

Letter to the Editor

IL-13 mediates IL-33-dependent mast cell and type 2 innate lymphoid cell effects on bronchial epithelial cells

To the Editor:

Type 2 inflammation, characterized by increased expression of the cytokines IL-4, IL-5, and IL-13 and eosinophilic infiltration of the airways, is a feature of some patients with asthma and is prominent in patients with frequent exacerbations.¹ We and others have shown that “T_H2 high” asthmatic patients exhibit distinct IL-13-induced gene expression in airway epithelial cells including eosinophil chemokine (C-C) ligand 26 (CCL26), periostin (POSTN), a biomarker of systemic eosinophilic airway inflammation and subepithelial fibrosis in asthmatic patients, and an increased ratio of mucin (MUC)5AC to MUC5B (MUC5AC:MUC5B), all of which may contribute to disease pathology.²⁻⁴

Mast cells are localized to the airway epithelium in “T_H2 high” asthmatic patients, are associated with disease severity, and can be activated by epithelial cytokines including IL-33.⁵ IL-5 and IL-13-producing type 2 innate lymphoid cells (ILC2s) contribute significantly in animal models of type 2 inflammation and may potentially play a role in human asthma by responding to cytokines including IL-33, IL-25, and thymic stromal lymphopoietin.⁶ IL-33 is released after *in vitro* exposure to allergen extracts by human airway epithelial cells and in lungs of allergen-challenged mice, and has been detected in bronchoalveolar lavage fluid and airway smooth muscle in patients with asthma.⁷ However, specific effects of IL-33 on airway epithelium in the context of an inflammatory microenvironment have not been well characterized. As both mast cells and ILC2s have been found in human lungs, express the IL-33 receptor ST2, and produce IL-13, we sought to characterize the interactions of these cells with the airway epithelium in a proinflammatory context and determine the role

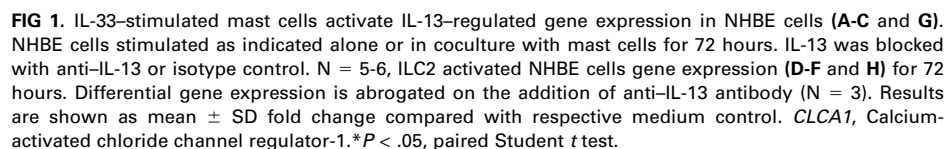
of IL-13-dependent and IL-13-independent pathways in airway gene expression.

We investigated global transcriptional patterns in IL-33-stimulated primary cultured *in vitro* differentiated human mast cells using gene expression microarrays, focusing on cytokines, chemokines, and growth factors (CCGFs),⁴ as they represent soluble mediators of intercellular communication (Table I). Detailed methods of culture and stimulation are given in this article’s Methods section in the Online Repository at www.jacionline.org. Consistent with previous reports,⁸ we found that IL-33-stimulated mast cells upregulated multiple non-type 2 proinflammatory mediators compared with controls. However, IL-5 and IL-13 were among the top 5 most highly induced CCGF genes in mast cells on IL-33 stimulation, suggesting that a dominant response to IL-33 in mast cells is the increased expression of type 2 inflammatory cytokines. We not only detected significantly higher IL-5 (see Fig E1, A, in this article’s Online Repository at www.jacionline.org) and IL-13 protein (Fig E1, B) in supernatants from IL-33-treated mast cells compared with controls but also observed increased production of non-type 2 mediators TNF- α and IL-8 in supernatants from IL-33-stimulated mast cells (Fig E1, C and D).

To assess IL-33’s effects on ILC2s, we isolated lineage-negative human ILC2s from blood buffy coats (see Fig E2, A, in this article’s Online Repository at www.jacionline.org) and expanded them *in vitro* in the presence of IL-2, IL-7, IL-25, IL-33, and thymic stromal lymphopoietin. We then assessed the production of T_H2 cytokines in response to IL-33. IL-33 significantly enhanced IL-5 (Fig E2, B) and IL-13 (Fig E2, C) production from ILC2s, although substantial quantities of IL-5 and IL-13 were secreted from ILC2s even without IL-33 restimulation. IL-33 also significantly increased the production of TNF- α and IL-8 (see Fig E3, A and B, in this article’s Online Repository at www.jacionline.org) in ILC2s. IL-4 was detectable albeit at

TABLE I. CCGF genes differentially expressed in mast cells after 24 h of IL-33 stimulation

Agilent gene ID	Entrez gene ID	Fold change	Adjusted P value	Gene name
A_24_P209047	<i>IL5</i>	352.1	2.6×10^{-08}	Interleukin 5
A_23_P315364	<i>CXCL2</i>	114.6	2.5×10^{-08}	Chemokine (C-X-C motif) ligand 2
A_23_P251031	<i>IL13</i>	73.0	1.3×10^{-08}	Interleukin 13
A_32_P87013	<i>CXCL8</i>	61.0	2.4×10^{-07}	Interleukin 8
A_23_P49759	<i>CCL1</i>	27.9	5.9×10^{-09}	Chemokine (C-C motif) ligand 1
A_24_P183150	<i>CXCL3</i>	17.1	1.3×10^{-13}	Chemokine (C-X-C motif) ligand 3
A_23_P71037	<i>IL6</i>	16.0	1.0×10^{-06}	Interleukin 6
A_23_P72096	<i>IL1A</i>	8.8	3.7×10^{-08}	Interleukin 1, alpha
A_23_P79518	<i>IL1B</i>	8.1	1.1×10^{-04}	Interleukin 1, beta
A_23_P51936	<i>TNFRSF9</i>	7.8	3.7×10^{-03}	TNF receptor superfamily, member 9
A_24_P411121	<i>TNFRSF18</i>	7.7	7.0×10^{-08}	TNF receptor superfamily, member 18
A_23_P207564	<i>CCL4</i>	7.6	2.5×10^{-05}	Chemokine (C-C motif) ligand 4
A_24_P133253	<i>KITLG</i>	5.3	4.1×10^{-05}	KIT ligand
A_23_P138352	<i>WNT2B</i>	4.3	1.3×10^{-05}	Wingless-type mouse mammary tumor virus integration site family, member 2B
A_23_P76102	<i>GDF11</i>	4.0	3.3×10^{-05}	Growth differentiation factor 11
A_24_P228130	<i>CCL3L3</i>	3.9	1.1×10^{-03}	Chemokine (C-C motif) ligand 3-like 3
A_23_P376488	<i>TNF</i>	3.8	4.0×10^{-04}	TNF
A_23_P152838	<i>CCL5</i>	3.4	1.4×10^{-03}	Chemokine (C-C motif) ligand 5
A_23_P72817	<i>GDF3</i>	3.0	2.6×10^{-03}	Growth differentiation factor 3
A_24_P151121	<i>A1BG</i>	2.0	1.1×10^{-03}	Alpha-1-B glycoprotein



we assessed the effects of ILC2-NHBE cells coculture without additional IL-33. We cocultured NHBE cells with IL-33-stimulated mast cells or mature ILC2s and examined the expression of IL-13-regulated genes CCL26, POSTN, MUC5AC, and MUC5B. In NHBE cells alone, IL-33 did not change the expression of CCL26 (Fig 1, A), POSTN (Fig 1, B), or MUC5AC: MUC5B (Fig 1, C). In the presence of mast cells, IL-33 treatment significantly upregulated CCL26, POSTN, and MUC5AC: MUC5B compared with mast cell-NHBE cells medium control. Anti-IL-13 strongly and significantly suppressed differential

expression of CCL26, MUC5AC:MUC5B, and POSTN compared with control antibody. ILC2 coculture led to significantly increased expression of CCL26 (Fig 1, D) and POSTN (Fig 1, E), which was blocked by the addition of anti-IL-13, suggesting a predominant role of IL-13 in this system. We observed a trend toward an increase in MUC5AC:MUC5B (Fig 1, F), which was reduced by blocking IL-13 although this did not reach nominal statistical significance. IL-33-treated NHBE cells in the presence of mast cells had higher levels of IL-13 and periostin in basolateral supernatants compared with control (see Fig E4, B and C, in this article's Online Repository at www.jacionline.org), suggesting that the effects in coculture were due to IL-13.

On a genomewide transcriptional level, genes that were differentially expressed in NHBE cells when cocultured in the presence of IL-33-stimulated mast cells or ILC2s correlated positively and linearly with genes differentially expressed in NHBE cells directly stimulated with IL-13 alone (Fig 1, G, and Table E1, and Fig 1, H, and Table E2, respectively, in this article's Online Repository at www.jacionline.org). We did not observe differential expression of genes that were dependent on IL-33 nor dependent on ILC2 in the context of IL-13 blockade, suggesting that transcriptional effects in NHBE cells were predominantly dependent on IL-13.

Although our studies focused on IL-13, we cannot completely rule out potential effects of IL-4. Although mast cells have been reported to express IL-4, we did not detect IL-4 in our mast cell cultures (data not shown). Non-type 2 mediators including IL-8 and TNF- α were also induced in IL-33-activated mast cells and ILC2s, and may be involved in severe asthma via the recruitment of neutrophils and smooth muscle activation.⁹ Furthermore, the presence of other immune cells in the airway in an IL-33 milieu may result in an abundance of non-type 2 mediators, which could affect differential gene expression not otherwise seen in the coculture system. Thus, further studies need to be conducted *in vivo* to examine the effects of anti-IL-13 on airway inflammation, mucus expression, and hyperreactivity in response to IL-33.

In conclusion, we have shown that IL-33-activated mast cells and ILC2s drive predominantly IL-13-regulated gene expression when cocultured with NHBE cells, which initiates a transcriptional program that can subsequently exacerbate airway pathology and contribute to fibrosis, eosinophilia, and mucous metaplasia. Although mast cells and ILC2s produce a diverse set of cytokines and other mediators of intercellular communication in response to IL-33, the predominant effect on airway epithelium in this *in vitro* coculture system is mediated by IL-13.

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Genentech, Inc supported this research.

Disclosure of potential conflict of interest: D. R. Nagarkar and R. Soriano are employed by Genentech, Inc, and receive stock/stock options as part of compensation for employment. V. Ramirez-Carrozzi and R. Pappu are employed by Genentech, Inc, receive stock/stock options as part of compensation for employment, and have patent applications pending through Genentech. D. F. Choy is employed by Genentech, Inc, holds stock options for Roche Group as part of compensation for employment, and is a named inventor on planned patents related to a diagnostic that may predict asthmatic clinical response to anti-IL-13 through Genentech. A. R. Abbas and J. R. Arron are employed by Genentech, Inc, hold stock/stock options in Roche Group as part of compensation for employment, and are named inventors on patents related to asthma diagnosis and treatment through Genentech. Z. Modrusan is employed by Genentech and has stock/stock options from Roche as part of compensation for employment. The rest of the authors declare that they have no relevant conflicts of interest.

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<http://dx.doi.org/10.1016/j.jaci.2015.01.036>

ONLINE REPOSITORY

IL-13 mediates IL-33 dependent mast cell and ILC2 effects on bronchial epithelial cells

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Funding: This research was funded by Genentech, Inc.

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METHODS

NHBE culture and stimulation

6.5 mm diameter 0.4 μ M pore density transwell plates from Corning Life Sciences (Corning, NY), were collagen coated using 100 μ g/ml PureCol from Advanced BioMatrix (San Diego, CA). NHBE from five donors were seeded in transwells and maintained in serum-free bronchial epithelial cell growth medium (BEGM, Lonza) for 96 hours or until confluent. Thereafter the apical media was removed, and cells were fed basolaterally with Pneumacult complete air liquid interface (ALI) medium (Stem Cell) and differentiated for a period of 21 days. In mast cell co-culture studies, NHBE were cultured alone in ALI media or in presence of mast cells (5×10^5 cells/ml, 1:5 ratio) in 50% ALI and 50% mast cell culture medium, and stimulated with IL-13 (10 ng/ml), or IL-33 (10 ng/ml). IL-13 in culture was neutralized with the addition of anti-IL-13 (228B/C, 10 μ g/ml) or equivalent concentrations of mouse isotype control (eBioscience) for a period of 72 hours. RNA was extracted from NHBE for gene expression analysis and basolateral supernatants were collected for measurement of protein. For ILC2 co-culture studies, NHBE were cultured alone in ALI media or with ILC2s (1×10^5 cells/ml, 1:1 ratio) in 50% ALI and 50% Yssel's media containing 1 ng/ml IL-2 and IL-7 for a period of 72 hours.

Generation of primary cultured *in vitro* derived mast cells , culture, and stimulation

Peripheral blood derived CD34⁺ cells derived from 10 donors were purchased from Stemcell Technologies (Vancouver, BC, Canada) and were differentiated into primary cultured *in vitro* CD34⁺ cell derived human mast cells for a period of 12 weeks in the presence of IL-6 and SCF as described previously.¹ At 0 weeks, the cells were suspended in serum-free Iscove's methylcellulose medium (MethoCult SFBIT H4236, Stemcell Technologies) containing 200

44 ng/ml SCF, 50 ng/ml IL-6, 5 ng/ml IL-3, 11 μ M 2-mercaptoethanol (2-ME, Invitrogen (Carlsbad,
45 CA)), 100 U/ml penicillin, and 100 μ g/ml streptomycin (Invitrogen), and then incubated at 37°C
46 in 5% CO₂. At 2 weeks of culture, fresh methylcellulose medium containing 200 ng/ml SCF, 50
47 ng/ml IL-6, 11 μ M 2-ME, 100 U/ml penicillin, and 100 μ g/ml streptomycin was layered over the
48 methylcellulose cultures. At 4 weeks, a 1 ml aliquot of IMDM, supplemented with 200 ng/ml
49 SCF, 50 ng/ml IL-6, insulin-transferrin-selenium (Invitrogen), 55 μ M 2-ME, 100 U/ml penicillin,
50 and 100 μ g/ml streptomycin was layered over the methylcellulose cultures. At 6 weeks, all cells
51 were retrieved after dissolving the methylcellulose medium with PBS. The cells were then
52 suspended and cultured in IMDM supplemented with 100 ng/ml SCF, 50 ng/ml IL-6, 0.1% BSA,
53 insulin-transferrin-selenium, 55 μ M 2-ME, 100 U/ml penicillin, and 100 μ g/ml streptomycin, and
54 the culture medium was replaced a week later. After an additional week of culture, the culture
55 medium was switched to IMDM supplemented with 100 ng/ml SCF, 50 ng/ml IL-6, 5% FBS
56 (Invitrogen), 55 μ M 2-ME, 100 U/ml penicillin, and 100 μ g/ml streptomycin. The culture
57 medium was changed weekly thereafter, and the cells were incubated for an additional 5-7
58 weeks. By the end of 12 weeks majority of non-mast cells are expected to undergo attrition.² The
59 final purity of the mast cells was determined by measuring Fc ϵ RI expression using flow
60 cytometry after 12 weeks of culture following 48 hours treatment with 1 μ g/ml myeloma IgE
61 (EMD Millipore, Billerica, MA) and was 90 %. We generated mast cells from 10 independent
62 donors in this manner. For microarray studies of IL-33 stimulated mast cells, mast cells from 2
63 donors (1 x 10⁶ cells/ml) were stimulated with 10 ng/ml IL-33 in duplicate for a period of 24
64 hours. RNA was then collected for microarray analysis. For determining IL-13 responses, mast
65 cells were stimulated with IL-33 as indicated for 48 hours, and cell free supernatants were
66 collected for protein analysis.

67

68 **Isolation and culture of ILC2s**

69 ILC2s from 5 donors were isolated from blood buffy coats and sorted for lineage negative
70 CRTH2⁺, CD161⁺ cells as previously described and gated for CD127.³ Peripheral blood
71 mononuclear cells (PBMCs) were isolated after Ficoll Paque (GE Healthcare, Pittsburgh, PA)
72 centrifugation in Greiner Leukosep tubes (Sigma). Cells were labeled with Fluorescein
73 thioisocyanate (FITC)-conjugated CD3 (eBioscience, San Diego, CA), CD14, CD16, and CD19
74 (all BD Biosciences, San Jose, CA) antibodies, incubated with anti-FITC microbeads (Miltenyi
75 Biotec, Auburn, CA), and depleted with SuperMacs II Separators magnets (Miltenyi). The
76 depleted cell fraction was then stained with FITC labeled-anti-CD1a, anti-CD4, anti-CD14, anti-
77 CD16, anti-CD19, anti-CD34, anti-CD56, anti-TCR $\gamma\delta$, Alexafluor (AF)-647-labeled anti-
78 CRTH2 (all from BD Biosciences), FITC anti-CD3, anti-CD11c, anti-CD94, anti-CD123, anti-
79 TCR $\alpha\beta$, anti-Fc ϵ R1, phycoerythrin (PE)-conjugated anti-CD161 (all from eBioscience), and
80 PE.indotricarbocyanine (Cy)-7 conjugated anti-CD127 (Beckman Coulter, Brea, CA) for 30
81 minutes and sorted for lineage negative CRTH2⁺, CD161⁺ cells. The resultant fraction was then
82 resuspended in an in-house generated Yssel's T cell medium containing 1% human AB serum
83 (Life Technologies, Grand Island, NY), IL-2 (50 ng/ml), and IL-7 (50 ng/ml). For expansion of
84 cells, ILC2s were cultured in Yssel's medium containing IL-2, IL-7, IL-33, and IL-25 (50 ng/ml
85 each) and TSLP (20 ng/ml) for 7-10 days. A total of 5 donors of ILC2s were isolated. For
86 stimulation, ILC2s (2×10^5 cells/ml) were rested for 24 hours in fresh medium containing 1
87 ng/ml IL-2 and IL-7, and then stimulated in fresh media containing 1 ng/ml IL-2 and IL-7 alone
88 with IL-33 or co-cultured with NHBE for 72 hours. Cell free supernatants were collected for
89 cytokine measurements. In control studies, epithelial cells were stimulated with IL-2 and IL-7

alone, however this did not significantly alter CCL26 (0.4 cycle higher), MUC5AC (0.4 cycle higher), MUC5B (0.9 cycle higher) or POSTN (1 cycle higher) expression.

Gene expression analysis

Total RNA was extracted from NHBE or mast cells using the Qiagen RNeasy Kit (Germantown, MD). Thereafter cDNA was generated using iScript Reverse Transcription Supermix from Biorad (Hercules, CA). Amplification of cDNA was performed using Taqman Gene Expression Assays (Applied Biosystems, Foster City, CA). Fold changes in gene expression unless otherwise indicated were compared to respective medium control. For microarray analysis, RNA from NHBE or mast cell samples were submitted for Agilent single round amplification. The assays numbers for qPCR were as follows: MUC5AC, Hs00873651_mH; MUC5B, Hs00861595_m1; CCL26, Hs00171146_m1; and POSTN, Hs01566734_m1

Microarray Analysis and Statistics

The quantity and quality of total RNA samples were determined, respectively, using an ND-1000 spectrophotometer (Thermo Scientific, Wilmington, DE, USA) and Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA, USA). A Cy dye-labeled cRNA preparation and array hybridization were prepared as per the manufacturer's (Agilent Technologies) instructions. Briefly, total RNA sample was converted to double-stranded cDNA and then to Cy dye-labeled cRNA using an Agilent Quick Amp Labeling kit. The labeled cRNA was purified using an RNeasy mini kit (Qiagen). cRNA yield and Cy dye incorporation were determined using the ND-

113 1000 spectrophotometer (Thermo Scientific). A 750ng weight of the labeled cRNA was
114 fragmented and hybridized to Agilent Whole Human Genome 4 × 44 Kv2 arrays. All samples
115 were labeled with Cy5 dye and hybridized against a Cy3 dye-labeled universal human reference
116 (Stratagene, La Jolla, CA, USA). Samples were hybridized for 17 h at 65 °C. Following
117 hybridization, the arrays were washed, dried and scanned using an Agilent scanner. The Agilent
118 Feature Extraction software version 11.5 was used to analyze the acquired array images. All
119 statistical calculations were performed using the R Project software package, version 2.15.1
120 (<http://www.R-project.org>). Array quality control was assessed using arrayQualityMetrics
121 package for R. Microarrays were normalized and probe intensities transformed using the vsn
122 package of Bioconductor⁴. Independent filtering⁵ of microarray data was conducted using the
123 genefilter package to increase statistical power to detect true positives while maintaining type I
124 error control.⁶ As array features that are invariant or do not correspond to an Entrez gene
125 transcript are uninformative for differential gene expression analysis, filtering on the basis of
126 annotation and expression variability was conducted. Briefly, filtering was conducted as
127 follows: 1) Only array features representing Entrez or CCGf⁷ genes were retained 2) Multiple
128 array features corresponding to a single Entez gene were reduced to a single array feature on the
129 basis of highest IQR and 3) The 25th percentile most variable (IQR) genes were retained for
130 differential expression analysis of NHBE experiements. Linear model test statistics of gene
131 expression microarray data was performed with the limma⁸ package of Bioconductor. In brief,
132 this method utilizes an empirical Bayes approach equivalent to shrinkage of the estimated sample
133 variances towards a pooled estimate, resulting in far more stable inference when the number of
134 arrays is limited⁸. Differential expression test statistics were estimated as a linear contrast of a

model including treatment as a factor. Adjusted *P*-values to account for multiple hypothesis testing was addressed utilizing the method of Benjamini and Hochberg⁹.

Cytokine measurements

The concentrations of IL-5, IL-13, IL-4, IL-10, and TNF- α in cell-free supernatants from stimulated mast cells or from basolateral supernatants from co-culture studies were measured by a Meso Scale Discovery Th1/Th2 10-plex panel (MSD, Rockville, MD) according to the manufacturer's instructions. 25 μ l of each sample was used for cytokine detection. The limit of detection for each is cytokine 2.4 pg/ml.

FIGURE LEGENDS

Figure E1. IL-33 stimulates Th2 and non-Th2 cytokine production in human mast cells.

Primary human mast cells were stimulated with IL-33 for 48 hours. IL-5 (A), IL-13 (B), TNF- α (C), and IL-8 (D) production in supernatants was measured by MSD. Results are shown as mean $\pm$ SD, N=5-7 independent mast cell donors, *p<0.05, paired Student's *t* test.

Figure E2. Isolation of peripheral blood derived ILC2s. FACS sorting of lineage⁻ cells that were positive for CRTH2, CD161, and CD127 (A). Cells were expanded in the presence of IL-2, IL-7, IL-25, IL-33, and TSLP for 10 days, rested for 24 hours in IL-2 and IL-7 only, and re-stimulated with indicated concentrations of IL-33 for 72 hours. Cytokines were measured via MSD (B-C). Results are shown as mean $\pm$ SD, N=4 donors, *p<0.05, paired Student's *t* test.

Figure E3. Cytokine production in ILC2s after IL-33 treatment. ILC2s were cultured with indicated doses of IL-33 for 72 hours. TNF- α (A), IL-8 (B) and IL-4 (C) production in cell free supernatants was measured with an MSD panel. Results are shown as mean $\pm$ SD, N=4 independent donors, *p<0.05, paired Students *t* test.

Figure E4. Experimental schematic of NHBE co-culture studies (A). Induction of IL-13 (B) and periostin (C) in IL-33 stimulated mast cells in co-culture supernatants at 72 hours. Cell free supernatants from basolateral compartment were subjected to MSD or ELISA. Results are shown as mean $\pm$ SD, N=3 independent experiments, *p<0.05, 1 way-ANOVA.

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Table E1: Genes differentially expressed in IL-33 treated NHBE in the presence of mast cells compared to medium control

Agilent Gene ID	Entrez Gene ID	Fold Change	Adjusted p value	Gene Name
A_23_P215484	CCL26	87.1	5.9E-05	chemokine (C-C motif) ligand 26
A_33_P3511265	POSTN	79.2	5.9E-05	periostin, osteoblast specific factor
A_23_P144126	FETUB	73.5	1.5E-04	fetuin B
A_23_P51217	CLCA1	52.2	5.9E-05	chloride channel accessory 1
A_23_P139434	PRB2	26.8	1.5E-02	proline-rich protein BstNI subfamily 2
A_23_P46639	C8A	24.8	1.5E-04	complement component 8, alpha polypeptide
A_23_P90626	CYTIP	22.2	6.9E-05	cytohesin 1 interacting protein
A_23_P78595	CEACAM21	14.8	2.2E-02	carcinoembryonic antigen-related cell adhesion molecule 21
A_23_P111583	CD36	14.4	6.9E-05	CD36 molecule (thrombospondin receptor)
A_33_P3270104	FAM26D	13.7	3.4E-02	family with sequence similarity 26, member D
A_24_P87036	ANO1	10.7	1.1E-03	anoctamin 1, calcium activated chloride channel
A_33_P3287223	DPP4	10.2	1.7E-04	dipeptidyl-peptidase 4
A_23_P144096	CISH	10.0	1.5E-04	cytokine inducible SH2-containing protein
A_23_P112859	CST1	9.8	5.4E-03	cystatin SN
A_33_P3263432	ITGA10	9.7	2.7E-04	integrin, alpha 10
A_23_P80040	PROCR	8.7	1.5E-04	protein C receptor, endothelial
A_23_P21495	FCGBP	8.6	1.1E-03	Fc fragment of IgG binding protein
A_23_P341567	SLC9B2	8.6	1.1E-03	solute carrier family 9, subfamily B (cation proton antiporter 2), member 2
A_23_P8913	CA2	8.1	4.6E-04	carbonic anhydrase II
A_33_P3423854	C8B	7.8	2.3E-04	complement component 8, beta polypeptide
A_24_P240259	LRRC31	7.6	4.5E-03	leucine rich repeat containing 31
A_23_P502464	NOS2	7.4	4.1E-03	nitric oxide synthase 2, inducible
A_33_P3367860	CHRM1	6.6	2.5E-03	cholinergic receptor, muscarinic 1
A_23_P313981	SERPINB10	6.4	7.5E-03	serpin peptidase inhibitor, clade B (ovalbumin), member 10
A_33_P3672756	LOC284561	6.0	4.5E-03	uncharacterized LOC284561
A_33_P3322804	NTRK2	5.9	1.6E-03	neurotrophic tyrosine kinase, receptor, type 2

A_24_P245379	SERPINB2	5.8	1.6E-04	serpin peptidase inhibitor, clade B (ovalbumin), member 2
A_23_P127978	B3GNT6	5.7	2.8E-02	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase)
A_23_P17065	CCL20	5.4	3.0E-03	chemokine (C-C motif) ligand 20
A_23_P420196	SOCS1	5.4	4.5E-04	suppressor of cytokine signaling 1
A_23_P331560	SLC26A4	5.1	1.9E-02	solute carrier family 26, member 4
A_23_P203972	FZD10	5.1	2.1E-03	frizzled family receptor 10
A_24_P53778	ITLN2	5.1	3.7E-03	intelectin 2
A_24_P237175	CST2	5.0	2.0E-02	cystatin SA
A_33_P3309832	C10orf81	4.5	4.2E-02	chromosome 10 open reading frame 81
A_24_P365526	HCK	4.5	2.2E-02	hemopoietic cell kinase
A_23_P36531	TSPAN8	4.4	6.4E-04	tetraspanin 8
A_23_P324754	KIAA1199	4.4	9.9E-04	KIAA1199
A_33_P3295358	ANGPTL4	4.4	2.2E-02	angiopoietin-like 4
A_33_P3260125	LDLRAD2	4.4	4.4E-03	low density lipoprotein receptor class A domain containing 2
A_23_P56703	C2orf89	4.3	3.3E-04	chromosome 2 open reading frame 89
A_24_P365721	SLC6A14	4.3	4.6E-04	solute carrier family 6 (amino acid transporter), member 14
A_23_P80570	AADAC	4.2	1.3E-02	arylacetamide deacetylase (esterase)
A_23_P323751	FAM83D	4.2	5.4E-04	family with sequence similarity 83, member D
A_23_P111194	SPDEF	4.1	1.5E-04	SAM pointed domain containing ets transcription factor
A_33_P3298326	FSHB	4.0	5.1E-03	follicle stimulating hormone, beta polypeptide
A_33_P3216570	MUC5AC	3.9	3.1E-02	mucin 5AC, oligomeric mucus/gel-forming
A_33_P3360311	GYS2	3.9	3.8E-02	glycogen synthase 2 (liver)
A_23_P86470	CH25H	3.9	6.4E-04	cholesterol 25-hydroxylase
A_32_P157391	FOLH1B	3.9	2.3E-02	folate hydrolase 1B
A_23_P138706	ADRA2A	3.9	1.0E-02	adrenergic, alpha-2A-, receptor
A_33_P3370763	SARM1	3.9	2.5E-02	sterile alpha and TIR motif containing 1
A_23_P393099	TFF3	3.8	1.5E-03	trefoil factor 3 (intestinal)
A_24_P192727	KAZALD1	3.8	3.2E-04	Kazal-type serine peptidase inhibitor domain 1
A_33_P3821350	PRO2012	3.8	1.2E-02	uncharacterized protein PRO2012

A_32_P164593	ZMAT4	3.7	1.2E-03	zinc finger, matrin-type 4
A_23_P419696	LYPD1	3.7	1.2E-02	LY6/PLAUR domain containing 1
A_33_P3367396	FAM177B	3.7	2.7E-02	family with sequence similarity 177, member B
A_23_P153301	CEACAM5	3.6	6.4E-04	carcinoembryonic antigen-related cell adhesion molecule 5
A_23_P157136	SCIN	3.6	1.9E-02	scinderin
A_23_P74012	SPRR1A	3.6	3.6E-02	small proline-rich protein 1A
A_32_P196263	ADAMTS9	3.6	4.7E-03	ADAM metalloproteinase with thrombospondin type 1 motif, 9
A_33_P3356776	GOLGA7B	3.5	2.0E-02	golgin A7 family, member B
A_33_P3330463	FAM170B	3.5	2.3E-02	family with sequence similarity 170, member B
A_23_P302005	STON1	3.5	9.9E-04	stonin 1
A_33_P3283480	CTSC	3.5	9.3E-04	cathepsin C
A_23_P314101	SUSD2	3.5	2.0E-03	sushi domain containing 2
A_23_P105973	SERPINA11	3.4	1.5E-04	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11
A_23_P73571	MUM1L1	3.4	4.7E-03	melanoma associated antigen (mutated) 1-like 1
A_33_P3294509	CD44	3.4	5.4E-04	CD44 molecule (Indian blood group)
A_23_P127584	NNMT	3.4	2.4E-03	nicotinamide N-methyltransferase
A_23_P5601	DOK1	3.4	4.8E-04	docking protein 1, 62kDa (downstream of tyrosine kinase 1)
A_32_P66804	PTPRN2	3.4	3.9E-03	protein tyrosine phosphatase, receptor type, N polypeptide 2
A_23_P151907	PCSK6	3.4	3.4E-03	proprotein convertase subtilisin/kexin type 6
A_33_P3284345	NRG1	3.4	4.4E-03	neuregulin 1
A_32_P324933	LINC00282	3.3	4.3E-02	long intergenic non-protein coding RNA 282
A_23_P501193	KCNJ16	3.3	3.0E-02	potassium inwardly-rectifying channel, subfamily J, member 16
A_23_P142174	FOXA3	3.3	7.3E-03	forkhead box A3
A_23_P70307	SMOC2	3.3	8.3E-03	SPARC related modular calcium binding 2
A_23_P2271	PTH1LH	3.2	1.4E-02	parathyroid hormone-like hormone
A_23_P58266	S100P	3.2	4.6E-04	S100 calcium binding protein P
A_23_P9711	HS3ST4	3.2	1.8E-02	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
A_24_P46130	ACPP	3.2	4.6E-03	acid phosphatase, prostate

A_23_P105562	VWF	3.2	1.4E-03	von Willebrand factor
A_33_P3708309	LOC285638	3.2	1.7E-02	uncharacterized LOC285638
A_23_P63209	HSD11B1	3.1	3.9E-02	hydroxysteroid (11-beta) dehydrogenase 1
A_23_P13753	NFE2	3.1	4.8E-04	nuclear factor (erythroid-derived 2), 45kDa
A_33_P3376838	PAPPA2	3.1	2.1E-02	pappalysin 2
A_23_P32233	KLF4	3.1	1.1E-03	Kruppel-like factor 4 (gut)
A_24_P416177	ADCY7	3.0	5.1E-03	adenylate cyclase 7
A_24_P63347	PF4V1	3.0	4.7E-03	platelet factor 4 variant 1
A_23_P10206	HAS2	3.0	4.8E-04	hyaluronan synthase 2
A_24_P217572	EDNRA	3.0	2.0E-02	endothelin receptor type A
A_23_P19673	SGK1	3.0	5.4E-04	serum/glucocorticoid regulated kinase 1
A_24_P350589	RNF150	3.0	2.3E-03	ring finger protein 150
A_23_P321354	TMEM71	3.0	3.9E-03	transmembrane protein 71
A_23_P12363	ROR1	3.0	3.2E-03	receptor tyrosine kinase-like orphan receptor 1
A_24_P404840	GJB1	3.0	3.8E-03	gap junction protein, beta 1, 32kDa
A_33_P3350726	PPARG	3.0	7.8E-03	peroxisome proliferator-activated receptor gamma
A_33_P3315149	C15orf34	3.0	4.5E-02	chromosome 15 open reading frame 34
A_23_P69329	HYAL1	3.0	5.8E-04	hyaluronoglucosaminidase 1
A_23_P253602	BMX	2.9	5.4E-04	BMX non-receptor tyrosine kinase
A_23_P82567	PRSS58	2.9	1.7E-02	protease, serine, 58
A_24_P942370	GALNT4	2.9	7.1E-03	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)
A_33_P3252394	GADD45G	2.9	4.8E-04	growth arrest and DNA-damage-inducible, gamma
A_23_P127891	BDNF	2.9	5.2E-03	brain-derived neurotrophic factor
A_33_P3313835	PP14571	2.9	2.0E-02	uncharacterized LOC100130449
A_23_P43898	EPHX4	2.9	1.6E-02	epoxide hydrolase 4
A_23_P119478	EBI3	2.8	1.9E-02	Epstein-Barr virus induced 3
A_23_P253321	PNOC	2.8	6.7E-03	prepronociceptin
A_23_P40453	CBR3	2.8	4.6E-04	carbonyl reductase 3
A_23_P132175	RTN4R	2.8	5.4E-04	reticulon 4 receptor
A_23_P5945	DHX35	2.7	4.6E-04	DEAH (Asp-Glu-Ala-His) box polypeptide 35
A_23_P329198	OBFC2A	2.7	6.4E-04	oligonucleotide/oligosaccharide-binding fold containing 2A

A_23_P99906	HOMER2	2.7	2.1E-03	homer homolog 2 (Drosophila)
A_32_P29118	SEMA3D	2.7	1.2E-02	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D
A_23_P216920	NEK6	2.7	9.6E-04	NIMA (never in mitosis gene a)-related kinase 6
A_23_P49448	FA2H	2.7	4.8E-04	fatty acid 2-hydroxylase
A_23_P87049	SORL1	2.7	7.9E-04	sortilin-related receptor, L(DLR class) A repeats containing
A_23_P64372	TCN1	2.7	2.5E-02	transcobalamin I (vitamin B12 binding protein, R binder family)
A_23_P161297	OGDHL	2.7	3.0E-03	oxoglutarate dehydrogenase-like
A_23_P315206	CCBL1	2.7	5.4E-04	cysteine conjugate-beta lyase, cytoplasmic
A_23_P376172	C1orf64	2.6	1.5E-03	chromosome 1 open reading frame 64
A_23_P381261	ADCY4	2.6	4.4E-02	adenylate cyclase 4
A_23_P24948	KCNE3	2.6	3.2E-02	potassium voltage-gated channel, Isk-related family, member 3
A_33_P3331511	LINC00173	2.6	2.0E-02	long intergenic non-protein coding RNA 173
A_23_P41424	SLC39A8	2.6	7.4E-03	solute carrier family 39 (zinc transporter), member 8
A_24_P245838	MGAT3	2.5	2.9E-03	mannosyl (beta-1,4)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase
A_23_P72096	IL1A	2.5	1.4E-02	interleukin 1, alpha
A_24_P253251	SLC7A1	2.5	1.3E-03	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
A_33_P3299416	GRASP	2.5	5.5E-04	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein
A_33_P3391220	SULT1C2P1	2.5	4.2E-02	sulfotransferase family, cytosolic, 1C, member 2 pseudogene 1
A_33_P3277447	SLC26A2	2.5	1.6E-03	solute carrier family 26 (sulfate transporter), member 2
A_24_P188377	CD55	2.5	5.7E-04	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
A_23_P115726	SLC16A9	2.5	2.0E-03	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)
A_23_P215549	PON3	2.5	3.5E-03	paraoxonase 3
A_33_P3361348	ALOX15	2.5	1.2E-02	arachidonate 15-lipoxygenase
A_24_P265506	NTRK1	2.5	6.9E-03	neurotrophic tyrosine kinase,

				receptor, type 1
A_23_P368338	BET3L	2.5	6.9E-03	BET3 like (S. cerevisiae)
A_32_P175739	HK2	2.5	1.7E-03	hexokinase 2
A_23_P76291	PRR4	2.5	6.9E-03	proline rich 4 (lacrimal)
A_23_P210425	MYL9	2.4	3.8E-03	myosin, light chain 9, regulatory
A_33_P3308105	GGH	2.4	1.1E-03	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
A_23_P42746	NCF1	2.4	1.6E-02	neutrophil cytosolic factor 1
A_23_P251151	NELL1	2.4	3.5E-02	NEL-like 1 (chicken)
A_23_P335495	ANO7	2.4	3.2E-02	anoctamin 7
A_23_P162525	UTP20	2.4	4.1E-03	UTP20, small subunit (SSU) processome component, homolog (yeast)
A_23_P255376	CCDC109B	2.4	1.1E-03	coiled-coil domain containing 109B
A_23_P114883	FMOD	2.4	3.2E-03	fibromodulin
A_33_P3703501	GALNT10	2.4	1.2E-03	UDP-N-acetyl-alpha-D- galactosamine:polypeptide N- acetylgalactosaminyltransferase 10 (GalNAc-T10)
A_24_P36890	RAP1GAP	2.3	1.5E-02	RAP1 GTPase activating protein
A_23_P62115	TIMP1	2.3	5.4E-04	TIMP metalloproteinase inhibitor 1
A_23_P74449	HPDL	2.3	2.0E-03	4-hydroxyphenylpyruvate dioxygenase-like
A_23_P216489	GNE	2.3	1.1E-03	glucosamine (UDP-N-acetyl)-2- epimerase/N-acetylmannosamine kinase
A_24_P181055	ST3GAL4	2.3	1.7E-03	ST3 beta-galactoside alpha-2,3- sialyltransferase 4
A_24_P197537	PDE8B	2.3	1.2E-02	phosphodiesterase 8B
A_23_P254254	SGSH	2.3	5.7E-04	N-sulfoglucosamine sulfohydrolase
A_24_P170439	TREML3	2.3	1.2E-02	triggering receptor expressed on myeloid cells-like 3
A_23_P130194	PYCR1	2.3	6.4E-04	pyrroline-5-carboxylate reductase 1
A_33_P3288104	DAAM2	2.3	1.9E-02	dishevelled associated activator of morphogenesis 2
A_23_P152620	TNFSF13	2.3	4.2E-02	tumor necrosis factor (ligand) superfamily, member 13
A_32_P234145	SHC4	2.3	3.0E-02	SHC (Src homology 2 domain containing) family, member 4
A_32_P47643	FAM110C	2.3	3.3E-03	family with sequence similarity 110, member C

A_33_P3345708	CREB3L4	2.3	3.6E-03	cAMP responsive element binding protein 3-like 4
A_23_P8640	GPER	2.3	1.2E-02	G protein-coupled estrogen receptor 1
A_23_P124946	CMYA5	2.3	7.4E-03	cardiomyopathy associated 5
A_24_P321068	SLC31A1	2.3	3.0E-03	solute carrier family 31 (copper transporters), member 1
A_24_P940166	PAPSS2	2.3	2.2E-02	3'-phosphoadenosine 5'-phosphosulfate synthase 2
A_23_P72668	SDPR	2.2	1.8E-02	serum deprivation response
A_33_P3308749	LAMA4	2.2	1.8E-02	laminin, alpha 4
A_23_P117506	DHRS7	2.2	1.7E-03	dehydrogenase/reductase (SDR family) member 7
A_23_P214026	FBN2	2.2	6.2E-03	fibrillin 2
A_33_P3413962	PFKP	2.2	2.1E-03	phosphofructokinase, platelet
A_33_P3355208	CROT	2.2	1.5E-02	carnitine O-octanoyltransferase
A_23_P79978	SLC24A3	2.2	1.5E-02	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
A_24_P388528	ST6GAL1	2.2	3.2E-03	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1
A_23_P64611	P2RY6	2.2	1.5E-02	pyrimidinergic receptor P2Y, G-protein coupled, 6
A_32_P25437	SLC12A2	2.2	2.0E-03	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
A_32_P159651	KAT2B	2.2	7.5E-03	K(lysine) acetyltransferase 2B
A_23_P97365	LRRC8D	2.2	1.1E-03	leucine rich repeat containing 8 family, member D
A_23_P69226	TMEM111	2.2	7.9E-04	transmembrane protein 111
A_33_P3832341	SCARNA22	2.2	3.1E-02	small Cajal body-specific RNA 22
A_23_P16469	PLAUR	2.1	1.1E-03	plasminogen activator, urokinase receptor
A_32_P106194	TMEM92	2.1	2.9E-02	transmembrane protein 92
A_32_P207169	C1orf133	2.1	4.7E-03	chromosome 1 open reading frame 133
A_33_P3666884	PNPLA7	2.1	1.4E-02	patatin-like phospholipase domain containing 7
A_23_P156497	ELOVL5	2.1	1.4E-03	ELOVL fatty acid elongase 5
A_24_P149036	DPYSL3	2.1	1.7E-02	dihydropyrimidinase-like 3
A_23_P106016	PRKD1	2.1	1.2E-02	protein kinase D1
A_24_P43876	C9orf40	2.1	2.8E-03	chromosome 9 open reading frame 40
A_33_P3573141	LOC440149	2.1	1.9E-02	uncharacterized LOC440149
A_23_P79518	IL1B	2.1	6.9E-03	interleukin 1, beta

A_23_P217319	FGF13	2.1	7.5E-03	fibroblast growth factor 13
A_33_P3371089	SGTB	2.1	4.1E-03	small glutamine-rich tetratricopeptide repeat (TPR)- containing, beta
A_23_P409553	PPM1A	2.1	2.8E-02	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1A
A_33_P3338724	LENG9	2.1	2.8E-03	leukocyte receptor cluster (LRC) member 9
A_33_P3309526	PTPRC	2.0	3.4E-02	protein tyrosine phosphatase, receptor type, C
A_33_P3423121	RDX	2.0	4.0E-02	radixin
A_23_P256784	MUC2	2.0	3.2E-02	mucin 2, oligomeric mucus/gel- forming
A_23_P210253	DGKD	2.0	6.4E-03	diacylglycerol kinase, delta 130kDa
A_23_P56659	DQX1	2.0	1.6E-03	DEAQ box RNA-dependent ATPase 1
A_23_P3956	C1QTNF1	2.0	3.2E-02	C1q and tumor necrosis factor related protein 1
A_23_P168610	TSPAN13	2.0	7.9E-03	tetraspanin 13
A_23_P58132	RHOH	2.0	1.2E-03	ras homolog family member H
A_23_P357185	CHDH	2.0	4.2E-03	choline dehydrogenase
A_24_P696761	LEMD1	2.0	2.0E-02	LEM domain containing 1
A_32_P128701	USP53	2.0	1.2E-02	ubiquitin specific peptidase 53
A_33_P3282434	SLC16A1	2.0	2.5E-03	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
A_23_P312920	POU2AF1	2.0	6.4E-03	POU class 2 associating factor 1
A_33_P3261595	ANKRD34B	2.0	2.6E-02	ankyrin repeat domain 34B
A_23_P58993	MOCS1	2.0	2.8E-02	molybdenum cofactor synthesis 1
A_23_P108437	FZD5	2.0	3.8E-03	frizzled family receptor 5
A_24_P319374	GPA33	2.0	1.6E-02	glycoprotein A33 (transmembrane)
A_23_P39840	VAMP5	2.0	1.1E-03	vesicle-associated membrane protein 5 (myobrevin)
A_24_P115507	SARDH	2.0	1.2E-02	sarcosine dehydrogenase
A_33_P3272231	MFSD2A	2.0	1.3E-03	major facilitator superfamily domain containing 2A
A_24_P37409	DUSP2	2.0	2.2E-02	dual specificity phosphatase 2
A_23_P2317	DDN	1.9	4.2E-02	dendrin
A_32_P161762	RUNX2	1.9	2.1E-03	runt-related transcription factor 2
A_23_P256107	HPSE	1.9	3.2E-03	heparanase
A_24_P316430	NT5E	1.9	1.2E-02	5'-nucleotidase, ecto (CD73)
A_23_P382835	P2RY1	1.9	2.0E-02	purinergic receptor P2Y, G- protein coupled, 1

A_23_P41267	LOC401127	1.9	1.2E-03	WD repeat domain 5 pseudogene
A_32_P87013	IL8	1.9	1.8E-02	interleukin 8
A_33_P3399788	SERPINA3	1.9	3.8E-02	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
A_33_P3219651	BMPER	1.9	2.9E-02	BMP binding endothelial regulator
A_33_P3307187	NPAS3	1.9	2.0E-02	neuronal PAS domain protein 3
A_33_P3241204	CALHM3	1.9	3.8E-02	calcium homeostasis modulator 3
A_33_P3361037	MYO5C	1.9	1.2E-02	myosin VC
A_23_P250274	LRRC8A	1.9	7.5E-03	leucine rich repeat containing 8 family, member A
A_23_P57364	TFF2	1.9	1.5E-02	trefoil factor 2
A_23_P211909	PLS1	1.9	1.5E-02	plastin 1
A_23_P1602	CDC42EP2	1.9	1.5E-03	CDC42 effector protein (Rho GTPase binding) 2
A_33_P3396389	IL1R1	1.9	2.1E-02	interleukin 1 receptor, type I
A_33_P3215768	GALNT6	1.9	6.2E-03	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
A_24_P299474	ODZ2	1.9	8.9E-03	odz, odd Oz/ten-m homolog 2 (Drosophila)
A_23_P333138	MON2	1.9	2.2E-02	MON2 homolog (S. cerevisiae)
A_23_P14804	TSPAN3	1.9	1.6E-03	tetraspanin 3
A_23_P429184	GNPNAT1	1.9	6.9E-03	glucosamine-phosphate N-acetyltransferase 1
A_23_P355536	USP54	1.9	1.6E-02	ubiquitin specific peptidase 54
A_23_P401055	SOX2	1.9	4.3E-03	SRY (sex determining region Y)-box 2
A_23_P144384	GALNT7	1.9	7.8E-03	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)
A_24_P100517	SAPCD2	1.9	1.7E-03	suppressor APC domain containing 2
A_33_P3384932	NUDT8	1.9	2.2E-03	nudix (nucleoside diphosphate linked moiety X)-type motif 8
A_33_P3224819	SLC45A4	1.8	4.1E-03	solute carrier family 45, member 4
A_23_P19226	DSE	1.8	2.2E-02	dermatan sulfate epimerase
A_33_P3213822	KCNK2	1.8	1.4E-02	potassium channel, subfamily K, member 2
A_23_P48596	RNASE1	1.8	2.3E-02	ribonuclease, RNase A family, 1 (pancreatic)
A_33_P3256793	KIAA1324	1.8	7.4E-03	KIAA1324

A_23_P93213	SLC22A7	1.8	3.7E-02	solute carrier family 22 (organic anion transporter), member 7
A_33_P3246833	IL1RN	1.8	2.0E-02	interleukin 1 receptor antagonist
A_23_P159907	MAGED4B	1.8	3.4E-02	melanoma antigen family D, 4B
A_33_P3358957	PAPL	1.8	2.2E-03	iron/zinc purple acid phosphatase-like protein
A_33_P3260634	PLCB4	1.8	7.5E-03	phospholipase C, beta 4
A_23_P29939	SNCA	1.8	2.9E-03	synuclein, alpha (non A4 component of amyloid precursor)
A_33_P3405068	NAV1	1.8	2.0E-02	neuron navigator 1
A_33_P3353979	SYT15	1.8	4.0E-02	synaptotagmin XV
A_23_P62932	ATP1B1	1.8	8.1E-03	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide
A_33_P3405424	IL4I1	1.8	4.1E-02	interleukin 4 induced 1
A_23_P211504	KDEL3	1.8	2.2E-03	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
A_24_P366526	SYNGR2	1.8	1.0E-02	synaptogyrin 2
A_23_P163087	NID2	1.8	1.4E-02	nidogen 2 (osteonidogen)
A_32_P91042	LOC100129034	1.8	3.6E-02	uncharacterized LOC100129034
A_33_P3226832	F3	1.8	1.0E-02	coagulation factor III (thromboplastin, tissue factor)
A_23_P146572	NPDC1	1.8	1.2E-02	neural proliferation, differentiation and control, 1
A_24_P12626	CAV1	1.8	1.5E-02	caveolin 1, caveolae protein, 22kDa
A_23_P1691	MMP1	1.8	2.0E-02	matrix metalloproteinase 1 (interstitial collagenase)
A_23_P322704	FAM177A1	1.8	1.1E-02	family with sequence similarity 177, member A1
A_33_P3277110	SLC5A3	1.8	4.6E-03	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3
A_23_P131899	SDCBP2	1.8	7.4E-03	syndecan binding protein (syntenin) 2
A_33_P3290394	IL2RG	1.8	1.3E-02	interleukin 2 receptor, gamma
A_33_P3297946	LOC283693	1.8	4.7E-02	actin, gamma pseudogene
A_33_P3236177	ANG	1.8	3.0E-03	angiogenin, ribonuclease, RNase A family, 5
A_23_P121657	HS3ST1	1.8	4.4E-03	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
A_23_P122674	PAK1IP1	1.8	4.0E-03	PAK1 interacting protein 1
A_23_P316381	ACOX3	1.8	7.4E-03	acyl-CoA oxidase 3, pristanoyl
A_33_P3410806	CLDN10	1.7	2.0E-02	claudin 10
A_24_P344961	AMOT	1.7	1.9E-02	angiomin
A_33_P3251093	SLC36A1	1.7	1.1E-02	solute carrier family 36

				(proton/amino acid symporter), member 1
A_23_P59613	FZD9	1.7	2.5E-02	frizzled family receptor 9
A_33_P3313899	LOC728228	1.7	4.4E-02	uncharacterized LOC728228
A_23_P356494	SPINK5	1.7	3.5E-02	serine peptidase inhibitor, Kazal type 5
A_23_P50591	KCNK6	1.7	1.1E-02	potassium channel, subfamily K, member 6
A_23_P408094	MXD1	1.7	8.7E-03	MAX dimerization protein 1
A_33_P3219090	INSIG1	1.7	4.3E-03	insulin induced gene 1
A_33_P3409477	UBASH3B	1.7	3.6E-02	ubiquitin associated and SH3 domain containing B
A_23_P127948	ADM	1.7	1.9E-02	adrenomedullin
A_33_P3313476	ZAR1L	1.7	2.8E-02	zygote arrest 1-like
A_23_P165783	MLPH	1.7	8.0E-03	melanophilin
A_33_P3789693	MGC24103	1.7	4.3E-02	uncharacterized MGC24103
A_23_P49041	TMEM62	1.7	2.0E-02	transmembrane protein 62
A_23_P358917	CYP3A7	1.7	4.3E-02	cytochrome P450, family 3, subfamily A, polypeptide 7
A_23_P142345	PRTN3	1.7	4.8E-02	proteinase 3
A_32_P46214	SLC9A9	1.7	6.9E-03	solute carrier family 9 (sodium/hydrogen exchanger), member 9
A_24_P189533	ENDOD1	1.7	1.1E-02	endonuclease domain containing 1
A_23_P253350	C8orf4	1.7	3.1E-02	chromosome 8 open reading frame 4
A_33_P3406899	TRAK1	1.7	1.7E-02	trafficking protein, kinesin binding 1
A_23_P40847	CHST2	1.7	1.3E-02	carbohydrate (N- acetylglucosamine-6-O) sulfotransferase 2
A_33_P3254634	PDIA5	1.7	1.6E-02	protein disulfide isomerase family A, member 5
A_33_P3224380	DLG1	1.7	2.0E-02	discs, large homolog 1 (Drosophila)
A_23_P500799	CASP6	1.7	1.3E-02	caspase 6, apoptosis-related cysteine peptidase
A_24_P408457	NAGA	1.7	2.8E-02	N-acetylgalactosaminidase, alpha-
A_24_P251599	CAV3	1.7	7.9E-03	caveolin 3
A_23_P31407	AGR2	1.6	7.4E-03	anterior gradient 2 homolog (Xenopus laevis)
A_23_P130158	WNT3	1.6	2.3E-02	wingless-type MMTV integration site family, member 3
A_23_P376372	MARVELD3	1.6	3.3E-02	MARVEL domain containing 3

A_33_P3422888	CLEC16A	1.6	3.1E-02	C-type lectin domain family 16, member A
A_33_P3335233	HKDC1	1.6	3.5E-02	hexokinase domain containing 1
A_23_P160154	GALE	1.6	8.0E-03	UDP-galactose-4-epimerase
A_23_P120103	KCNS3	1.6	2.5E-02	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
A_23_P118203	ZG16B	1.6	2.2E-02	zymogen granule protein 16 homolog B (rat)
A_23_P204947	GJB2	1.6	1.2E-02	gap junction protein, beta 2, 26kDa
A_23_P142738	TMEM178	1.6	4.8E-02	transmembrane protein 178
A_33_P3225843	CCDC149	1.6	1.5E-02	coiled-coil domain containing 149
A_33_P3367392	FAM167B	1.6	9.6E-03	family with sequence similarity 167, member B
A_33_P3263666	ANKRD9	1.6	4.0E-03	ankyrin repeat domain 9
A_23_P128375	C12orf34	1.6	2.8E-02	chromosome 12 open reading frame 34
A_23_P160460	UAP1	1.6	7.3E-03	UDP-N-acetylglucosamine pyrophosphorylase 1
A_23_P359647	NFAT5	1.6	2.2E-02	nuclear factor of activated T-cells 5, tonicity-responsive
A_33_P3225066	DNAJC12	1.6	3.9E-02	DnaJ (Hsp40) homolog, subfamily C, member 12
A_33_P3400578	HLF	1.6	3.2E-02	hepatic leukemia factor
A_23_P32404	ISG20	1.6	7.3E-03	interferon stimulated exonuclease gene 20kDa
A_23_P5831	HPCAL1	1.6	9.9E-03	hippocalcin-like 1
A_24_P250922	PTGS2	1.6	2.8E-02	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
A_23_P34375	TCEA3	1.6	8.0E-03	transcription elongation factor A (SII), 3
A_33_P3275751	SEC14L1	1.6	8.0E-03	SEC14-like 1 (S. cerevisiae)
A_23_P114947	RGS2	1.6	1.2E-02	regulator of G-protein signaling 2, 24kDa
A_23_P35414	PPP1R3C	1.6	3.2E-02	protein phosphatase 1, regulatory subunit 3C
A_23_P333218	ERGIC1	1.6	1.4E-02	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1
A_23_P205531	RNASE4	1.6	1.5E-02	ribonuclease, RNase A family, 4
A_23_P145485	ULBP2	1.6	4.3E-02	UL16 binding protein 2
A_33_P3257993	RNF125	1.6	3.0E-02	ring finger protein 125, E3 ubiquitin protein ligase
A_33_P3423551	IER3	1.6	1.0E-02	immediate early response 3

A_33_P3840512	SLC25A15	1.6	1.9E-02	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
A_23_P153529	TRPM4	1.6	7.5E-03	transient receptor potential cation channel, subfamily M, member 4
A_23_P256735	CPQ	1.6	7.8E-03	carboxypeptidase Q
A_23_P251043	SYNDIG1	1.6	7.0E-03	synapse differentiation inducing 1
A_24_P105191	HS6ST2	1.6	2.7E-02	heparan sulfate 6-O-sulfotransferase 2
A_24_P146670	SLK	1.6	3.4E-02	STE20-like kinase
A_33_P3276718	HGF	1.6	4.1E-02	hepatocyte growth factor (hepapoietin A; scatter factor)
A_23_P12343	GSTM3	1.6	6.0E-03	glutathione S-transferase mu 3 (brain)
A_23_P67367	DHDH	1.6	3.8E-02	dihydrodiol dehydrogenase (dimeric)
A_23_P205567	PRKCH	1.6	5.6E-03	protein kinase C, eta
A_24_P130041	CYP51A1	1.6	1.2E-02	cytochrome P450, family 51, subfamily A, polypeptide 1
A_23_P93988	ARHGEF5	1.6	9.3E-03	Rho guanine nucleotide exchange factor (GEF) 5
A_23_P74330	MGC4473	1.6	1.3E-02	uncharacterized LOC79100
A_23_P8452	LFNG	1.6	4.6E-02	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
A_23_P10121	SFRP1	1.6	9.9E-03	secreted frizzled-related protein 1
A_23_P302654	CEP72	1.6	1.3E-02	centrosomal protein 72kDa
A_23_P129903	TRIM16L	1.6	1.0E-02	tripartite motif containing 16-like
A_23_P415401	KLF9	1.6	6.9E-03	Kruppel-like factor 9
A_23_P74278	PDE4B	1.6	4.3E-02	phosphodiesterase 4B, cAMP-specific
A_33_P3282556	TMEM204	1.6	3.9E-02	transmembrane protein 204
A_23_P102706	SNPH	1.6	1.1E-02	syntaphilin
A_33_P3246418	MDFI	1.6	2.0E-02	MyoD family inhibitor
A_33_P3287567	BCAP29	1.5	1.3E-02	B-cell receptor-associated protein 29
A_23_P76364	CD9	1.5	1.6E-02	CD9 molecule
A_23_P1072	ATP1A1	1.5	1.0E-02	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide
A_23_P103110	MAFF	1.5	7.9E-03	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
A_23_P30315	TRIM7	1.5	2.7E-02	tripartite motif containing 7
A_23_P215132	WDR91	1.5	2.0E-02	WD repeat domain 91
A_23_P105307	DGKA	1.5	3.9E-02	diacylglycerol kinase, alpha

				80kDa
A_23_P360079	NCKAP5	1.5	2.0E-02	NCK-associated protein 5
A_23_P108948	MREG	1.5	4.3E-03	melanoregulin
A_33_P3242543	MAOA	1.5	5.6E-03	monoamine oxidase A
A_23_P142872	TCF7L1	1.5	1.9E-02	transcription factor 7-like 1 (T-cell specific, HMG-box)
A_33_P3305571	TNFRSF6B	1.5	4.4E-02	tumor necrosis factor receptor superfamily, member 6b, decoy
A_23_P155477	C3orf18	1.5	1.5E-02	chromosome 3 open reading frame 18
A_23_P127579	PTS	1.5	2.0E-02	6-pyruvoyltetrahydropterin synthase
A_23_P160240	ACP6	1.5	8.0E-03	acid phosphatase 6, lysophosphatidic
A_33_P3257222	COMTD1	1.5	1.0E-02	catechol-O-methyltransferase domain containing 1
A_23_P147918	S100A16	1.5	8.3E-03	S100 calcium binding protein A16
A_23_P54736	GNG13	1.5	1.9E-02	guanine nucleotide binding protein (G protein), gamma 13
A_33_P3298387	PLK1	1.5	1.2E-02	polo-like kinase 1
A_33_P3233565	UROS	1.5	1.7E-02	uroporphyrinogen III synthase
A_24_P245298	TNFSF12	1.5	1.9E-02	tumor necrosis factor (ligand) superfamily, member 12
A_23_P68121	PSD4	1.5	4.2E-02	pleckstrin and Sec7 domain containing 4
A_32_P197489	KLF13	1.5	1.9E-02	Kruppel-like factor 13
A_23_P120316	MTHFD2	1.5	6.9E-03	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
A_23_P105535	POC1B	1.5	8.1E-03	POC1 centriolar protein homolog B (Chlamydomonas)
A_23_P64828	OAS1	1.5	1.2E-02	2'-5'-oligoadenylate synthetase 1, 40/46kDa
A_23_P408108	MTERF	1.5	1.4E-02	mitochondrial transcription termination factor
A_23_P369701	FAM108C1	1.5	1.2E-02	family with sequence similarity 108, member C1
A_24_P2948	RUSC1	1.5	9.4E-03	RUN and SH3 domain containing 1
A_23_P69738	RASL11B	1.5	2.8E-02	RAS-like, family 11, member B
A_23_P428842	TMEM44	1.5	7.5E-03	transmembrane protein 44
A_24_P408736	GALNT5	1.5	3.6E-02	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase

				5 (GalNAc-T5)
A_33_P3489737	NLN	1.5	4.2E-02	neurolysin (metallopeptidase M3 family)
A_33_P3260605	CTNNAL1	1.5	4.4E-02	catenin (cadherin-associated protein), alpha-like 1
A_24_P65507	STRA13	1.5	1.2E-02	stimulated by retinoic acid 13 homolog (mouse)
A_33_P3415191	ATP8B1	1.5	1.1E-02	ATPase, aminophospholipid transporter, class I, type 8B, member 1
A_23_P166297	ABCG1	1.5	2.5E-02	ATP-binding cassette, sub-family G (WHITE), member 1
A_23_P327499	LHFPL1	1.5	3.8E-02	lipoma HMGIC fusion partner-like 1
A_23_P92082	TKT	1.5	9.2E-03	transketolase
A_23_P314584	MAPKAPK3	1.5	8.0E-03	mitogen-activated protein kinase-activated protein kinase 3
A_23_P128215	SOCS2	1.5	2.1E-02	suppressor of cytokine signaling 2
A_23_P79331	TMBIM1	1.5	7.9E-03	transmembrane BAX inhibitor motif containing 1
A_23_P29096	PDE9A	1.5	3.7E-02	phosphodiesterase 9A
A_32_P129752	TMEM30B	1.5	3.0E-02	transmembrane protein 30B
A_23_P318904	SERTAD4	1.5	1.9E-02	SERTA domain containing 4
A_24_P300777	ADAM8	1.5	1.4E-02	ADAM metallopeptidase domain 8
A_23_P62807	SCCPDH	1.5	3.1E-02	saccharopine dehydrogenase (putative)
A_32_P46981	HSBP1L1	1.5	2.8E-02	heat shock factor binding protein 1-like 1
A_23_P52336	UNC5B	1.5	2.6E-02	unc-5 homolog B (C. elegans)
A_23_P41390	SH3TC1	1.5	1.2E-02	SH3 domain and tetratricopeptide repeats 1
A_23_P68106	TMSB10	1.5	1.6E-02	thymosin beta 10
A_33_P3278347	C21orf88	1.5	2.2E-02	chromosome 21 open reading frame 88
A_33_P3389286	SFN	1.5	1.4E-02	stratifin
A_23_P133691	RRAGD	1.5	2.6E-02	Ras-related GTP binding D
A_32_P208120	CAMK1D	1.5	3.1E-02	calcium/calmodulin-dependent protein kinase ID
A_23_P205228	ATP7B	1.5	1.2E-02	ATPase, Cu ⁺⁺ transporting, beta polypeptide
A_33_P3405022	LETM1	1.5	7.7E-03	leucine zipper-EF-hand containing transmembrane protein 1
A_24_P34155	RUNX1	1.5	3.8E-02	runt-related transcription factor 1
A_24_P103886	IDI1	1.5	9.9E-03	isopentenyl-diphosphate delta

				isomerase 1
A_23_P108501	EPHA4	1.5	2.1E-02	EPH receptor A4
A_23_P55998	SLC1A5	1.5	1.6E-02	solute carrier family 1 (neutral amino acid transporter), member 5
A_23_P64792	KCNMB4	1.5	1.9E-02	potassium large conductance calcium-activated channel, subfamily M, beta member 4
A_33_P3237359	HMGB3	1.5	1.9E-02	high mobility group box 3
A_23_P104563	CPT1A	1.5	1.4E-02	carnitine palmitoyltransferase 1A (liver)
A_33_P3376341	LRRC24	1.5	1.1E-02	leucine rich repeat containing 24
A_24_P117029	LDLR	1.5	2.2E-02	low density lipoprotein receptor
A_23_P313632	FUT8	1.5	4.0E-02	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
A_23_P5903	SLCO4A1	1.5	4.1E-02	solute carrier organic anion transporter family, member 4A1
A_32_P141682	EVPLL	1.5	2.0E-02	envoplakin-like
A_33_P3314231	CRYBA2	1.5	3.8E-02	crystallin, beta A2
A_23_P154875	BACE2	1.5	2.0E-02	beta-site APP-cleaving enzyme 2
A_23_P141770	NAPG	1.5	4.3E-02	N-ethylmaleimide-sensitive factor attachment protein, gamma
A_23_P79302	LYPD6B	1.5	2.6E-02	LY6/PLAUR domain containing 6B
A_33_P3360728	BLVRB	1.5	2.0E-02	biliverdin reductase B (flavin reductase (NADPH))
A_23_P160177	ATP1A4	1.5	2.3E-02	ATPase, Na ⁺ /K ⁺ transporting, alpha 4 polypeptide
A_24_P72518	AHCYL2	1.4	4.2E-02	adenosylhomocysteinase-like 2
A_23_P89902	RTN2	1.4	3.2E-02	reticulon 2
A_23_P17870	TMEM184B	1.4	1.7E-02	transmembrane protein 184B
A_23_P78018	ABCA5	1.4	2.0E-02	ATP-binding cassette, sub-family A (ABC1), member 5
A_32_P151544	KRT18	1.4	1.2E-02	keratin 18
A_23_P11685	PLA2G4A	1.4	1.5E-02	phospholipase A2, group IVA (cytosolic, calcium-dependent)
A_23_P256158	ADRA2C	1.4	2.7E-02	adrenergic, alpha-2C-, receptor
A_23_P203391	ASRGL1	1.4	2.9E-02	asparaginase like 1
A_23_P140602	NGRN	1.4	4.4E-02	neugrin, neurite outgrowth associated
A_24_P269062	SPRY4	1.4	3.7E-02	sprouty homolog 4 (Drosophila)
A_23_P146367	C9orf89	1.4	3.4E-02	chromosome 9 open reading frame 89
A_23_P373708	KRT18P55	1.4	1.6E-02	keratin 18 pseudogene 55

A_23_P80839	MAP6D1	1.4	3.3E-02	MAP6 domain containing 1
A_23_P25684	RDH11	1.4	2.3E-02	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)
A_24_P287075	MAP4K2	1.4	4.8E-02	mitogen-activated protein kinase kinase kinase 2
A_24_P381136	PACSIN3	1.4	2.8E-02	protein kinase C and casein kinase substrate in neurons 3
A_23_P352266	BCL2	1.4	3.2E-02	B-cell CLL/lymphoma 2
A_23_P94301	TSTA3	1.4	1.7E-02	tissue specific transplantation antigen P35B
A_23_P211212	COL18A1	1.4	2.9E-02	collagen, type XVIII, alpha 1
A_24_P202717	PLEKHJ1	1.4	2.2E-02	pleckstrin homology domain containing, family J member 1
A_33_P3215953	MPZL1	1.4	3.2E-02	myelin protein zero-like 1
A_23_P376096	TICAM1	1.4	2.1E-02	toll-like receptor adaptor molecule 1
A_23_P255884	GSN	1.4	1.3E-02	gelsolin
A_23_P20777	RBM18	1.4	1.4E-02	RNA binding motif protein 18
A_23_P126103	CTH	1.4	1.5E-02	cystathionase (cystathionine gamma-lyase)
A_23_P137035	PIR	1.4	2.2E-02	pirin (iron-binding nuclear protein)
A_23_P142878	ATOH8	1.4	4.2E-02	atonal homolog 8 (Drosophila)
A_23_P91850	IL20RB	1.4	4.1E-02	interleukin 20 receptor beta
A_24_P371962	AMD1	1.4	2.5E-02	adenosylmethionine decarboxylase 1
A_23_P67913	GMPPA	1.4	2.6E-02	GDP-mannose pyrophosphorylase A
A_24_P37441	PDK1	1.4	3.9E-02	pyruvate dehydrogenase kinase, isozyme 1
A_33_P3408221	LOC729799	1.4	2.9E-02	SEC14-like 1 pseudogene
A_33_P3464555	LOC283070	1.4	3.0E-02	uncharacterized LOC283070
A_23_P120281	EDAR	1.4	1.4E-02	ectodysplasin A receptor
A_23_P401076	SUSD3	1.4	3.7E-02	sushi domain containing 3
A_23_P217958	HK1	1.4	2.0E-02	hexokinase 1
A_24_P355267	SLC25A25	1.4	2.6E-02	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25
A_23_P102060	SSFA2	1.4	1.2E-02	sperm specific antigen 2
A_23_P361773	CCND3	1.4	2.6E-02	cyclin D3
A_33_P3378126	FBXO32	1.4	3.4E-02	F-box protein 32
A_33_P3272921	ARID3A	1.4	2.6E-02	AT rich interactive domain 3A (BRIGHT-like)
A_23_P256542	FAM162A	1.4	1.8E-02	family with sequence similarity 162, member A

A_23_P152125	MVD	1.4	2.7E-02	mevalonate (diphospho) decarboxylase
A_33_P3281816	CAP1	1.4	4.6E-02	CAP, adenylate cyclase-associated protein 1 (yeast)
A_23_P143994	FANCD2	1.4	4.0E-02	Fanconi anemia, complementation group D2
A_32_P113508	ATG16L1	1.4	3.6E-02	ATG16 autophagy related 16-like 1 (<i>S. cerevisiae</i>)
A_33_P3240936	BACE1	1.4	2.7E-02	beta-site APP-cleaving enzyme 1
A_23_P101093	COPZ2	1.4	1.6E-02	coatamer protein complex, subunit zeta 2
A_23_P203900	SCARB1	1.4	4.2E-02	scavenger receptor class B, member 1
A_24_P338648	ARL1	1.4	4.4E-02	ADP-ribosylation factor-like 1
A_23_P432360	PMM2	1.4	4.2E-02	phosphomannomutase 2
A_23_P66948	FAM59A	1.4	4.5E-02	family with sequence similarity 59, member A
A_23_P145114	GCLC	1.4	3.8E-02	glutamate-cysteine ligase, catalytic subunit
A_24_P248606	ACSL3	1.4	2.6E-02	acyl-CoA synthetase long-chain family member 3
A_23_P428129	CDKN1C	1.4	4.4E-02	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
A_23_P200239	YIPF1	1.4	1.6E-02	Yip1 domain family, member 1
A_23_P44166	DCXR	1.4	1.9E-02	dicarbonyl/L-xylulose reductase
A_23_P36345	STARD10	1.4	4.4E-02	StAR-related lipid transfer (START) domain containing 10
A_23_P19938	KDEL2	1.4	2.0E-02	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
A_24_P226008	MGLL	1.4	2.5E-02	monoglyceride lipase
A_23_P70571	SLC39A7	1.4	4.8E-02	solute carrier family 39 (zinc transporter), member 7
A_23_P150876	VPS37B	1.4	3.3E-02	vacuolar protein sorting 37 homolog B (<i>S. cerevisiae</i>)
A_23_P12884	GRK5	1.4	4.4E-02	G protein-coupled receptor kinase 5
A_24_P88763	LOXL3	1.4	2.1E-02	lysyl oxidase-like 3
A_24_P115511	RAB14	1.4	4.3E-02	RAB14, member RAS oncogene family
A_23_P101013	TMC6	1.3	3.1E-02	transmembrane channel-like 6
A_23_P373119	HMGB3P1	1.3	4.9E-02	high mobility group box 3 pseudogene 1
A_23_P319133	DNAJC10	1.3	2.7E-02	DnaJ (Hsp40) homolog, subfamily C, member 10
A_23_P61447	ETFDH	1.3	4.9E-02	electron-transferring-flavoprotein dehydrogenase

A_24_P915007	NACC1	1.3	3.8E-02	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing
A_24_P192627	MLLT3	1.3	4.1E-02	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3
A_23_P321959	SFT2D1	1.3	2.7E-02	SFT2 domain containing 1
A_23_P130531	CDC37	1.3	3.6E-02	cell division cycle 37 homolog (S. cerevisiae)
A_23_P119196	KLF2	1.3	2.8E-02	Kruppel-like factor 2 (lung)
A_23_P252783	SLC2A8	1.3	4.1E-02	solute carrier family 2 (facilitated glucose transporter), member 8
A_24_P167473	ARPC3	1.3	3.3E-02	actin related protein 2/3 complex, subunit 3, 21kDa
A_33_P3342410	EEF2K	1.3	2.6E-02	eukaryotic elongation factor-2 kinase
A_23_P414252	SNX8	1.3	4.2E-02	sorting nexin 8
A_23_P336198	GLCCI1	1.3	4.1E-02	glucocorticoid induced transcript 1
A_23_P106898	ORAI3	1.3	3.4E-02	ORAI calcium release-activated calcium modulator 3
A_23_P129101	HEXA	1.3	2.0E-02	hexosaminidase A (alpha polypeptide)
A_23_P148194	ADI1	1.3	4.4E-02	acireductone dioxygenase 1
A_23_P6344	SDF2L1	1.3	3.9E-02	stromal cell-derived factor 2-like 1
A_23_P320250	MYO19	1.3	2.3E-02	myosin XIX
A_23_P118493	TOM1L1	1.3	3.0E-02	target of myb1 (chicken)-like 1
A_23_P94795	TEAD4	1.3	3.1E-02	TEA domain family member 4
A_33_P3307886	TBXA2R	1.3	3.0E-02	thromboxane A2 receptor
A_23_P129956	DUSP3	1.3	4.4E-02	dual specificity phosphatase 3
A_23_P167096	VEGFC	1.3	3.3E-02	vascular endothelial growth factor C
A_23_P134614	COG5	1.3	3.6E-02	component of oligomeric golgi complex 5
A_23_P117163	RCBTB1	1.3	4.3E-02	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1
A_23_P38864	RABAC1	1.3	3.6E-02	Rab acceptor 1 (prenylated)
A_23_P24444	DHCR7	1.3	2.1E-02	7-dehydrocholesterol reductase
A_23_P345118	PIM1	1.3	3.3E-02	pim-1 oncogene
A_23_P115573	SHISA4	1.3	3.0E-02	shisa homolog 4 (Xenopus laevis)

A_23_P132936	SPCS3	1.3	4.0E-02	signal peptidase complex subunit 3 homolog (S. cerevisiae)
A_23_P116173	C11orf93	1.3	2.3E-02	chromosome 11 open reading frame 93
A_23_P120845	XPB1	1.3	2.8E-02	X-box binding protein 1
A_23_P158725	SLC16A3	1.3	3.0E-02	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)
A_24_P105564	PRKAB2	1.3	3.7E-02	protein kinase, AMP-activated, beta 2 non-catalytic subunit
A_32_P103945	B4GALT4	1.3	3.9E-02	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4
A_24_P141214	STOM	1.3	4.7E-02	stomatin
A_23_P11995	PRDX1	1.3	3.8E-02	peroxiredoxin 1
A_33_P3381827	OSBPL2	1.3	3.3E-02	oxysterol binding protein-like 2
A_23_P11279	ALG13	1.3	4.6E-02	asparagine-linked glycosylation 13 homolog (S. cerevisiae)
A_24_P181585	LRRC59	1.3	4.2E-02	leucine rich repeat containing 59
A_24_P109214	APOC1	1.3	4.0E-02	apolipoprotein C-I
A_24_P99795	ISOC2	1.3	3.5E-02	isochorismatase domain containing 2
A_33_P3424861	FAM118A	1.3	3.1E-02	family with sequence similarity 118, member A
A_23_P210900	ACSS2	1.3	3.9E-02	acyl-CoA synthetase short-chain family member 2
A_33_P3323453	HM13	1.3	3.8E-02	histocompatibility (minor) 13
A_33_P3362088	P2RX4	1.3	3.6E-02	purinergic receptor P2X, ligand-gated ion channel, 4
A_24_P87931	APOL1	1.3	3.4E-02	apolipoprotein L, 1
A_23_P139704	DUSP6	1.3	3.5E-02	dual specificity phosphatase 6
A_23_P5441	ABCB6	1.3	4.6E-02	ATP-binding cassette, sub-family B (MDR/TAP), member 6
A_23_P79999	ENTPD6	1.3	3.9E-02	ectonucleoside triphosphate diphosphohydrolase 6 (putative)
A_33_P3422113	ZSCAN12P1	1.2	4.1E-02	zinc finger and SCAN domain containing 12 pseudogene 1
A_23_P159539	ASMTL	1.2	3.9E-02	acetylserotonin O-methyltransferase-like
A_23_P32253	NFIL3	1.2	4.7E-02	nuclear factor, interleukin 3 regulated
A_23_P501547	ADCY6	1.2	3.9E-02	adenylate cyclase 6
A_23_P110791	CSF1R	1.2	4.7E-02	colony stimulating factor 1 receptor
A_23_P170467	USP3	0.8	4.9E-02	ubiquitin specific peptidase 3
A_33_P3243168	MZF1	0.8	4.7E-02	myeloid zinc finger 1

A_23_P46063	NME7	0.8	3.8E-02	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
A_23_P18372	B3GNT5	0.8	3.7E-02	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
A_23_P95764	PRPS1	0.8	3.5E-02	phosphoribosyl pyrophosphate synthetase 1
A_23_P133245	IK	0.8	4.6E-02	IK cytokine, down-regulator of HLA II
A_24_P151727	NONO	0.8	4.1E-02	non-POU domain containing, octamer-binding
A_23_P16078	PAFAH1B3	0.8	3.3E-02	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)
A_23_P31073	MYB	0.8	4.6E-02	v-myb myeloblastosis viral oncogene homolog (avian)
A_24_P342096	FAM27A	0.8	4.5E-02	family with sequence similarity 27, member A
A_23_P65532	PELI2	0.8	3.8E-02	pellino E3 ubiquitin protein ligase family member 2
A_24_P353794	GALNT2	0.8	3.8E-02	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)
A_23_P94683	NFX1	0.8	4.3E-02	nuclear transcription factor, X-box binding 1
A_23_P86100	KLHDC9	0.8	2.8E-02	kelch domain containing 9
A_33_P3209741	KATNAL2	0.8	4.5E-02	katanin p60 subunit A-like 2
A_23_P106822	NOB1	0.8	3.5E-02	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)
A_33_P3365037	ERCC1	0.8	4.0E-02	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
A_23_P253464	FAM175A	0.8	3.5E-02	family with sequence similarity 175, member A
A_23_P85543	RNF2	0.8	4.6E-02	ring finger protein 2
A_23_P14493	DNAAF2	0.8	4.3E-02	dynein, axonemal, assembly factor 2
A_33_P3351175	WNK2	0.8	4.7E-02	WNK lysine deficient protein kinase 2
A_33_P3253672	KCNH3	0.8	4.1E-02	potassium voltage-gated channel, subfamily H (eag-related), member 3
A_33_P3303649	MB	0.8	4.2E-02	myoglobin
A_23_P38959	VAV1	0.8	3.8E-02	vav 1 guanine nucleotide exchange factor

A_33_P3350056	MT1X	0.8	3.8E-02	metallothionein 1X
A_33_P3347168	TBL1X	0.8	2.8E-02	transducin (beta)-like 1X-linked
A_24_P763243	EEF1A1	0.8	3.8E-02	eukaryotic translation elongation factor 1 alpha 1
A_23_P91140	PECR	0.8	2.7E-02	peroxisomal trans-2-enoyl-CoA reductase
A_23_P27346	SMAD4	0.8	4.8E-02	SMAD family member 4
A_23_P111000	PSMB9	0.8	4.4E-02	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)
A_23_P135611	DALRD3	0.8	4.6E-02	DALR anticodon binding domain containing 3
A_23_P122197	CCNB1	0.8	4.9E-02	cyclin B1
A_33_P3411848	CNFN	0.8	3.7E-02	cornifelin
A_33_P3242014	PHC1	0.8	2.4E-02	polyhomeotic homolog 1 (Drosophila)
A_23_P343411	AGRN	0.8	3.2E-02	agrin
A_23_P135499	CLIC4	0.8	4.8E-02	chloride intracellular channel 4
A_23_P99917	WDR73	0.8	4.9E-02	WD repeat domain 73
A_23_P115149	WDR77	0.8	2.9E-02	WD repeat domain 77
A_33_P3272698	DUSP23	0.8	2.9E-02	dual specificity phosphatase 23
A_23_P413803	POC5	0.8	3.5E-02	POC5 centriolar protein homolog (Chlamydomonas)
A_33_P3399090	DIXDC1	0.8	2.8E-02	DIX domain containing 1
A_23_P1043	C1orf106	0.8	2.8E-02	chromosome 1 open reading frame 106
A_33_P3315314	MT1H	0.8	4.1E-02	metallothionein 1H
A_23_P48585	SALL2	0.8	4.3E-02	sal-like 2 (Drosophila)
A_23_P201400	PPOX	0.8	2.8E-02	protoporphyrinogen oxidase
A_24_P712350	CHML	0.8	3.2E-02	choroideremia-like (Rab escort protein 2)
A_33_P3331491	LOC728392	0.8	4.6E-02	uncharacterized LOC728392
A_33_P3409886	VAMP2	0.8	3.9E-02	vesicle-associated membrane protein 2 (synaptobrevin 2)
A_33_P3251703	CRIP1	0.8	4.8E-02	cysteine-rich protein 1 (intestinal)
A_23_P24903	P2RY2	0.8	2.6E-02	purinergic receptor P2Y, G-protein coupled, 2
A_33_P3345663	PPP1R21	0.8	2.7E-02	protein phosphatase 1, regulatory subunit 21
A_33_P3305790	NOS3	0.8	3.1E-02	nitric oxide synthase 3 (endothelial cell)
A_23_P411833	WDR90	0.8	2.1E-02	WD repeat domain 90
A_23_P71855	C5	0.8	4.7E-02	complement component 5

A_23_P153197	TGIF1	0.8	2.3E-02	TGFB-induced factor homeobox 1
A_23_P120594	ACSS1	0.8	2.8E-02	acyl-CoA synthetase short-chain family member 1
A_23_P24723	TMEM138	0.8	3.4E-02	transmembrane protein 138
A_23_P37983	MT1B	0.8	4.0E-02	metallothionein 1B
A_33_P3231888	C5orf15	0.8	3.4E-02	chromosome 5 open reading frame 15
A_24_P82957	RNF114	0.8	2.9E-02	ring finger protein 114
A_24_P497186	IRF2BP2	0.8	2.2E-02	interferon regulatory factor 2 binding protein 2
A_23_P427217	JMJD1C	0.8	4.4E-02	jumonji domain containing 1C
A_33_P3417195	C17orf82	0.8	3.5E-02	chromosome 17 open reading frame 82
A_33_P3214298	IMPDH2	0.8	2.0E-02	IMP (inosine 5'-monophosphate) dehydrogenase 2
A_33_P3315554	ANKMY1	0.8	3.3E-02	ankyrin repeat and MYND domain containing 1
A_23_P3602	NUDT7	0.8	4.3E-02	nudix (nucleoside diphosphate linked moiety X)-type motif 7
A_23_P90172	PPP1R15A	0.8	4.6E-02	protein phosphatase 1, regulatory subunit 15A
A_23_P106391	THAP10	0.8	3.2E-02	THAP domain containing 10
A_33_P3323323	ZNF497	0.8	4.3E-02	zinc finger protein 497
A_23_P142849	RND3	0.8	2.1E-02	Rho family GTPase 3
A_23_P127522	HYLS1	0.8	2.9E-02	hydroletharus syndrome 1
A_32_P113114	ZNF561	0.8	4.7E-02	zinc finger protein 561
A_23_P149992	PDLIM1	0.8	3.9E-02	PDZ and LIM domain 1
A_23_P42265	APOM	0.8	4.6E-02	apolipoprotein M
A_33_P3308914	CIB2	0.8	3.8E-02	calcium and integrin binding family member 2
A_33_P3369844	CD24	0.8	3.1E-02	CD24 molecule
A_23_P124742	CHKA	0.8	4.7E-02	choline kinase alpha
A_23_P157038	CNPY4	0.8	4.1E-02	canopy 4 homolog (zebrafish)
A_23_P381102	CCDC74B	0.8	3.4E-02	coiled-coil domain containing 74B
A_33_P3302115	CAPRIN1	0.8	4.7E-02	cell cycle associated protein 1
A_23_P250607	PLS3	0.8	1.8E-02	plastin 3
A_33_P3290343	CYP1B1	0.8	2.2E-02	cytochrome P450, family 1, subfamily B, polypeptide 1
A_23_P379649	BMF	0.8	4.7E-02	Bcl2 modifying factor
A_23_P95594	NAT1	0.8	4.8E-02	N-acetyltransferase 1 (arylamine N-acetyltransferase)
A_24_P48587	PSENEN	0.7	2.8E-02	presenilin enhancer 2 homolog (C. elegans)

A_23_P5983	PLTP	0.7	2.2E-02	phospholipid transfer protein
A_23_P168882	TP53INP1	0.7	3.8E-02	tumor protein p53 inducible nuclear protein 1
A_33_P3216008	SKA3	0.7	2.1E-02	spindle and kinetochore associated complex subunit 3
A_23_P210886	BCL2L1	0.7	2.4E-02	BCL2-like 1
A_23_P327022	MDFIC	0.7	3.8E-02	MyoD family inhibitor domain containing
A_23_P254179	ADNP	0.7	1.5E-02	activity-dependent neuroprotector homeobox
A_23_P348524	C20orf201	0.7	3.5E-02	chromosome 20 open reading frame 201
A_32_P52816	TM7SF3	0.7	3.7E-02	transmembrane 7 superfamily member 3
A_23_P164047	MMD	0.7	4.4E-02	monocyte to macrophage differentiation-associated
A_33_P3316278	ABCC6P1	0.7	3.8E-02	ATP-binding cassette, sub-family C, member 6 pseudogene 1
A_33_P3262758	UNC93B1	0.7	3.1E-02	unc-93 homolog B1 (C. elegans)
A_33_P3272291	AKR1C4	0.7	3.9E-02	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)
A_23_P214969	CITED2	0.7	4.8E-02	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
A_23_P111701	GNG11	0.7	3.2E-02	guanine nucleotide binding protein (G protein), gamma 11
A_23_P110412	TMEM150C	0.7	4.3E-02	transmembrane protein 150C
A_23_P40989	USP13	0.7	3.5E-02	ubiquitin specific peptidase 13 (isopeptidase T-3)
A_23_P250478	PDK3	0.7	2.1E-02	pyruvate dehydrogenase kinase, isozyme 3
A_24_P396197	PRKCSH	0.7	4.7E-02	protein kinase C substrate 80K-H
A_23_P387552	RARG	0.7	3.1E-02	retinoic acid receptor, gamma
A_33_P3789382	LOC84989	0.7	3.4E-02	uncharacterized LOC84989
A_23_P54055	AJUBA	0.7	2.7E-02	ajuba LIM protein
A_23_P141362	FZD2	0.7	3.4E-02	frizzled family receptor 2
A_32_P193646	RBMX	0.7	3.0E-02	RNA binding motif protein, X-linked
A_24_P245322	PRKAR1A	0.7	3.4E-02	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)

A_23_P30666	TNFRSF21	0.7	3.4E-02	tumor necrosis factor receptor superfamily, member 21
A_33_P3237927	ARHGAP4	0.7	1.4E-02	Rho GTPase activating protein 4
A_23_P138480	C10orf95	0.7	3.7E-02	chromosome 10 open reading frame 95
A_23_P501822	JUP	0.7	4.0E-02	junction plakoglobin
A_24_P250535	TMX4	0.7	3.9E-02	thioredoxin-related transmembrane protein 4
A_33_P3311755	KIF23	0.7	2.4E-02	kinesin family member 23
A_23_P215956	MYC	0.7	2.2E-02	v-myc myelocytomatosis viral oncogene homolog (avian)
A_23_P434944	ILF3	0.7	1.9E-02	interleukin enhancer binding factor 3, 90kDa
A_33_P3238543	MAFG-AS1	0.7	2.2E-02	MAFG antisense RNA 1 (non-protein coding)
A_23_P162807	MRPS31	0.7	2.7E-02	mitochondrial ribosomal protein S31
A_23_P385126	DEPDC7	0.7	2.6E-02	DEP domain containing 7
A_33_P3322288	AZI2	0.7	3.4E-02	5-azacytidine induced 2
A_23_P111860	RADIL	0.7	4.8E-02	Ras association and DIL domains
A_23_P76882	CCNB1IP1	0.7	2.3E-02	cyclin B1 interacting protein 1, E3 ubiquitin protein ligase
A_24_P225468	ANP32E	0.7	2.2E-02	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
A_23_P18604	LAP3	0.7	4.2E-02	leucine aminopeptidase 3
A_33_P3336422	LOC729013	0.7	4.7E-02	uncharacterized LOC729013
A_23_P50108	NDC80	0.7	4.2E-02	NDC80 kinetochore complex component homolog (S. cerevisiae)
A_23_P383986	CHST15	0.7	1.9E-02	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15
A_33_P3369190	PAM	0.7	2.7E-02	peptidylglycine alpha-amidating monooxygenase
A_24_P295963	SLC38A2	0.7	2.6E-02	solute carrier family 38, member 2
A_33_P3359306	MTA1	0.7	1.6E-02	metastasis associated 1
A_23_P117662	HDC	0.7	4.4E-02	histidine decarboxylase
A_23_P114084	PHEX	0.7	2.0E-02	phosphate regulating endopeptidase homolog, X-linked
A_24_P239731	B4GALT5	0.7	1.4E-02	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
A_23_P501831	C5orf4	0.7	2.2E-02	chromosome 5 open reading

				frame 4
A_23_P136964	RPGR	0.7	2.9E-02	retinitis pigmentosa GTPase regulator
A_33_P3286349	C19orf51	0.7	3.3E-02	chromosome 19 open reading frame 51
A_24_P317762	LY6E	0.7	3.5E-02	lymphocyte antigen 6 complex, locus E
A_23_P209449	FZD7	0.7	3.9E-02	frizzled family receptor 7
A_23_P89509	SPAG5	0.7	1.9E-02	sperm associated antigen 5
A_24_P50753	NUDT4	0.7	1.9E-02	nudix (nucleoside diphosphate linked moiety X)-type motif 4
A_33_P3681776	LOC255512	0.7	3.4E-02	uncharacterized LOC255512
A_33_P3449097	TSPAN10	0.7	3.8E-02	tetraspanin 10
A_23_P118	EXTL2	0.7	2.8E-02	exostoses (multiple)-like 2
A_23_P210763	JAG1	0.7	4.3E-02	jagged 1
A_23_P501933	CACNG6	0.7	3.7E-02	calcium channel, voltage-dependent, gamma subunit 6
A_24_P838448	LINC00340	0.7	4.5E-02	long intergenic non-protein coding RNA 340
A_23_P29248	TST	0.7	1.7E-02	thiosulfate sulfurtransferase (rhodanese)
A_23_P368558	TMEM131	0.7	3.8E-02	transmembrane protein 131
A_33_P3260614	PLCB2	0.7	3.4E-02	phospholipase C, beta 2
A_23_P48936	SMAD3	0.7	2.3E-02	SMAD family member 3
A_23_P26810	TP53	0.7	3.9E-02	tumor protein p53
A_33_P3255914	MYLIP	0.7	4.0E-02	myosin regulatory light chain interacting protein
A_33_P3802116	LOC157860	0.7	2.0E-02	uncharacterized LOC157860
A_24_P59667	JAK3	0.7	4.1E-02	Janus kinase 3
A_33_P3253975	ACAT1	0.7	1.7E-02	acetyl-CoA acetyltransferase 1
A_23_P76488	EMP1	0.7	2.4E-02	epithelial membrane protein 1
A_23_P214222	MARCKS	0.7	3.3E-02	myristoylated alanine-rich protein kinase C substrate
A_33_P3288649	HOXA10	0.7	4.0E-02	homeobox A10
A_23_P318300	ZAK	0.7	2.0E-02	sterile alpha motif and leucine zipper containing kinase AZK
A_33_P3308137	C7orf46	0.7	2.4E-02	chromosome 7 open reading frame 46
A_23_P105012	HRASLS2	0.7	2.9E-02	HRAS-like suppressor 2
A_33_P3288189	RHOBTB3	0.7	3.6E-02	Rho-related BTB domain containing 3
A_32_P231179	TEKT4	0.7	2.9E-02	tektin 4
A_24_P56240	CPNE8	0.7	1.6E-02	copine VIII
A_33_P3594214	OR7E104P	0.7	3.2E-02	olfactory receptor, family 7, subfamily E, member 104

				pseudogene
A_24_P143171	TMEM47	0.7	4.1E-02	transmembrane protein 47
A_23_P36753	ALDH2	0.7	1.8E-02	aldehyde dehydrogenase 2 family (mitochondrial)
A_24_P296808	PNMAL1	0.7	3.1E-02	paraneoplastic Ma antigen family-like 1
A_23_P44569	ABCC2	0.7	4.7E-02	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
A_33_P3234697	LXN	0.7	2.5E-02	latexin
A_23_P100539	ABCC6	0.7	1.6E-02	ATP-binding cassette, sub-family C (CFTR/MRP), member 6
A_23_P168240	PRPF4B	0.7	3.8E-02	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
A_23_P52986	VWCE	0.7	3.5E-02	von Willebrand factor C and EGF domains
A_24_P941166	ZNF425	0.7	2.8E-02	zinc finger protein 425
A_23_P335905	STK36	0.7	1.2E-02	serine/threonine kinase 36
A_23_P102000	CXCR4	0.7	1.4E-02	chemokine (C-X-C motif) receptor 4
A_24_P61490	NKX2-1	0.7	4.7E-02	NK2 homeobox 1
A_23_P136671	UGT2B7	0.7	3.9E-02	UDP glucuronosyltransferase 2 family, polypeptide B7
A_23_P171143	TSPAN6	0.7	1.5E-02	tetraspanin 6
A_33_P3287631	CTSB	0.7	2.8E-02	cathepsin B
A_24_P205364	SHMT1	0.7	8.7E-03	serine hydroxymethyltransferase 1 (soluble)
A_23_P500501	FGFR3	0.7	2.1E-02	fibroblast growth factor receptor 3
A_23_P168761	PTPRZ1	0.7	2.7E-02	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
A_23_P159255	PTPRM	0.7	1.4E-02	protein tyrosine phosphatase, receptor type, M
A_33_P3257165	YPEL1	0.7	4.9E-02	yippee-like 1 (Drosophila)
A_23_P48628	ZBTB25	0.7	4.0E-02	zinc finger and BTB domain containing 25
A_33_P3209591	AQP3	0.7	2.8E-02	aquaporin 3 (Gill blood group)
A_23_P383915	BTBD16	0.7	2.8E-02	BTB (POZ) domain containing 16
A_23_P97990	HTRA1	0.7	2.2E-02	HtrA serine peptidase 1
A_24_P287941	PSMC3IP	0.7	1.4E-02	PSMC3 interacting protein
A_24_P408047	PLEKHA4	0.7	2.0E-02	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4

A_24_P118196	GXYLT2	0.7	4.6E-02	glucoside xylosyltransferase 2
A_23_P257971	AKR1C1	0.7	3.0E-02	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
A_33_P3399593	CCDC134	0.7	1.8E-02	coiled-coil domain containing 134
A_23_P151653	APEX1	0.7	1.2E-02	APEX nuclease (multifunctional DNA repair enzyme) 1
A_24_P261259	PFKFB3	0.7	2.8E-02	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
A_32_P221799	HIST1H2AM	0.7	4.1E-02	histone cluster 1, H2am
A_24_P20630	LEF1	0.7	3.8E-02	lymphoid enhancer-binding factor 1
A_24_P491397	LDLRAD1	0.7	1.2E-02	low density lipoprotein receptor class A domain containing 1
A_23_P202837	CCND1	0.7	2.5E-02	cyclin D1
A_33_P3875565	LOC100270679	0.7	3.4E-02	uncharacterized LOC100270679
A_23_P134854	CLDN23	0.7	2.0E-02	claudin 23
A_23_P146576	GBGT1	0.7	1.5E-02	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1
A_23_P259586	TTK	0.7	2.6E-02	TTK protein kinase
A_32_P125771	RGS22	0.7	3.6E-02	regulator of G-protein signaling 22
A_23_P134237	RARRES2	0.7	4.5E-02	retinoic acid receptor responder (tazarotene induced) 2
A_23_P904	BEND5	0.7	2.5E-02	BEN domain containing 5
A_23_P27606	IL27RA	0.7	1.9E-02	interleukin 27 receptor, alpha
A_32_P86739	C10orf114	0.7	2.4E-02	chromosome 10 open reading frame 114
A_23_P138541	AKR1C3	0.7	2.6E-02	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
A_23_P434809	S100A8	0.7	9.3E-03	S100 calcium binding protein A8
A_23_P124417	BUB1	0.7	2.3E-02	budding uninhibited by benzimidazoles 1 homolog (yeast)
A_23_P96158	KRT17	0.7	2.3E-02	keratin 17
A_23_P60387	NOTCH1	0.7	2.8E-02	notch 1
A_32_P447001	FLJ27352	0.7	4.0E-02	uncharacterized LOC145788
A_23_P2705	LPAR6	0.7	2.5E-02	lysophosphatidic acid receptor 6
A_33_P3270311	HECW2	0.7	1.9E-02	HECT, C2 and WW domain

				containing E3 ubiquitin protein ligase 2
A_23_P63026	LGALS8	0.7	1.4E-02	lectin, galactoside-binding, soluble, 8
A_33_P3274478	UNC119B	0.7	1.9E-02	unc-119 homolog B (C. elegans)
A_23_P216501	TPM2	0.7	4.8E-02	tropomyosin 2 (beta)
A_23_P161507	MTL5	0.7	3.6E-02	metallothionein-like 5, testis-specific (tesmin)
A_33_P3398331	MMP24	0.7	3.1E-02	matrix metalloproteinase 24 (membrane-inserted)
A_24_P406986	SLC43A3	0.7	2.0E-02	solute carrier family 43, member 3
A_24_P802145	IRS1	0.7	3.5E-02	insulin receptor substrate 1
A_24_P348806	PLEKHA7	0.7	2.7E-02	pleckstrin homology domain containing, family A member 7
A_23_P213562	F2R	0.7	2.7E-02	coagulation factor II (thrombin) receptor
A_23_P201808	PPAP2B	0.7	2.4E-02	phosphatidic acid phosphatase type 2B
A_23_P24129	DKK1	0.7	4.0E-02	dickkopf 1 homolog (Xenopus laevis)
A_23_P136573	ST3GAL5	0.7	2.7E-02	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
A_32_P923011	FAM138A	0.7	2.8E-02	family with sequence similarity 138, member A
A_33_P3809606	FLJ45671	0.7	2.9E-02	uncharacterized LOC400212
A_33_P3303031	FLJ40606	0.7	2.3E-02	uncharacterized LOC643549
A_23_P113572	CD19	0.7	2.3E-02	CD19 molecule
A_24_P134816	BCL9L	0.7	2.1E-02	B-cell CLL/lymphoma 9-like
A_32_P96036	MEX3A	0.7	1.7E-02	mex-3 homolog A (C. elegans)
A_23_P156180	SLC22A4	0.7	2.0E-02	solute carrier family 22 (organic cation/ergothioneine transporter), member 4
A_23_P214533	ZNF323	0.7	1.4E-02	zinc finger protein 323
A_23_P500892	TUB	0.7	4.8E-02	tubby homolog (mouse)
A_23_P31064	MOXD1	0.7	2.5E-02	monooxygenase, DBH-like 1
A_23_P344481	STOX1	0.7	4.6E-02	storkhead box 1
A_33_P3590259	CXCL14	0.7	3.3E-02	chemokine (C-X-C motif) ligand 14
A_32_P116556	ZNF469	0.7	3.4E-02	zinc finger protein 469
A_24_P911676	SOX4	0.7	4.1E-02	SRY (sex determining region Y)-box 4
A_23_P96369	CXorf57	0.7	4.7E-02	chromosome X open reading frame 57
A_24_P358591	C2orf70	0.7	2.5E-02	chromosome 2 open reading frame 70

A_23_P381017	WBSCR27	0.7	4.0E-02	Williams Beuren syndrome chromosome region 27
A_23_P129466	ATF7IP2	0.7	1.8E-02	activating transcription factor 7 interacting protein 2

Table E2: Genes differentially expressed in NHBE in the presence of ILC2s compared to NHBE alone

Agilent Gene ID	Entrez Gene ID	Fold Change	Adjusted p Value	Gene Name
A_23_P51217	CLCA1	619.8	2.10E-04	chloride channel accessory 1
A_33_P3270104	FAM26D	176	2.70E-03	family with sequence similarity 26, member D
A_23_P139434	PRB2	158.7	9.80E-04	proline-rich protein BstNI subfamily 2
A_23_P215484	CCL26	127.2	7.20E-03	chemokine (C-C motif) ligand 26
A_33_P3217776	PRB4	106.6	1.30E-03	proline-rich protein BstNI subfamily 4
A_23_P351148	SH2D1B	105.5	1.70E-03	SH2 domain containing 1B
A_33_P3511265	POSTN	88.8	1.50E-03	periostin, osteoblast specific factor
A_23_P90626	CYTIP	73	8.50E-04	cytohesin 1 interacting protein
A_33_P3263432	ITGA10	63.5	2.40E-04	integrin, alpha 10
A_23_P8913	CA2	39.5	6.60E-04	carbonic anhydrase II
A_24_P87036	ANO1	39.2	5.10E-03	anoctamin 1, calcium activated chloride channel
A_23_P112859	CST1	37.3	2.80E-03	cystatin SN
A_23_P56703	C2orf89	36.7	2.40E-04	chromosome 2 open reading frame 89
A_23_P341567	SLC9B2	35.7	2.10E-04	solute carrier family 9, subfamily B (cation proton antiporter 2), member 2
A_32_P167076	CAPN14	30.5	3.20E-03	calpain 14
A_23_P39525	FAM124B	30.3	2.10E-03	family with sequence similarity 124B
A_23_P144096	CISH	23.3	1.50E-03	cytokine inducible SH2-containing protein
A_23_P9711	HS3ST4	22.1	1.50E-03	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
A_23_P420196	SOCS1	21.6	2.40E-04	suppressor of cytokine signaling 1
A_23_P111583	CD36	20.5	6.80E-03	CD36 molecule (thrombospondin receptor)
A_24_P245379	SERPINB2	19.3	7.20E-03	serpin peptidase inhibitor, clade B (ovalbumin), member 2
A_23_P19673	SGK1	18.2	6.60E-04	serum/glucocorticoid regulated kinase 1
A_23_P331560	SLC26A4	17.1	1.50E-03	solute carrier family 26, member 4
A_23_P212568	TRAT1	16.5	9.20E-03	T cell receptor associated transmembrane adaptor 1
A_23_P80040	PROCR	15.3	2.80E-03	protein C receptor, endothelial
A_23_P41424	SLC39A8	15.1	5.40E-04	solute carrier family 39 (zinc transporter), member 8
A_33_P3252394	GADD45G	15.1	1.30E-03	growth arrest and DNA-damage-

				inducible, gamma
A_24_P237175	CST2	14.4	4.80E-03	cystatin SA
A_32_P196263	ADAMTS9	14.3	6.40E-04	ADAM metallopeptidase with thrombospondin type 1 motif, 9
A_23_P314101	SUSD2	14.2	1.00E-02	sushi domain containing 2
A_23_P36531	TSPAN8	14.1	1.20E-03	tetraspanin 8
A_24_P265506	NTRK1	13.9	3.40E-03	neurotrophic tyrosine kinase, receptor, type 1
A_23_P46639	C8A	13.9	6.60E-04	complement component 8, alpha polypeptide
A_23_P338479	CD274	13.5	2.70E-03	CD274 molecule
A_33_P3287223	DPP4	12.5	9.60E-04	dipeptidyl-peptidase 4
A_23_P5601	DOK1	12.4	6.40E-04	docking protein 1, 62kDa (downstream of tyrosine kinase 1)
A_33_P3396404	CLLU1OS	12.3	1.60E-02	chronic lymphocytic leukemia up-regulated 1 opposite strand
A_24_P365721	SLC6A14	11.9	8.30E-03	solute carrier family 6 (amino acid transporter), member 14
A_33_P3258593	PRB1	11.4	2.40E-04	proline-rich protein BstNI subfamily 1
A_32_P163147	VSIG1	11.0	1.20E-02	V-set and immunoglobulin domain containing 1
A_33_P3356776	GOLGA7B	10.8	3.70E-03	golgin A7 family, member B
A_23_P21495	FCGBP	10.5	5.10E-03	Fc fragment of IgG binding protein
A_32_P157391	FOLH1B	10.1	1.50E-03	folate hydrolase 1B
A_33_P3256334	PRB3	10	1.10E-03	proline-rich protein BstNI subfamily 3
A_23_P368338	BET3L	9.6	9.80E-03	BET3 like (<i>S. cerevisiae</i>)
A_23_P105973	SERPINA11	9.5	9.60E-04	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11
A_23_P79978	SLC24A3	9.5	1.10E-03	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
A_33_P3260125	LDLRAD2	9.1	4.30E-03	low density lipoprotein receptor class A domain containing 2
A_23_P216712	TRPM6	9.0	1.70E-02	transient receptor potential cation channel, subfamily M, member 6
A_33_P3357818	HTR1D	8.6	1.50E-03	5-hydroxytryptamine (serotonin) receptor 1D, G protein-coupled
A_32_P66881	TLR4	8.4	7.90E-03	toll-like receptor 4
A_23_P58266	S100P	7.7	3.80E-03	S100 calcium binding protein P
A_33_P3240249	LOC100129125	7.7	1.30E-02	uncharacterized LOC100129125
A_23_P105562	VWF	7.6	2.70E-03	von Willebrand factor
A_33_P3471466	C14orf166B	7.5	1.50E-02	chromosome 14 open reading frame 166B
A_23_P124946	CMYA5	7.3	1.10E-02	cardiomyopathy associated 5

A_33_P3280603	PPP4R1L	6.8	2.60E-03	protein phosphatase 4, regulatory subunit 1-like
A_23_P73571	MUM1L1	6.5	1.10E-02	melanoma associated antigen (mutated) 1-like 1
A_33_P3744415	LOC154092	6.5	1.40E-02	uncharacterized LOC154092
A_24_P416177	ADCY7	6.5	1.90E-03	adenylate cyclase 7
A_33_P3610406	ECEL1P2	6.4	5.50E-03	endothelin converting enzyme-like 1, pseudogene 2
A_33_P3284345	NRG1	6.3	1.40E-03	neuregulin 1
A_23_P32233	KLF4	6.3	8.90E-04	Kruppel-like factor 4 (gut)
A_33_P3268472	CTSC	6.2	9.70E-03	cathepsin C
A_24_P181055	ST3GAL4	6.2	1.60E-03	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
A_33_P3312466	BTNL9	6.2	9.20E-03	butyrophilin-like 9
A_33_P3322804	NTRK2	6.1	9.50E-03	neurotrophic tyrosine kinase, receptor, type 2
A_23_P161297	OGDHL	6.1	6.20E-03	oxoglutarate dehydrogenase-like
A_23_P13753	NFE2	6.1	8.80E-03	nuclear factor (erythroid-derived 2), 45kDa
A_23_P142878	ATOH8	6.1	1.70E-03	atonal homolog 8 (Drosophila)
A_23_P81676	WISP3	6.1	1.10E-02	WNT1 inducible signaling pathway protein 3
A_33_P3254811	C3orf70	6.1	1.40E-02	chromosome 3 open reading frame 70
A_24_P192727	KAZALD1	6.1	1.40E-03	Kazal-type serine peptidase inhibitor domain 1
A_23_P111194	SPDEF	6.0	2.50E-03	SAM pointed domain containing ets transcription factor
A_23_P203972	FZD10	5.9	2.20E-03	frizzled family receptor 10
A_23_P127891	BDNF	5.9	1.20E-02	brain-derived neurotrophic factor
A_23_P69329	HYAL1	5.9	8.90E-04	hyaluronoglucosaminidase 1
A_23_P76291	PRR4	5.9	9.80E-04	proline rich 4 (lacrimal)
A_23_P36397	CYP27B1	5.9	2.70E-03	cytochrome P450, family 27, subfamily B, polypeptide 1
A_23_P329198	OBFC2A	5.8	1.50E-03	oligonucleotide/oligosaccharide-binding fold containing 2A
A_23_P26847	SOX9	5.8	9.00E-03	SRY (sex determining region Y)-box 9
A_23_P47616	FOLH1	5.8	6.80E-03	folate hydrolase (prostate-specific membrane antigen) 1
A_23_P12343	GSTM3	5.6	1.40E-03	glutathione S-transferase mu 3 (brain)
A_23_P38537	KRT16	5.5	1.40E-03	keratin 16
A_23_P99906	HOMER2	5.5	1.70E-03	homer homolog 2 (Drosophila)
A_23_P324754	KIAA1199	5.3	1.00E-02	KIAA1199
A_33_P3216570	MUC5AC	5.3	1.50E-02	mucin 5AC, oligomeric mucus/gel-forming

A_23_P80570	AADAC	5.3	1.50E-02	arylacetamide deacetylase (esterase)
A_32_P66804	PTPRN2	5.2	9.00E-03	protein tyrosine phosphatase, receptor type, N polypeptide 2
A_23_P58228	ODAM	5.2	8.80E-03	odontogenic, ameloblast associated
A_23_P115726	SLC16A9	5.2	1.10E-03	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)
A_23_P1602	CDC42EP2	5.1	6.90E-03	CDC42 effector protein (Rho GTPase binding) 2
A_23_P142174	FOXA3	4.9	2.30E-03	forkhead box A3
A_32_P175739	HK2	4.9	1.50E-03	hexokinase 2
A_24_P77968	FLNC	4.9	5.60E-03	filamin C, gamma
A_23_P64792	KCNMB4	4.8	7.50E-03	potassium large conductance calcium-activated channel, subfamily M, beta member 4
A_23_P216920	NEK6	4.8	1.50E-03	NIMA (never in mitosis gene a)-related kinase 6
A_33_P3373775	BCL2L15	4.8	3.40E-03	BCL2-like 15
A_23_P62709	SPRR3	4.8	7.20E-03	small proline-rich protein 3
A_24_P388528	ST6GAL1	4.8	1.50E-03	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1
A_23_P87049	SORL1	4.7	2.70E-03	sortilin-related receptor, L(DLR class) A repeats containing
A_33_P3423854	C8B	4.7	7.20E-03	complement component 8, beta polypeptide
A_23_P74449	HPDL	4.7	6.10E-03	4-hydroxyphenylpyruvate dioxygenase-like
A_32_P159651	KAT2B	4.6	5.50E-03	K(lysine) acetyltransferase 2B
A_23_P101642	PTPRH	4.6	7.70E-03	protein tyrosine phosphatase, receptor type, H
A_23_P427296	LOC100132319	4.5	1.30E-02	uncharacterized LOC100132319
A_23_P3956	C1QTNF1	4.5	2.70E-03	C1q and tumor necrosis factor related protein 1
A_23_P422911	HS6ST3	4.5	1.70E-02	heparan sulfate 6-O-sulfotransferase 3
A_23_P151907	PCSK6	4.5	6.30E-03	proprotein convertase subtilisin/kexin type 6
A_23_P335495	ANO7	4.5	2.70E-03	anoctamin 7
A_23_P255884	GSN	4.5	1.40E-03	gelsolin
A_23_P117506	DHRS7	4.5	2.70E-03	dehydrogenase/reductase (SDR family) member 7
A_23_P41114	CSTA	4.4	1.50E-02	cystatin A (stefin A)
A_23_P56659	DQX1	4.3	1.40E-03	DEAQ box RNA-dependent ATPase 1
A_24_P404840	GJB1	4.3	7.70E-03	gap junction protein, beta 1, 32kDa

A_23_P10206	HAS2	4.2	1.60E-02	hyaluronan synthase 2
A_23_P39840	VAMP5	4.2	1.40E-03	vesicle-associated membrane protein 5 (myobrevin)
A_33_P3418170	DDX58	4.2	4.10E-03	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
A_33_P3258046	TAC4	4.1	5.60E-03	tachykinin 4 (hemokinin)
A_23_P315206	CCBL1	4.1	9.80E-04	cysteine conjugate-beta lyase, cytoplasmic
A_24_P366526	SYNGR2	4.1	5.40E-03	synaptogyrin 2
A_33_P3282434	SLC16A1	4.1	3.80E-03	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
A_23_P71170	TRPV6	4.1	4.40E-03	transient receptor potential cation channel, subfamily V, member 6
A_32_P25437	SLC12A2	4.1	6.80E-03	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
A_23_P384329	DENND4A	4.1	1.60E-02	DENN/MADD domain containing 4A
A_33_P3235147	DLX5	4	1.50E-02	distal-less homeobox 5
A_33_P3272231	MFSD2A	4	1.30E-03	major facilitator superfamily domain containing 2A
A_33_P3703501	GALNT10	4	6.80E-03	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)
A_24_P217572	EDNRA	4	5.30E-03	endothelin receptor type A
A_33_P3302892	NID2	4	9.20E-03	nidogen 2 (osteonidogen)
A_23_P115407	GSTM1	4	3.20E-03	glutathione S-transferase mu 1
A_33_P3666884	PNPLA7	4	3.70E-03	patatin-like phospholipase domain containing 7
A_23_P40453	CBR3	4	1.80E-03	carbonyl reductase 3
A_32_P9543	APOBEC3A	4	1.50E-03	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A
A_33_P3294509	CD44	3.9	8.10E-03	CD44 molecule (Indian blood group)
A_23_P355536	USP54	3.9	1.30E-03	ubiquitin specific peptidase 54
A_23_P156497	ELOVL5	3.9	1.50E-03	ELOVL fatty acid elongase 5
A_24_P942370	GALNT4	3.9	7.50E-03	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)
A_23_P68106	TMSB10	3.9	1.00E-02	thymosin beta 10
A_23_P69226	TMEM111	3.9	1.50E-03	transmembrane protein 111
A_23_P323751	FAM83D	3.9	3.20E-03	family with sequence similarity 83, member D

A_24_P188377	CD55	3.8	1.40E-03	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
A_24_P109644	LOC220077	3.8	1.10E-02	dedicator of cytokinesis 1 pseudogene
A_23_P398943	KIR3DX1	3.8	1.30E-02	killer cell immunoglobulin-like receptor, three domains, X1
A_33_P3320443	CRHR1	3.8	6.80E-03	corticotropin releasing hormone receptor 1
A_33_P3239295	PRODH	3.7	1.30E-02	proline dehydrogenase (oxidase) 1
A_33_P3308744	LAMA4	3.7	9.00E-03	laminin, alpha 4
A_24_P153840	FGD3	3.7	1.00E-02	FYVE, RhoGEF and PH domain containing 3
A_23_P49448	FA2H	3.7	1.50E-02	fatty acid 2-hydroxylase
A_24_P940166	PAPSS2	3.7	4.10E-03	3'-phosphoadenosine 5'-phosphosulfate synthase 2
A_23_P168610	TSPAN13	3.6	6.80E-03	tetraspanin 13
A_24_P36890	RAP1GAP	3.6	1.40E-02	RAP1 GTPase activating protein
A_33_P3339148	FLJ16126	3.6	1.40E-02	uncharacterized LOC645010
A_23_P215549	PON3	3.6	5.50E-03	paraoxonase 3
A_23_P132175	RTN4R	3.6	2.20E-03	reticulon 4 receptor
A_23_P39799	LOXL3	3.5	1.20E-02	lysyl oxidase-like 3
A_23_P138706	ADRA2A	3.5	4.90E-03	adrenergic, alpha-2A-, receptor
A_23_P408787	C1orf150	3.5	9.50E-03	chromosome 1 open reading frame 150
A_32_P141238	ANO2	3.5	9.50E-03	anoctamin 2
A_33_P3241051	ADAMTS17	3.5	8.80E-03	ADAM metallopeptidase with thrombospondin type 1 motif, 17
A_23_P322704	FAM177A1	3.4	2.80E-03	family with sequence similarity 177, member A1
A_23_P168551	SLC29A4	3.4	1.50E-03	solute carrier family 29 (nucleoside transporters), member 4
A_23_P97365	LRRC8D	3.4	3.40E-03	leucine rich repeat containing 8 family, member D
A_23_P58132	RHOH	3.4	2.70E-03	ras homolog family member H
A_33_P3236642	MIA3	3.3	1.70E-02	melanoma inhibitory activity family, member 3
A_23_P216489	GNE	3.3	5.10E-03	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
A_23_P12199	FAM46B	3.3	3.50E-03	family with sequence similarity 46, member B
A_33_P3277447	SLC26A2	3.3	9.30E-03	solute carrier family 26 (sulfate transporter), member 2
A_33_P3247624	REP15	3.3	9.20E-03	RAB15 effector protein
A_23_P255376	CCDC109B	3.3	5.10E-03	coiled-coil domain containing 109B

A_33_P3413962	PFKP	3.3	1.70E-03	phosphofructokinase, platelet
A_23_P146572	NPDC1	3.3	5.60E-03	neural proliferation, differentiation and control, 1
A_33_P3338724	LENG9	3.2	2.70E-03	leukocyte receptor cluster (LRC) member 9
A_33_P3361348	ALOX15	3.2	1.50E-02	arachidonate 15-lipoxygenase
A_23_P211504	KDELR3	3.2	5.20E-03	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
A_24_P24444	EXOG	3.2	9.50E-03	endo/exonuclease (5'-3'), endonuclease G-like
A_23_P160460	UAP1	3.2	8.10E-03	UDP-N-acetylglucosamine pyrophosphorylase 1
A_33_P3313835	PP14571	3.2	1.50E-02	uncharacterized LOC100130449
A_33_P3308105	GGH	3.2	9.80E-03	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
A_23_P64611	P2RY6	3.2	6.10E-03	pyrimidinergic receptor P2Y, G-protein coupled, 6
A_24_P253251	SLC7A1	3.2	4.30E-03	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
A_23_P254254	SGSH	3.2	9.20E-03	N-sulfoglucosamine sulfohydrolase
A_32_P207169	C1orf133	3.1	6.50E-03	chromosome 1 open reading frame 133
A_33_P3290249	OR2M5	3.1	1.20E-02	olfactory receptor, family 2, subfamily M, member 5
A_23_P108437	FZD5	3.1	1.50E-03	frizzled family receptor 5
A_23_P48740	DIO2	3.1	1.50E-02	deiodinase, iodothyronine, type II
A_33_P3342081	PRDM1	3.1	5.50E-03	PR domain containing 1, with ZNF domain
A_23_P43898	EPHX4	3.1	9.30E-03	epoxide hydrolase 4
A_23_P86470	CH25H	3.1	4.40E-03	cholesterol 25-hydroxylase
A_23_P16469	PLAUR	3.1	4.80E-03	plasminogen activator, urokinase receptor
A_23_P128728	ARG2	2.9	6.80E-03	arginase, type II
A_24_P344961	AMOT	2.9	6.90E-03	angiomotin
A_24_P137522	USP53	2.9	5.50E-03	ubiquitin specific peptidase 53
A_24_P130041	CYP51A1	2.9	1.50E-03	cytochrome P450, family 51, subfamily A, polypeptide 1
A_33_P3371089	SGTB	2.9	4.30E-03	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta
A_23_P5831	HPCAL1	2.9	2.10E-03	hippocalcin-like 1
A_33_P3228807	SPEG	2.9	1.60E-02	SPEG complex locus
A_23_P14804	TSPAN3	2.9	2.30E-03	tetraspanin 3

A_23_P26759	CANT1	2.9	6.20E-03	calcium activated nucleotidase 1
A_23_P5945	DHX35	2.9	3.40E-03	DEAH (Asp-Glu-Ala-His) box polypeptide 35
A_23_P357546	PNKD	2.8	1.10E-02	paroxysmal nonkinesigenic dyskinesia
A_23_P123172	OR2A9P	2.8	2.70E-03	olfactory receptor, family 2, subfamily A, member 9 pseudogene
A_33_P3251093	SLC36A1	2.8	6.70E-03	solute carrier family 36 (proton/amino acid symporter), member 1
A_23_P215132	WDR91	2.8	7.20E-03	WD repeat domain 91
A_23_P60146	PDGFRL	2.8	1.10E-02	platelet-derived growth factor receptor-like
A_23_P13907	IGF1	2.8	5.50E-03	insulin-like growth factor 1 (somatomedin C)
A_24_P300777	ADAM8	2.8	9.20E-03	ADAM metallopeptidase domain 8
A_23_P429184	GNPNAT1	2.7	4.90E-03	glucosamine-phosphate N-acetyltransferase 1
A_23_P127579	PTS	2.7	2.50E-03	6-pyruvoyltetrahydropterin synthase
A_33_P3373046	ZNF772	2.7	1.50E-02	zinc finger protein 772
A_33_P3225066	DNAJC12	2.7	9.20E-03	DnaJ (Hsp40) homolog, subfamily C, member 12
A_33_P3246418	MDFI	2.7	9.20E-03	MyoD family inhibitor
A_24_P43876	C9orf40	2.7	1.20E-02	chromosome 9 open reading frame 40
A_32_P230196	AGAP7	2.7	1.30E-02	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7
A_23_P359277	ELOVL7	2.7	2.70E-03	ELOVL fatty acid elongase 7
A_24_P351283	MREG	2.7	1.00E-02	melanoregulin
A_33_P3254634	PDIA5	2.6	4.50E-03	protein disulfide isomerase family A, member 5
A_24_P929322	FLJ42393	2.6	8.10E-03	uncharacterized LOC401105
A_23_P148584	DOCK11	2.6	3.80E-03	dedicator of cytokinesis 11
A_23_P131899	SDCBP2	2.6	5.20E-03	syndecan binding protein (syntenin) 2
A_33_P3242543	MAOA	2.6	3.70E-03	monoamine oxidase A
A_33_P3376341	LRRC24	2.6	7.80E-03	leucine rich repeat containing 24
A_23_P51202	ZNF436	2.6	2.70E-03	zinc finger protein 436
A_23_P250274	LRRC8A	2.6	6.40E-03	leucine rich repeat containing 8 family, member A
A_33_P3241984	PTPN22	2.6	1.00E-02	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
A_33_P3290394	IL2RG	2.6	4.10E-03	interleukin 2 receptor, gamma
A_23_P114947	RGS2	2.6	4.80E-03	regulator of G-protein signaling 2, 24kDa

A_23_P167599	FAM134B	2.6	2.90E-03	family with sequence similarity 134, member B
A_32_P91042	LOC100129034	2.6	9.00E-03	uncharacterized LOC100129034
A_23_P13797	C12orf49	2.6	7.10E-03	chromosome 12 open reading frame 49
A_23_P62807	SCCPDH	2.6	3.20E-03	saccharopine dehydrogenase (putative)
A_23_P63232	CREB3L4	2.6	5.10E-03	cAMP responsive element binding protein 3-like 4
A_23_P162525	UTP20	2.6	1.30E-02	UTP20, small subunit (SSU) processome component, homolog (yeast)
A_24_P62505	GLT25D2	2.6	1.30E-02	glycosyltransferase 25 domain containing 2
A_24_P117029	LDLR	2.6	2.20E-03	low density lipoprotein receptor
A_33_P3358957	PAPL	2.6	4.40E-03	iron/zinc purple acid phosphatase-like protein
A_23_P211909	PLS1	2.5	9.20E-03	plastin 1
A_32_P46214	SLC9A9	2.5	1.70E-02	solute carrier family 9 (sodium/hydrogen exchanger), member 9
A_23_P130194	PYCR1	2.5	5.30E-03	pyrroline-5-carboxylate reductase 1
A_23_P56578	VIT	2.5	6.20E-03	vitrin
A_23_P152428	MARVELD3	2.5	1.50E-02	MARVEL domain containing 3
A_24_P321068	SLC31A1	2.5	6.80E-03	solute carrier family 31 (copper transporters), member 1
A_23_P256107	HPSE	2.5	5.30E-03	heparanase
A_23_P153301	CEACAM5	2.5	6.90E-03	carcinoembryonic antigen-related cell adhesion molecule 5
A_23_P26954	VAT1	2.5	8.40E-03	vesicle amine transport protein 1 homolog (T. californica)
A_33_P3360728	BLVRB	2.5	4.90E-03	biliverdin reductase B (flavin reductase (NADPH))
A_23_P1072	ATP1A1	2.5	3.80E-03	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide
A_24_P307626	ATP1A4	2.5	4.90E-03	ATPase, Na ⁺ /K ⁺ transporting, alpha 4 polypeptide
A_23_P369701	FAM108C1	2.5	6.80E-03	family with sequence similarity 108, member C1
A_23_P205567	PRKCH	2.5	4.50E-03	protein kinase C, eta
A_23_P76364	CD9	2.5	6.20E-03	CD9 molecule
A_23_P325924	FAM59B	2.5	1.30E-02	family with sequence similarity 59, member B
A_24_P453921	DPY19L1P1	2.5	1.40E-02	dpy-19-like 1 pseudogene 1 (C. elegans)
A_23_P12884	GRK5	2.4	6.20E-03	G protein-coupled receptor kinase 5
A_33_P3413905	ADM2	2.4	4.30E-03	adrenomedullin 2

A_23_P153529	TRPM4	2.4	2.70E-03	transient receptor potential cation channel, subfamily M, member 4
A_23_P312920	POU2AF1	2.4	9.20E-03	POU class 2 associating factor 1
A_23_P200239	YIPF1	2.4	1.50E-02	Yip1 domain family, member 1
A_23_P256735	CPQ	2.4	1.60E-02	carboxypeptidase Q
A_23_P16834	FNDC4	2.4	7.20E-03	fibronectin type III domain containing 4
A_24_P64126	CPNE3	2.4	1.10E-02	copine III
A_24_P72518	AHCYL2	2.4	7.10E-03	adenosylhomocysteinase-like 2
A_23_P10121	SFRP1	2.4	8.80E-03	secreted frizzled-related protein 1
A_32_P116840	CTAGE5	2.4	7.60E-03	CTAGE family, member 5
A_23_P19226	DSE	2.4	4.60E-03	dermatan sulfate epimerase
A_23_P120056	RTKN	2.4	1.30E-02	rhotekin
A_33_P3406899	TRAK1	2.4	5.30E-03	trafficking protein, kinesin binding 1
A_24_P197537	PDE8B	2.4	7.20E-03	phosphodiesterase 8B
A_23_P128215	SOCS2	2.4	8.10E-03	suppressor of cytokine signaling 2
A_23_P201319	DISP1	2.4	1.30E-02	dispatched homolog 1 (Drosophila)
A_33_P3210647	COL16A1	2.4	9.50E-03	collagen, type XVI, alpha 1
A_23_P31407	AGR2	2.4	8.80E-03	anterior gradient 2 homolog (Xenopus laevis)
A_23_P102060	SSFA2	2.4	7.10E-03	sperm specific antigen 2
A_23_P121657	HS3ST1	2.3	5.50E-03	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
A_33_P3215768	GALNT6	2.3	6.80E-03	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
A_33_P3224819	SLC45A4	2.3	9.20E-03	solute carrier family 45, member 4
A_24_P147461	SERPINB8	2.3	7.80E-03	serpin peptidase inhibitor, clade B (ovalbumin), member 8
A_23_P253602	BMX	2.3	1.50E-02	BMX non-receptor tyrosine kinase
A_23_P93988	ARHGEF5	2.3	5.20E-03	Rho guanine nucleotide exchange factor (GEF) 5
A_23_P150876	VPS37B	2.3	9.60E-03	vacuolar protein sorting 37 homolog B (S. cerevisiae)
A_24_P2948	RUSC1	2.3	3.50E-03	RUN and SH3 domain containing 1
A_23_P30315	TRIM7	2.3	5.20E-03	tripartite motif containing 7
A_23_P160154	GALE	2.3	7.30E-03	UDP-galactose-4-epimerase
A_33_P3408420	MDGA2	2.3	1.20E-02	MAM domain containing glycosylphosphatidylinositol anchor 2
A_23_P152782	IFI35	2.3	3.70E-03	interferon-induced protein 35
A_23_P311232	CLASP1	2.3	3.70E-03	cytoplasmic linker associated protein 1

A_23_P401076	SUSD3	2.2	8.10E-03	sushi domain containing 3
A_23_P70355	SERPINB6	2.2	6.80E-03	serpin peptidase inhibitor, clade B (ovalbumin), member 6
A_33_P3260634	PLCB4	2.2	1.70E-02	phospholipase C, beta 4
A_23_P24444	DHCR7	2.2	7.90E-03	7-dehydrocholesterol reductase
A_23_P50591	KCNK6	2.2	3.70E-03	potassium channel, subfamily K, member 6
A_23_P146367	C9orf89	2.2	9.90E-03	chromosome 9 open reading frame 89
A_32_P221	C16orf78	2.2	1.50E-02	chromosome 16 open reading frame 78
A_23_P129903	TRIM16L	2.2	1.30E-02	tripartite motif containing 16-like
A_24_P38276	FZD1	2.2	5.50E-03	frizzled family receptor 1
A_33_P3275751	SEC14L1	2.2	5.10E-03	SEC14-like 1 (S. cerevisiae)
A_23_P211428	SMTN	2.2	1.70E-02	smoothelin
A_33_P3408320	CERS1	2.2	5.10E-03	ceramide synthase 1
A_23_P500799	CASP6	2.2	1.50E-02	caspase 6, apoptosis-related cysteine peptidase
A_33_P3352758	NHSL2	2.2	1.50E-02	NHS-like 2
A_33_P3263666	ANKRD9	2.2	1.30E-02	ankyrin repeat domain 9
A_23_P114883	FMOD	2.2	1.50E-02	fibromodulin
A_23_P125078	SLC26A11	2.2	1.30E-02	solute carrier family 26, member 11
A_24_P62615	CAP1	2.2	8.10E-03	CAP, adenylate cyclase-associated protein 1 (yeast)
A_23_P79331	TMBIM1	2.2	1.20E-02	transmembrane BAX inhibitor motif containing 1
A_32_P47643	FAM110C	2.2	1.60E-02	family with sequence similarity 110, member C
A_23_P78018	ABCA5	2.2	1.30E-02	ATP-binding cassette, sub-family A (ABC1), member 5
A_23_P67913	GMPPA	2.2	7.30E-03	GDP-mannose pyrophosphorylase A
A_23_P154875	BACE2	2.2	5.50E-03	beta-site APP-cleaving enzyme 2
A_33_P3384932	NUDT8	2.2	4.20E-03	nudix (nucleoside diphosphate linked moiety X)-type motif 8
A_32_P339640	C20orf197	2.2	9.20E-03	chromosome 20 open reading frame 197
A_23_P110184	MSMO1	2.1	1.50E-02	methylsterol monooxygenase 1
A_23_P147918	S100A16	2.1	1.30E-02	S100 calcium binding protein A16
A_23_P212617	TFRC	2.1	1.20E-02	transferrin receptor (p90, CD71)
A_23_P3038	GPX2	2.1	8.80E-03	glutathione peroxidase 2 (gastrointestinal)
A_24_P141214	STOM	2.1	4.80E-03	stomatin
A_33_P3257222	COMTD1	2.1	7.50E-03	catechol-O-methyltransferase domain containing 1

A_24_P65507	STRA13	2.1	1.30E-02	stimulated by retinoic acid 13 homolog (mouse)
A_23_P215060	PODXL	2.1	5.50E-03	podocalyxin-like
A_24_P169773	CTAGE4	2.1	7.70E-03	CTAGE family, member 4
A_33_P3317664	MGAT1	2.1	8.10E-03	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
A_23_P105307	DGKA	2.1	1.30E-02	diacylglycerol kinase, alpha 80kDa
A_23_P92082	TKT	2.1	1.40E-02	transketolase
A_32_P34920	FOXD1	2.1	1.10E-02	forkhead box D1
A_24_P40907	PPAPDC2	2.1	8.40E-03	phosphatidic acid phosphatase type 2 domain containing 2
A_23_P128375	C12orf34	2.1	8.90E-03	chromosome 12 open reading frame 34
A_23_P218434	ZNF226	2.1	8.80E-03	zinc finger protein 226
A_23_P316381	ACOX3	2.1	6.80E-03	acyl-CoA oxidase 3, pristanoyl
A_23_P52402	PITRM1	2.1	6.50E-03	pitrilysin metallopeptidase 1
A_23_P49041	TMEM62	2.1	1.40E-02	transmembrane protein 62
A_23_P32029	SLC35D2	2.1	1.00E-02	solute carrier family 35, member D2
A_33_P3215953	MPZL1	2.1	1.30E-02	myelin protein zero-like 1
A_23_P415401	KLF9	2.1	6.80E-03	Kruppel-like factor 9
A_33_P3233565	UROS	2.1	9.20E-03	uroporphyrinogen III synthase
A_33_P3287567	BCAP29	2.1	7.60E-03	B-cell receptor-associated protein 29
A_23_P202905	TIRAP	2.1	1.20E-02	toll-interleukin 1 receptor (TIR) domain containing adaptor protein
A_23_P134614	COG5	2.1	9.00E-03	component of oligomeric golgi complex 5
A_23_P105535	POC1B	2.1	8.80E-03	POC1 centriolar protein homolog B (Chlamydomonas)
A_24_P103886	IDI1	2.1	8.10E-03	isopentenyl-diphosphate delta isomerase 1
A_33_P3259423	WDR55	2.1	6.80E-03	WD repeat domain 55
A_23_P359647	NFAT5	2.1	5.50E-03	nuclear factor of activated T-cells 5, tonicity-responsive
A_23_P133691	RRAGD	2	1.30E-02	Ras-related GTP binding D
A_24_P48204	SECTM1	2	1.60E-02	secreted and transmembrane 1
A_23_P144384	GALNT7	2	1.70E-02	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)
A_24_P277295	RAB43	2	1.60E-02	RAB43, member RAS oncogene family
A_23_P19592	PGM3	2	9.90E-03	phosphoglucomutase 3
A_33_P3256391	CRB3	2	6.90E-03	crumbs homolog 3 (Drosophila)

A_24_P332623	CTAGE11P	2	6.80E-03	CTAGE family, member 11, pseudogene
A_23_P118493	TOM1L1	2	5.50E-03	target of myb1 (chicken)-like 1
A_23_P44166	DCXR	2	9.10E-03	dicarbonyl/L-xylulose reductase
A_33_P3387155	LOC374443	2	1.10E-02	CLR pseudogene
A_23_P54517	TYRO3	2	6.20E-03	TYRO3 protein tyrosine kinase
A_23_P313632	FUT8	2	1.50E-02	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
A_24_P57528	SLC39A11	2	1.30E-02	solute carrier family 39 (metal ion transporter), member 11
A_33_P3245439	CD40	2	8.80E-03	CD40 molecule, TNF receptor superfamily member 5
A_33_P3338121	LAMB3	2	1.20E-02	laminin, beta 3
A_24_P37441	PK1	2	1.00E-02	pyruvate dehydrogenase kinase, isozyme 1
A_23_P210253	DGKD	2	1.50E-02	diacylglycerol kinase, delta 130kDa
A_33_P3280531	CRAT	2	1.30E-02	carnitine O-acetyltransferase
A_23_P62932	ATP1B1	2	1.50E-02	ATPase, Na+/K+ transporting, beta 1 polypeptide
A_23_P349083	FCHO2	2	7.30E-03	FCH domain only 2
A_23_P94301	TSTA3	2	1.20E-02	tissue specific transplantation antigen P35B
A_33_P3245183	HRH1	2	6.20E-03	histamine receptor H1
A_24_P146892	ORAI1	2	7.90E-03	ORAI calcium release-activated calcium modulator 1
A_23_P333218	ERGIC1	2	8.10E-03	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1
A_33_P3278347	C21orf88	2	5.50E-03	chromosome 21 open reading frame 88
A_23_P65481	TEP1	1.9	8.70E-03	telomerase-associated protein 1
A_23_P160240	ACP6	1.9	1.20E-02	acid phosphatase 6, lysophosphatidic
A_23_P19938	KDEL2	1.9	7.20E-03	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
A_23_P211252	LSS	1.9	1.30E-02	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
A_23_P43255	FAM49B	1.9	1.40E-02	family with sequence similarity 49, member B
A_23_P44139	PRIM2	1.9	9.50E-03	primase, DNA, polypeptide 2 (58kDa)
A_33_P3362088	P2RX4	1.9	9.20E-03	purinergic receptor P2X, ligand-gated ion channel, 4
A_23_P135742	C1orf170	1.9	9.90E-03	chromosome 1 open reading frame 170
A_23_P159382	SEC24D	1.9	1.10E-02	SEC24 family, member D (S.

				cerevisiae)
A_23_P65651	WARS	1.9	6.80E-03	tryptophanyl-tRNA synthetase
A_23_P306105	GALNT1	1.9	1.50E-02	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)
A_23_P120845	XBP1	1.9	1.60E-02	X-box binding protein 1
A_24_P185314	NAPG	1.9	9.60E-03	N-ethylmaleimide-sensitive factor attachment protein, gamma
A_23_P64828	OAS1	1.9	1.40E-02	2'-5'-oligoadenylate synthetase 1, 40/46kDa
A_24_P167642	GCH1	1.9	1.40E-02	GTP cyclohydrolase 1
A_24_P915007	NACC1	1.9	6.90E-03	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing
A_24_P563545	SLC30A7	1.9	1.50E-02	solute carrier family 30 (zinc transporter), member 7
A_23_P210330	LGALSL	1.9	1.00E-02	lectin, galactoside-binding-like
A_32_P52911	ADI1	1.9	1.30E-02	acireductone dioxygenase 1
A_33_P3412479	HPS1	1.9	9.70E-03	Hermansky-Pudlak syndrome 1
A_23_P432360	PMM2	1.9	9.20E-03	phosphomannomutase 2
A_23_P408108	MTERF	1.9	1.00E-02	mitochondrial transcription termination factor
A_23_P63798	KLF6	1.9	1.70E-02	Kruppel-like factor 6
A_23_P126167	KCNN3	1.9	1.50E-02	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3
A_23_P32404	ISG20	1.9	1.70E-02	interferon stimulated exonuclease gene 20kDa
A_33_P3217465	MID1IP1	1.9	6.80E-03	MID1 interacting protein 1
A_23_P327519	STARD4	1.9	1.60E-02	StAR-related lipid transfer (START) domain containing 4
A_23_P132915	FAM114A1	1.9	1.30E-02	family with sequence similarity 114, member A1
A_33_P3274696	SLC52A2	1.9	1.50E-02	solute carrier family 52, riboflavin transporter, member 2
A_23_P212458	SEC61A1	1.9	9.30E-03	Sec61 alpha 1 subunit (S. cerevisiae)
A_23_P258393	PPM1M	1.8	1.30E-02	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1M
A_23_P630	MSTO1	1.8	1.70E-02	misato homolog 1 (Drosophila)
A_23_P256542	FAM162A	1.8	9.60E-03	family with sequence similarity 162, member A
A_23_P86943	SRPR	1.8	1.40E-02	signal recognition particle receptor (docking protein)
A_24_P202717	PLEKHJ1	1.8	1.70E-02	pleckstrin homology domain containing, family J member 1

A_32_P129752	TMEM30B	1.8	9.40E-03	transmembrane protein 30B
A_23_P314584	MAPKAPK3	1.8	1.30E-02	mitogen-activated protein kinase-activated protein kinase 3
A_23_P130531	CDC37	1.8	7.50E-03	cell division cycle 37 homolog (S. cerevisiae)
A_23_P42718	NFE2L3	1.8	9.90E-03	nuclear factor (erythroid-derived 2)-like 3
A_23_P55998	SLC1A5	1.8	9.20E-03	solute carrier family 1 (neutral amino acid transporter), member 5
A_23_P25684	RDH11	1.8	1.00E-02	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)
A_33_P3350413	SVIL	1.8	1.60E-02	supervillin
A_23_P151870	GLCE	1.8	1.10E-02	glucuronic acid epimerase
A_24_P916718	ZNF467	1.8	1.50E-02	zinc finger protein 467
A_23_P56228	GMIP	1.8	1.40E-02	GEM interacting protein
A_23_P205389	MOAP1	1.8	9.20E-03	modulator of apoptosis 1
A_23_P106898	ORAI3	1.8	1.60E-02	ORAI calcium release-activated calcium modulator 3
A_23_P45560	GPR143	1.8	1.70E-02	G protein-coupled receptor 143
A_23_P402952	CTAGE15P	1.8	1.70E-02	CTAGE family, member 15, pseudogene
A_23_P160720	BATF3	1.8	1.60E-02	basic leucine zipper transcription factor, ATF-like 3
A_33_P3279158	NBPF6	1.8	1.40E-02	neuroblastoma breakpoint family, member 6
A_23_P117163	RCBTB1	1.8	1.30E-02	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1
A_24_P48898	APOL2	1.8	1.50E-02	apolipoprotein L, 2
A_33_P3389153	STK10	1.8	1.30E-02	serine/threonine kinase 10
A_24_P832156	FAM120AOS	1.8	7.20E-03	family with sequence similarity 120A opposite strand
A_23_P169178	TESK1	1.8	1.40E-02	testis-specific kinase 1
A_23_P165783	MLPH	1.8	1.00E-02	melanophilin
A_33_P3395369	AMD1	1.8	1.50E-02	adenosylmethionine decarboxylase 1
A_23_P135857	EIF2AK3	1.8	1.30E-02	eukaryotic translation initiation factor 2-alpha kinase 3
A_23_P431789	ARF4	1.8	1.10E-02	ADP-ribosylation factor 4
A_23_P210900	ACSS2	1.8	8.10E-03	acyl-CoA synthetase short-chain family member 2
A_32_P208120	CAMK1D	1.8	7.90E-03	calcium/calmodulin-dependent protein kinase ID
A_23_P66948	FAM59A	1.8	9.30E-03	family with sequence similarity 59, member A
A_33_P3209646	WDFY2	1.8	1.20E-02	WD repeat and FYVE domain containing 2

A_32_P95223	FDPSL2A	1.8	9.20E-03	MGC44478
A_24_P167473	ARPC3	1.7	8.70E-03	actin related protein 2/3 complex, subunit 3, 21kDa
A_24_P722216	DHTKD1	1.7	8.70E-03	dehydrogenase E1 and transketolase domain containing 1
A_23_P202587	KIAA1598	1.7	1.00E-02	KIAA1598
A_33_P3229288	ACE	1.7	1.30E-02	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1
A_24_P100517	SAPCD2	1.7	1.60E-02	suppressor APC domain containing 2
A_23_P137035	PIR	1.7	1.40E-02	pirin (iron-binding nuclear protein)
A_33_P3307886	TBXA2R	1.7	1.00E-02	thromboxane A2 receptor
A_23_P39237	ZFP36	1.7	1.30E-02	zinc finger protein 36, C3H type, homolog (mouse)
A_24_P301557	LPIN2	1.7	1.60E-02	lipin 2
A_24_P414376	KLF3	1.7	1.50E-02	Kruppel-like factor 3 (basic)
A_24_P288424	SLMO2	1.7	9.00E-03	slowmo homolog 2 (Drosophila)
A_23_P20035	GPR146	1.7	1.20E-02	G protein-coupled receptor 146
A_24_P356601	HEXIM1	1.7	1.40E-02	hexamethylene bis-acetamide inducible 1
A_23_P79999	ENTPD6	1.7	1.70E-02	ectonucleoside triphosphate diphosphohydrolase 6 (putative)
A_33_P3508717	LOC729678	1.7	1.20E-02	uncharacterized LOC729678
A_23_P121716	ANXA3	1.7	1.00E-02	annexin A3
A_33_P3602006	ADAT2	1.7	1.70E-02	adenosine deaminase, tRNA- specific 2
A_24_P194154	UPF1	1.7	1.00E-02	UPF1 regulator of nonsense transcripts homolog (yeast)
A_24_P277657	GMPR	1.7	1.70E-02	guanosine monophosphate reductase
A_23_P256205	ABLIM3	1.7	9.20E-03	actin binding LIM protein family, member 3
A_24_P114183	FDPS	1.7	1.50E-02	farnesyl diphosphate synthase
A_24_P99216	LRP10	1.7	1.70E-02	low density lipoprotein receptor- related protein 10
A_33_P3340490	FLJ46906	1.7	1.30E-02	uncharacterized LOC441172
A_23_P253421	AUP1	1.7	9.40E-03	ancient ubiquitous protein 1
A_23_P211522	SYNGR1	1.7	1.30E-02	synaptogyrin 1
A_33_P3244803	ACOX1	1.7	1.30E-02	acyl-CoA oxidase 1, palmitoyl
A_33_P3289286	TMEM57	1.7	1.50E-02	transmembrane protein 57
A_24_P132787	RAB18	1.7	1.30E-02	RAB18, member RAS oncogene family
A_23_P160729	AP4B1	1.7	9.80E-03	adaptor-related protein complex 4, beta 1 subunit
A_23_P78980	B3GNT3	1.7	1.60E-02	UDP-GlcNAc:betaGal beta-1,3-N- acetylglucosaminyltransferase 3

A_23_P2181	CYB5R2	1.7	1.50E-02	cytochrome b5 reductase 2
A_23_P156842	EEF1E1	1.7	1.60E-02	eukaryotic translation elongation factor 1 epsilon 1
A_24_P198629	LINS	1.7	1.30E-02	lines homolog (Drosophila)
A_24_P231494	DNPEP	1.7	1.60E-02	aspartyl aminopeptidase
A_23_P416894	PION	1.7	1.40E-02	pigeon homolog (Drosophila)
A_23_P106922	CHST6	1.6	1.70E-02	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6
A_23_P29257	H1F0	1.6	1.30E-02	H1 histone family, member 0
A_23_P2884	PIGH	1.6	1.60E-02	phosphatidylinositol glycan anchor biosynthesis, class H
A_33_P3422113	ZSCAN12P1	1.6	1.60E-02	zinc finger and SCAN domain containing 12 pseudogene 1
A_24_P29595	STXBP5	1.6	1.30E-02	syntaxin binding protein 5 (tomosyn)
A_24_P181585	LRRC59	1.6	1.00E-02	leucine rich repeat containing 59
A_24_P91852	DYNLT3	1.6	1.70E-02	dynein, light chain, Tctex-type 3
A_23_P19517	ITPR3	1.6	1.20E-02	inositol 1,4,5-trisphosphate receptor, type 3
A_24_P40229	CRNKL1	1.6	1.30E-02	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)
A_33_P3345936	CCDC9	1.6	1.60E-02	coiled-coil domain containing 9
A_24_P233915	MED8	1.6	1.00E-02	mediator complex subunit 8
A_24_P673786	PIP4K2A	1.6	1.40E-02	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha
A_23_P20777	RBM18	1.6	1.10E-02	RNA binding motif protein 18
A_24_P355267	SLC25A25	1.6	1.50E-02	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25
A_23_P145376	MAPK13	1.6	1.70E-02	mitogen-activated protein kinase 13
A_23_P91114	PREB	1.6	1.20E-02	prolactin regulatory element binding
A_32_P46981	HSBP1L1	1.6	1.40E-02	heat shock factor binding protein 1-like 1
A_23_P208009	SEC11C	1.6	1.60E-02	SEC11 homolog C (S. cerevisiae)
A_23_P15714	NSF	1.6	1.50E-02	N-ethylmaleimide-sensitive factor
A_23_P28969	CHMP4B	1.6	1.50E-02	charged multivesicular body protein 4B
A_23_P120316	MTHFD2	1.6	1.50E-02	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
A_23_P129486	MSRB1	1.6	1.50E-02	methionine sulfoxide reductase B1
A_32_P197621	GEMIN8P4	1.6	1.40E-02	gem (nuclear organelle) associated protein 8 pseudogene 4

A_23_P428842	TMEM44	1.6	1.50E-02	transmembrane protein 44
A_24_P20120	CCDC88A	1.6	1.20E-02	coiled-coil domain containing 88A
A_24_P248606	ACSL3	1.6	1.40E-02	acyl-CoA synthetase long-chain family member 3
A_23_P122216	LOX	1.6	1.60E-02	lysyl oxidase
A_23_P47790	METTL1	1.6	1.50E-02	methyltransferase like 1
A_23_P107036	TMEM11	1.6	1.50E-02	transmembrane protein 11
A_23_P204395	AACS	1.5	1.40E-02	acetoacetyl-CoA synthetase
A_24_P500891	AK2	1.5	1.70E-02	adenylate kinase 2
A_23_P147845	PDXDC1	1.5	1.60E-02	pyridoxal-dependent decarboxylase domain containing 1
A_23_P132936	SPCS3	1.5	1.50E-02	signal peptidase complex subunit 3 homolog (<i>S. cerevisiae</i>)
A_23_P115573	SHISA4	1.5	1.70E-02	shisa homolog 4 (<i>Xenopus laevis</i>)
A_33_P3230709	KIF1C	1.5	1.70E-02	kinesin family member 1C
A_33_P3424861	FAM118A	1.5	1.70E-02	family with sequence similarity 118, member A
A_23_P319133	DNAJC10	1.5	1.70E-02	DnaJ (Hsp40) homolog, subfamily C, member 10
A_23_P204702	TMBIM6	1.5	1.70E-02	transmembrane BAX inhibitor motif containing 6
A_23_P358995	IBTK	1.5	1.70E-02	inhibitor of Bruton agammaglobulinemia tyrosine kinase
A_23_P106822	NOB1	0.7	1.70E-02	NIN1/RPN12 binding protein 1 homolog (<i>S. cerevisiae</i>)
A_33_P3237634	TSC22D3	0.7	1.60E-02	TSC22 domain family, member 3
A_33_P3261869	NPM2	0.6	1.40E-02	nucleophosmin/nucleoplasmin 2
A_23_P109269	LAMA5	0.6	1.60E-02	laminin, alpha 5
A_24_P876408	C11orf95	0.6	1.70E-02	chromosome 11 open reading frame 95
A_23_P206441	FANCA	0.6	1.60E-02	Fanconi anemia, complementation group A
A_33_P3360540	AGPAT2	0.6	1.70E-02	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
A_23_P427217	JMJD1C	0.6	1.50E-02	jumonji domain containing 1C
A_33_P3260307	CARHSP1	0.6	1.30E-02	calcium regulated heat stable protein 1, 24kDa
A_23_P253524	CENPE	0.6	1.50E-02	centromere protein E, 312kDa
A_32_P26376	POGLUT1	0.6	1.10E-02	protein O-glucosyltransferase 1
A_23_P408955	E2F2	0.6	1.70E-02	E2F transcription factor 2
A_24_P119685	OBSCN	0.6	1.50E-02	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
A_32_P205110	FOXC1	0.6	1.50E-02	forkhead box C1
A_23_P124742	CHKA	0.6	1.10E-02	choline kinase alpha

A_23_P25873	WDHD1	0.6	1.50E-02	WD repeat and HMG-box DNA binding protein 1
A_24_P252996	FOLR3	0.6	1.30E-02	folate receptor 3 (gamma)
A_23_P7582	TCF7	0.6	1.50E-02	transcription factor 7 (T-cell specific, HMG-box)
A_23_P82913	TRMT12	0.6	1.30E-02	tRNA methyltransferase 12 homolog (S. cerevisiae)
A_23_P125265	KPNA2	0.6	9.70E-03	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
A_23_P87769	PARPBP	0.6	1.40E-02	PARP1 binding protein
A_33_P3227788	PANK1	0.6	9.50E-03	pantothenate kinase 1
A_23_P129466	ATF7IP2	0.6	1.50E-02	activating transcription factor 7 interacting protein 2
A_23_P31453	STEAP1	0.6	1.50E-02	six transmembrane epithelial antigen of the prostate 1
A_32_P3476	RPRML	0.6	1.00E-02	reprimo-like
A_23_P7791	OGFRL1	0.6	1.40E-02	opioid growth factor receptor-like 1
A_33_P3326285	GAS5	0.6	1.20E-02	growth arrest-specific 5 (non-protein coding)
A_32_P41553	C1orf182	0.6	1.70E-02	chromosome 1 open reading frame 182
A_23_P66241	MT1M	0.6	1.50E-02	metallothionein 1M
A_23_P357794	MTBP	0.6	1.30E-02	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa
A_23_P107744	S1PR5	0.6	1.20E-02	sphingosine-1-phosphate receptor 5
A_23_P377860	C21orf128	0.6	1.50E-02	chromosome 21 open reading frame 128
A_23_P48585	SALL2	0.6	7.10E-03	sal-like 2 (Drosophila)
A_23_P133956	KIFC1	0.5	1.70E-02	kinesin family member C1
A_24_P239606	GADD45B	0.5	1.50E-02	growth arrest and DNA-damage-inducible, beta
A_24_P53976	GLUL	0.5	1.30E-02	glutamate-ammonia ligase
A_33_P3319625	NFIA	0.5	1.60E-02	nuclear factor I/A
A_33_P3280927	SNHG7	0.5	1.20E-02	small nucleolar RNA host gene 7 (non-protein coding)
A_32_P221799	HIST1H2AM	0.5	1.40E-02	histone cluster 1, H2am
A_23_P156907	SOBP	0.5	9.50E-03	sine oculis binding protein homolog (Drosophila)
A_23_P67569	LPPR3	0.5	1.70E-02	lipid phosphate phosphatase-related protein type 3
A_23_P101505	KLK11	0.5	1.60E-02	kallikrein-related peptidase 11
A_24_P383609	NANOS1	0.5	1.50E-02	nanos homolog 1 (Drosophila)
A_23_P151150	FOXM1	0.5	9.00E-03	forkhead box M1
A_23_P502654	SHMT1	0.5	1.30E-02	serine hydroxymethyltransferase 1

				(soluble)
A_33_P3248794	NAB2	0.5	8.50E-03	NGFI-A binding protein 2 (EGR1 binding protein 2)
A_23_P50426	KANK2	0.5	9.00E-03	KN motif and ankyrin repeat domains 2
A_24_P50753	NUDT4	0.5	1.50E-02	nudix (nucleoside diphosphate linked moiety X)-type motif 4
A_23_P151529	C14orf132	0.5	9.70E-03	chromosome 14 open reading frame 132
A_33_P3335725	INSR	0.5	1.40E-02	insulin receptor
A_23_P7636	PTTG1	0.5	7.10E-03	pituitary tumor-transforming 1
A_33_P3269218	BAI2	0.5	1.70E-02	brain-specific angiogenesis inhibitor 2
A_23_P110802	CENPH	0.5	1.30E-02	centromere protein H
A_23_P217297	ZNF711	0.5	1.30E-02	zinc finger protein 711
A_32_P83845	HEY1	0.5	9.30E-03	hairy/enhancer-of-split related with YRPW motif 1
A_23_P501831	C5orf4	0.5	1.50E-02	chromosome 5 open reading frame 4
A_24_P108301	RTTN	0.5	1.50E-02	rotatin
A_23_P115482	UBE2T	0.5	1.50E-02	ubiquitin-conjugating enzyme E2T (putative)
A_24_P215765	ATP10A	0.5	1.10E-02	ATPase, class V, type 10A
A_23_P202810	OVOL1	0.5	1.60E-02	ovo-like 1(Drosophila)
A_23_P19663	CTGF	0.5	1.60E-02	connective tissue growth factor
A_23_P74088	MMP23B	0.5	9.30E-03	matrix metalloproteinase 23B
A_23_P375	CDCA8	0.5	1.30E-02	cell division cycle associated 8
A_23_P256956	KIF20A	0.5	1.00E-02	kinesin family member 20A
A_23_P68610	TPX2	0.5	7.20E-03	TPX2, microtubule-associated, homolog (Xenopus laevis)
A_23_P53588	WNT5B	0.5	5.50E-03	wingless-type MMTV integration site family, member 5B
A_23_P48936	SMAD3	0.5	1.20E-02	SMAD family member 3
A_33_P3397399	PPP3CB	0.5	1.00E-02	protein phosphatase 3, catalytic subunit, beta isozyme
A_23_P134835	CSGALNACT1	0.5	1.60E-02	chondroitin sulfate N-acetylgalactosaminyltransferase 1
A_33_P3296587	CP	0.5	6.90E-03	ceruloplasmin (ferroxidase)
A_23_P168761	PTPRZ1	0.5	5.70E-03	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
A_33_P3287939	C7orf46	0.5	1.60E-02	chromosome 7 open reading frame 46
A_33_P3236868	MT1X	0.5	7.10E-03	metallothionein 1X
A_32_P447001	FLJ27352	0.5	8.20E-03	uncharacterized LOC145788
A_33_P3355503	FOXL1	0.5	1.30E-02	forkhead box L1

A_24_P408047	PLEKHA4	0.5	9.80E-03	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4
A_33_P3381666	ABLM2	0.5	1.50E-02	actin binding LIM protein family, member 2
A_33_P3716128	SMC4	0.5	1.20E-02	structural maintenance of chromosomes 4
A_23_P500501	FGFR3	0.5	1.30E-02	fibroblast growth factor receptor 3
A_23_P76488	EMP1	0.5	1.50E-02	epithelial membrane protein 1
A_23_P107421	TK1	0.5	6.30E-03	thymidine kinase 1, soluble
A_33_P3384775	ZNF295	0.5	1.60E-02	zinc finger protein 295
A_33_P3262665	MAP7D3	0.5	8.10E-03	MAP7 domain containing 3
A_23_P434919	RAB42	0.5	1.60E-02	RAB42, member RAS oncogene family
A_33_P3313785	CCDC14	0.5	1.30E-02	coiled-coil domain containing 14
A_23_P104464	ALOX5	0.5	1.00E-02	arachidonate 5-lipoxygenase
A_23_P411296	CEBPB	0.5	6.80E-03	CCAAT/enhancer binding protein (C/EBP), beta
A_32_P96036	MEX3A	0.5	8.80E-03	mex-3 homolog A (C. elegans)
A_23_P110941	GSTA4	0.5	1.20E-02	glutathione S-transferase alpha 4
A_24_P381199	TRIM6	0.5	9.60E-03	tripartite motif containing 6
A_23_P134237	RARRES2	0.5	8.80E-03	retinoic acid receptor responder (tazarotene induced) 2
A_23_P24129	DKK1	0.5	1.10E-02	dickkopf 1 homolog (Xenopus laevis)
A_33_P3390187	NHLRC4	0.5	1.60E-02	NHL repeat containing 4
A_23_P5370	RPRM	0.5	7.90E-03	reprimin, TP53 dependent G2 arrest mediator candidate
A_33_P3344492	SCARNA1	0.5	1.00E-02	small Cajal body-specific RNA 1
A_33_P3317523	STMN1	0.4	7.30E-03	stathmin 1
A_32_P151800	FAM72D	0.4	1.40E-02	family with sequence similarity 72, member D
A_23_P18579	PTTG2	0.4	1.20E-02	pituitary tumor-transforming 2
A_32_P211045	DHFR	0.4	1.20E-02	dihydrofolate reductase
A_23_P349463	CHP2	0.4	1.70E-02	calcineurin B homologous protein 2
A_23_P25030	HSD17B6	0.4	3.70E-03	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)
A_33_P3314176	FAM46C	0.4	4.80E-03	family with sequence similarity 46, member C
A_23_P143981	FBLN2	0.4	1.20E-02	fibulin 2
A_23_P156861	RGS17	0.4	9.20E-03	regulator of G-protein signaling 17
A_23_P218626	NEU4	0.4	7.20E-03	sialidase 4
A_24_P281872	CXorf27	0.4	7.10E-03	chromosome X open reading frame 27

A_24_P11436	TTC22	0.4	6.50E-03	tetratricopeptide repeat domain 22
A_33_P3245290	AQP7P1	0.4	6.30E-03	aquaporin 7 pseudogene 1
A_23_P252740	DSCC1	0.4	1.50E-02	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
A_23_P334218	WDR67	0.4	6.80E-03	WD repeat domain 67
A_33_P3289296	TMEM37	0.4	7.30E-03	transmembrane protein 37
A_24_P226210	CEP120	0.4	6.80E-03	centrosomal protein 120kDa
A_23_P53126	LMO2	0.4	1.10E-02	LIM domain only 2 (rhombotin-like 1)
A_23_P133123	MND1	0.4	1.60E-02	meiotic nuclear divisions 1 homolog (S. cerevisiae)
A_33_P3374478	CASC4	0.4	1.60E-02	cancer susceptibility candidate 4
A_23_P8981	STAR	0.4	7.30E-03	steroidogenic acute regulatory protein
A_23_P395632	R3HDML	0.4	1.10E-02	R3H domain containing-like
A_24_P38347	DPYSL2	0.4	6.80E-03	dihydropyrimidinase-like 2
A_33_P3214159	CDH2	0.4	1.60E-02	cadherin 2, type 1, N-cadherin (neuronal)
A_23_P340263	RNF175	0.4	9.00E-03	ring finger protein 175
A_23_P436284	OSTBETA	0.4	1.70E-02	organic solute transporter beta
A_23_P215956	MYC	0.4	7.20E-03	v-myc myelocytomatosis viral oncogene homolog (avian)
A_24_P944049	CEP68	0.4	9.00E-03	centrosomal protein 68kDa
A_23_P71727	CKS2	0.4	1.30E-02	CDC28 protein kinase regulatory subunit 2
A_23_P54556	MKL2	0.4	9.00E-03	MKL/myocardin-like 2
A_23_P150281	TP53I11	0.4	4.50E-03	tumor protein p53 inducible protein 11
A_23_P122197	CCNB1	0.4	1.00E-02	cyclin B1
A_23_P134663	BAALC	0.4	1.40E-02	brain and acute leukemia, cytoplasmic
A_33_P3304983	PRKAR2B	0.4	9.50E-03	protein kinase, cAMP-dependent, regulatory, type II, beta
A_23_P50108	NDC80	0.4	3.40E-03	NDC80 kinetochore complex component homolog (S. cerevisiae)
A_32_P62997	PBK	0.4	1.60E-02	PDZ binding kinase
A_33_P3807062	HJURP	0.4	9.00E-03	Holliday junction recognition protein
A_33_P3219641	CEP78	0.4	1.20E-02	centrosomal protein 78kDa
A_23_P257971	AKR1C1	0.4	9.80E-03	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
A_33_P3344243	C4orf46	0.4	7.20E-03	chromosome 4 open reading frame 46
A_33_P3332547	SCHIP1	0.4	6.20E-03	schwannomin interacting protein 1

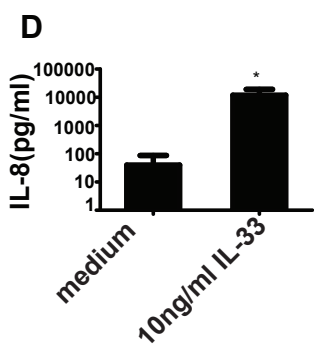
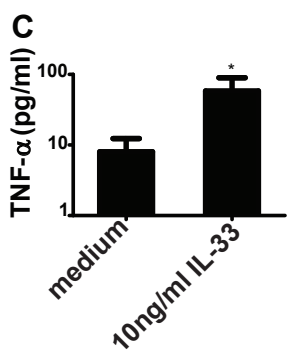
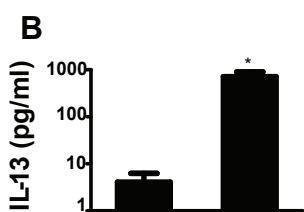
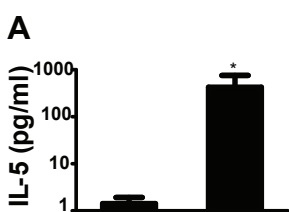
A_33_P3413741	OXTR	0.4	2.70E-03	oxytocin receptor
A_33_P3270657	FAM111B	0.4	7.80E-03	family with sequence similarity 111, member B
A_23_P19778	SLC13A4	0.4	1.30E-02	solute carrier family 13 (sodium/sulfate symporters), member 4
A_24_P184799	COCH	0.4	5.20E-03	coagulation factor C homolog, cochlin (Limulus polyphemus)
A_24_P322354	SKA1	0.4	1.50E-02	spindle and kinetochore associated complex subunit 1
A_24_P20630	LEF1	0.4	2.70E-03	lymphoid enhancer-binding factor 1
A_23_P102117	WNT10A	0.4	6.20E-03	wingless-type MMTV integration site family, member 10A
A_23_P413641	PREX1	0.4	1.30E-02	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1
A_23_P131676	CXCR7	0.4	5.50E-03	chemokine (C-X-C motif) receptor 7
A_33_P3278881	FLJ45340	0.4	1.30E-02	uncharacterized LOC402483
A_24_P274795	CDCA7L	0.4	1.10E-02	cell division cycle associated 7-like
A_23_P76234	RPH3A	0.4	1.50E-02	rabphilin 3A homolog (mouse)
A_23_P251421	CDCA7	0.4	1.50E-02	cell division cycle associated 7
A_23_P70448	HIST1H1A	0.4	6.20E-03	histone cluster 1, H1a
A_23_P258493	LMNB1	0.4	1.60E-02	lamin B1
A_33_P3274599	FAM138E	0.4	1.30E-02	family with sequence similarity 138, member E
A_23_P77908	SLC47A2	0.4	1.30E-02	solute carrier family 47, member 2
A_23_P57306	CHAF1B	0.4	1.30E-02	chromatin assembly factor 1, subunit B (p60)
A_33_P3313055	NOTCH3	0.4	9.00E-03	notch 3
A_24_P323598	ESCO2	0.4	3.20E-03	establishment of cohesion 1 homolog 2 (S. cerevisiae)
A_32_P116556	ZNF469	0.4	4.90E-03	zinc finger protein 469
A_33_P3596355	LOC644242	0.4	9.70E-03	uncharacterized LOC644242
A_23_P113572	CD19	0.4	7.90E-03	CD19 molecule
A_23_P115872	CEP55	0.4	6.80E-03	centrosomal protein 55kDa
A_23_P42282	C4B	0.4	9.20E-03	complement component 4B (Chido blood group)
A_23_P60387	NOTCH1	0.3	5.10E-03	notch 1
A_23_P121533	SPON2	0.3	4.10E-03	spondin 2, extracellular matrix protein
A_23_P118815	BIRC5	0.3	8.20E-03	baculoviral IAP repeat containing 5
A_33_P3220837	MAFB	0.3	7.10E-03	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
A_23_P167328	CD38	0.3	1.40E-02	CD38 molecule

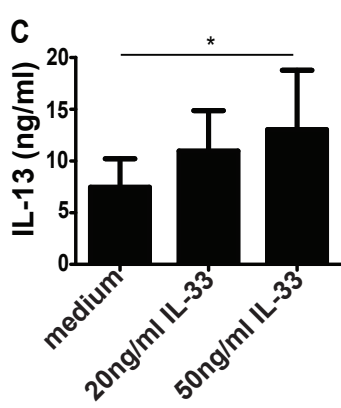
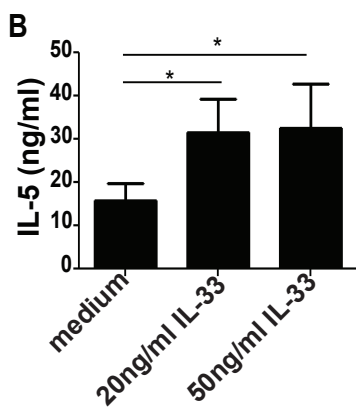
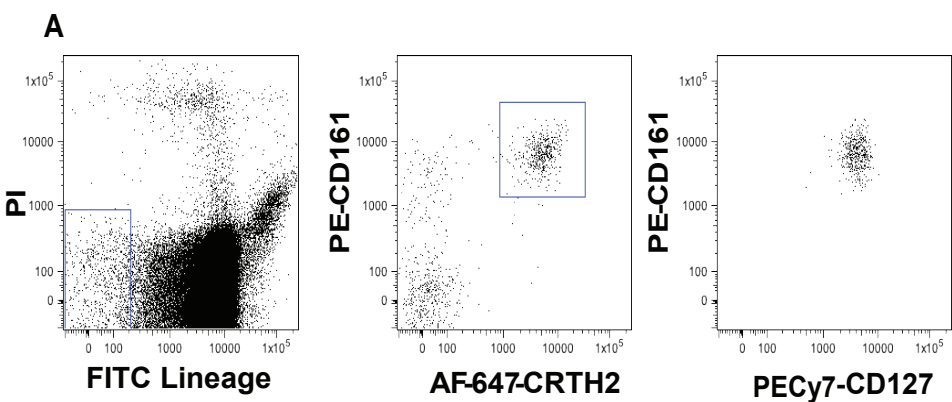
A_32_P61684	PAG1	0.3	1.00E-02	phosphoprotein associated with glycosphingolipid microdomains 1
A_33_P3332081	KHDRBS3	0.3	9.50E-03	KH domain containing, RNA binding, signal transduction associated 3
A_23_P258612	ATP8A2	0.3	1.70E-02	ATPase, aminophospholipid transporter, class I, type 8A, member 2
A_33_P3350488	NUSAP1	0.3	2.90E-03	nucleolar and spindle associated protein 1
A_33_P3400477	STIL	0.3	1.30E-02	SCL/TAL1 interrupting locus
A_33_P3288159	ASPM	0.3	1.20E-02	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
A_23_P214080	EGR1	0.3	1.40E-02	early growth response 1
A_23_P3681	NETO2	0.3	5.10E-03	neuropilin (NRP) and tolloid (TLL)-like 2
A_23_P385861	CDCA2	0.3	7.30E-03	cell division cycle associated 2
A_23_P65757	CCNB2	0.3	8.50E-03	cyclin B2
A_23_P94422	MELK	0.3	1.70E-02	maternal embryonic leucine zipper kinase
A_33_P3215239	KIF20B	0.3	1.20E-02	kinesin family member 20B
A_24_P129341	AKR1B10	0.3	7.20E-03	aldo-keto reductase family 1, member B10 (aldose reductase)
A_24_P462899	CENPW	0.3	1.20E-02	centromere protein W
A_33_P3269000	C8orf48	0.3	1.70E-02	chromosome 8 open reading frame 48
A_23_P104651	CDCA5	0.3	9.20E-03	cell division cycle associated 5
A_23_P253752	FAM54A	0.3	7.30E-03	family with sequence similarity 54, member A
A_23_P414654	RAB37	0.3	1.40E-02	RAB37, member RAS oncogene family
A_23_P74349	NUF2	0.3	1.70E-02	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
A_23_P60166	DEPTOR	0.3	3.20E-03	DEP domain containing MTOR-interacting protein
A_23_P216225	EGR3	0.3	1.20E-02	early growth response 3
A_33_P3409984	CDKL4	0.3	6.70E-03	cyclin-dependent kinase-like 4
A_23_P23292	RXRG	0.3	1.20E-02	retinoid X receptor, gamma
A_33_P3282390	GRM4	0.3	4.40E-03	glutamate receptor, metabotropic 4
A_33_P3279353	AZU1	0.3	3.50E-03	azurocidin 1
A_33_P3293598	LINC00410	0.3	1.50E-02	long intergenic non-protein coding RNA 410
A_23_P153964	INHBB	0.3	1.70E-03	inhibin, beta B
A_33_P3368945	LOC389332	0.3	8.50E-03	uncharacterized LOC389332
A_23_P163481	BUB1B	0.3	1.30E-02	budding uninhibited by

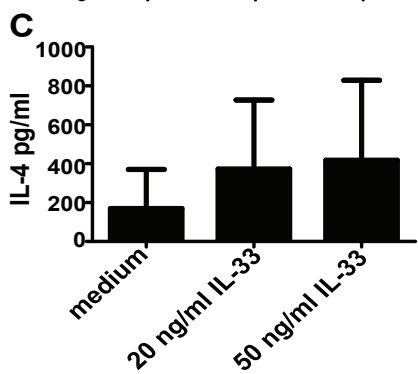
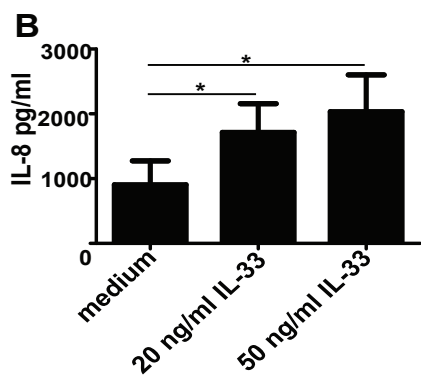
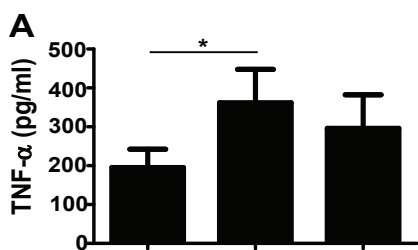
				benzimidazoles 1 homolog beta (yeast)
A_33_P3341499	WNT5A	0.3	6.80E-03	wingless-type MMTV integration site family, member 5A
A_23_P92860	CCNO	0.3	9.00E-03	cyclin O
A_24_P303145	ANKH	0.3	7.30E-03	ankylosis, progressive homolog (mouse)
A_24_P333697	KLK13	0.3	9.20E-03	kallikrein-related peptidase 13
A_23_P92441	MAD2L1	0.3	8.80E-03	MAD2 mitotic arrest deficient-like 1 (yeast)
A_23_P411335	SGOL2	0.3	1.30E-02	shugoshin-like 2 (S. pombe)
A_33_P3292769	NFAM1	0.3	1.00E-02	NFAT activating protein with ITAM motif 1
A_23_P111860	RADIL	0.3	5.70E-03	Ras association and DIL domains
A_33_P3380992	AKR1B15	0.3	6.90E-03	aldo-keto reductase family 1, member B15
A_33_P3327165	CCDC18	0.3	8.50E-03	coiled-coil domain containing 18
A_23_P103971	CYP4Z1	0.3	6.20E-03	cytochrome P450, family 4, subfamily Z, polypeptide 1
A_23_P156327	TGFBI	0.3	6.40E-03	transforming growth factor, beta-induced, 68kDa
A_23_P259586	TTK	0.3	9.60E-03	TTK protein kinase
A_23_P420281	PRKCB	0.3	8.80E-03	protein kinase C, beta
A_23_P159237	GPR20	0.3	1.50E-02	G protein-coupled receptor 20
A_32_P108889	DCLK1	0.3	1.50E-02	doublecortin-like kinase 1
A_23_P35871	E2F8	0.3	1.60E-02	E2F transcription factor 8
A_23_P88331	DLGAP5	0.3	8.70E-03	discs, large (Drosophila) homolog-associated protein 5
A_24_P500422	LOC730101	0.3	1.30E-02	uncharacterized LOC730101
A_24_P297539	UBE2C	0.3	7.30E-03	ubiquitin-conjugating enzyme E2C
A_23_P129133	OCA2	0.3	6.80E-03	oculocutaneous albinism II
A_23_P138507	CDK1	0.3	1.30E-02	cyclin-dependent kinase 1
A_33_P3214948	SPOCK2	0.3	7.20E-03	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2
A_23_P379614	OIP5	0.3	7.20E-03	Opa interacting protein 5
A_33_P3265359	HES6	0.3	1.50E-02	hairy and enhancer of split 6 (Drosophila)
A_24_P112941	LINGO1	0.3	1.10E-02	leucine rich repeat and Ig domain containing 1
A_33_P3355538	CERKL	0.3	2.60E-03	ceramide kinase-like
A_23_P392317	DLGAP2	0.3	1.40E-02	discs, large (Drosophila) homolog-associated protein 2
A_24_P792124	SCN9A	0.3	5.10E-03	sodium channel, voltage-gated, type IX, alpha subunit
A_23_P66481	RTN4RL1	0.3	1.30E-02	reticulon 4 receptor-like 1

A_23_P96325	ERCC6L	0.2	1.40E-02	excision repair cross-complementing rodent repair deficiency, complementation group 6-like
A_33_P3422822	GJC2	0.2	7.30E-03	gap junction protein, gamma 2, 47kDa
A_23_P215634	IGFBP3	0.2	6.30E-03	insulin-like growth factor binding protein 3
A_23_P500010	KLK12	0.2	8.30E-03	kallikrein-related peptidase 12
A_32_P77098	TMEM200B	0.2	5.10E-03	transmembrane protein 200B
A_24_P296808	PNMAL1	0.2	1.50E-02	paraneoplastic Ma antigen family-like 1
A_23_P356684	ANLN	0.2	1.30E-02	anillin, actin binding protein
A_23_P430658	HEYL	0.2	5.10E-03	hairy/enhancer-of-split related with YRPW motif-like
A_33_P3214849	KDEL2	0.2	1.00E-02	KDEL (Lys-Asp-Glu-Leu) containing 2
A_33_P3230548	KIF14	0.2	9.50E-03	kinesin family member 14
A_23_P40989	USP13	0.2	1.50E-02	ubiquitin specific peptidase 13 (isopeptidase T-3)
A_23_P50096	TYMS	0.2	7.20E-03	thymidylate synthetase
A_33_P3306068	MYCL1	0.2	5.30E-03	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)
A_23_P212469	ENTPD3	0.2	3.70E-03	ectonucleoside triphosphate diphosphohydrolase 3
A_33_P3291484	ST8SIA4	0.2	1.10E-02	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
A_23_P10385	DTL	0.2	1.10E-02	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
A_33_P3352522	FLJ41484	0.2	2.70E-03	uncharacterized LOC650669
A_24_P706953	TMEM213	0.2	1.50E-02	transmembrane protein 213
A_23_P207507	ABCC3	0.2	1.50E-02	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
A_33_P3214550	CXCR2	0.2	1.40E-03	chemokine (C-X-C motif) receptor 2
A_23_P328740	NEURL3	0.2	1.60E-02	neuralized homolog 3 (Drosophila) pseudogene
A_33_P3234202	DNASE1L3	0.2	1.50E-02	deoxyribonuclease I-like 3
A_23_P35219	NEK2	0.2	5.50E-03	NIMA (never in mitosis gene a)-related kinase 2
A_23_P200310	DEPDC1	0.2	1.30E-02	DEP domain containing 1
A_33_P3362128	LOC100129029	0.2	1.60E-02	uncharacterized LOC100129029
A_32_P140030	FOXN4	0.2	5.50E-03	forkhead box N4
A_23_P124417	BUB1	0.2	1.20E-02	budding uninhibited by benzimidazoles 1 homolog (yeast)
A_23_P116942	LAG3	0.2	1.20E-02	lymphocyte-activation gene 3

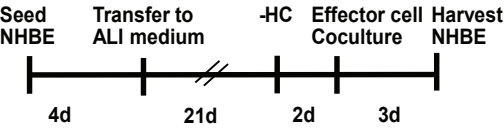
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A_23_P32165	LHX2	0.1	1.30E-02	LIM homeobox 2
A_23_P401606	EDIL3	0.1	7.10E-03	EGF-like repeats and discoidin I-like domains 3
A_24_P52697	H19	0.1	1.50E-02	H19, imprinted maternally expressed transcript (non-protein coding)
A_23_P139912	IGFBP6	0.1	1.50E-02	insulin-like growth factor binding protein 6
A_23_P166087	RASSF2	0.1	6.80E-03	Ras association (RalGDS/AF-6) domain family member 2



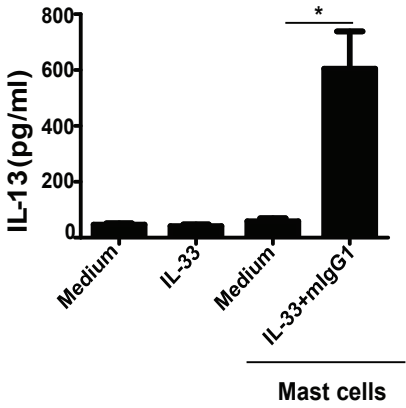




A



B



C

