

Guselkumab (an IL-23-specific mAb) demonstrates clinical and molecular response in patients with moderate-to-severe psoriasis[☆]

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Background: IL-23 expression is increased in psoriatic lesions and might regulate T_H17 T-cell counts in patients with psoriasis. **Objectives:** We sought to test a novel IL-23-specific therapeutic agent for the treatment of psoriasis.

Methods: In this randomized, double-blind, placebo-controlled study the safety, tolerability, and clinical response of guselkumab, an anti-IL-23-specific mAb, were evaluated in patients with moderate-to-severe plaque psoriasis. A total of 24 patients were randomized to receive a single dose of placebo or 10, 30, 100, or 300 mg of guselkumab. Clinical response was assessed by using the Psoriasis Area and Severity Index (PASI). Additionally, histologic analysis and gene expression in skin biopsy specimens from guselkumab-treated patients were compared with those from placebo-treated patients.

Results: At week 12, 50% (10 mg), 60% (30 and 100 mg), and 100% (300 mg) of guselkumab-treated patients, respectively, achieved a 75% improvement in PASI scores from baseline compared with 0% of placebo-treated patients. Improvements

in PASI scores were generally maintained through week 24 in all guselkumab-treated patients. The proportion of patients experiencing an adverse event was comparable between the combined guselkumab (13/20 [65.0%]) and placebo (2/4 [50.0%]) groups through week 24. Analysis of lesional and nonlesional skin biopsy specimens demonstrated decreases in epidermal thickness and T-cell and dendritic cell expression in guselkumab-treated patients compared with values seen in placebo-treated patients. At week 12, significant reductions in psoriasis gene expression and serum IL-17A levels were observed in guselkumab-treated patients.

Conclusion: IL-23 inhibition with a single dose of guselkumab results in clinical responses in patients with moderate-to-severe psoriasis, suggesting that neutralization of IL-23 alone is a promising therapy for psoriasis. (J Allergy Clin Immunol 2014;133:1032-40.)

Key words: Histology, IL-23, gene expression, guselkumab, psoriasis, Psoriasis Area and Severity Index, serum, skin, T cell, T_H17

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Psoriasis is the most common immune-mediated skin disorder.^{1,2} Psoriatic skin lesions contain increased infiltrates of T cells (T_H1, T_H17, and T_H22). Inflammatory CD11c⁺ dendritic cells (DCs) and macrophages in the skin become activated and release IL-12 and IL-23, which stimulate cytokine production from T cells. Epidermal T cells are responsible for secreting cytokines, including IFN-γ (T_H1), IL-17A and IL-17F (T_H17), IL-22 (T_H22), and TNF-α.³ The molecular disease profile of psoriasis, as defined by mRNA transcripts, contains hundreds of activated genes that can be linked to effects on individual or multiple cytokines.⁴ IFN-γ, IL-17A or IL-17F, and IL-22 have distinct effects on epidermal keratinocytes, which have been implicated as key regulators of psoriatic skin inflammation.³

IL-12 and IL-23 levels are increased in psoriatic lesions. It is believed that IL-12 modulates the excess T_H1 population, whereas IL-23 is the major regulator of T_H17 T cells. The role of IL-12/T_H1 T cells to sustain the psoriasis phenotype is debated because other inflammatory diseases thought to be T_H1-dependent proved to be IL-23/T_H17-mediated⁵ and because IL-17 antagonists can suppress the clinical, cellular, and molecular disease features of psoriasis.⁶ Conversely, the IL-23/T_H17 axis is hypothesized to be important in patients with psoriasis; however, IL-17 can also be produced in skin lesions independently of IL-23 by neutrophils and mast cells.⁷ Therefore,

Abbreviations used

AE:	Adverse event
DC:	Dendritic cell
IL-12R β 1:	IL-12 receptor β 1
IL-23R:	IL-23 receptor
KRT16:	Keratin 16
LCN2:	Lipocalin 2
PASI:	Psoriasis Area and Severity Index
PASI 75:	75% improvement in PASI score from baseline
PASI 90:	90% improvement in PASI score from baseline

the role of IL-23 in the pathogenesis of psoriasis can only be ascertained by means of selective antagonism of this cytokine.

IL-23 is a type 1 heterodimer comprised of p19 and p40 subunits that bind to the IL-23 receptor complex comprised of IL-23 receptor (IL-23R) and IL-12 receptor β 1 (IL-12R β 1). Binding of p19 (IL-23R) and p40 (IL-12R β 1) to their respective receptors activates the IL-23 signaling pathway in which IL-23R associates with Janus kinase 2 and IL-12R β 1 binds to tyrosine kinase 2 (Janus kinase protein).⁸ IL-23p19 and IL-12/23p40 mRNAs are strongly upregulated in human psoriatic lesions.⁹⁻¹¹ The main cellular source of IL-23 in psoriatic lesions appears to be myeloid DCs, which can be immature inflammatory cells or mature populations (DC-lysosomal-associated membrane proteins [LAMP]⁺^{12,13} or CD83⁺¹).

Guselkumab (CNTO 1959; Janssen Research & Development, LLC, Spring House, Pa) is an investigational human mAb specifically directed against IL-23. Here the proof-of-concept study of an anti-IL-23 mAb in patients with moderate-to-severe plaque psoriasis is reported. The objectives of this double-blind, placebo-controlled study were to assess the safety, tolerability, and clinical response to guselkumab in patients with moderate-to-severe plaque psoriasis. Histologic and gene expression studies of skin biopsy specimens were included in this study to evaluate which cellular and molecular disease features might be selectively regulated by IL-23 in patients with psoriasis.

METHODS

This phase 1, first-in-human, randomized, double-blind, placebo-controlled trial included 24 patients with moderate-to-severe plaque psoriasis and was conducted at 5 sites in the United States. Patient eligibility criteria are reported in the [Methods](#) section in this article's Online Repository at www.jacionline.org. All patients provided written informed consent, and institutional review boards/ethics committees approved the protocol.

Study design

At baseline, 24 patients were randomly assigned to receive subcutaneous injections of 10 mg (n = 5), 30 mg (n = 5), 100 mg (n = 5), or 300 mg (n = 5) of guselkumab or placebo (n = 4).

Study assessments

Safety and efficacy parameters were analyzed through week 24. Safety evaluations included adverse event (AE) assessments, vital sign measurements, electrocardiographic measurements, clinical laboratory tests, and physical examinations. Psoriasis Area and Severity Index (PASI) response measures the severity of psoriasis, ranging from a score of 0 (no psoriasis) to 72 (very severe).¹⁴ The proportion of patients achieving PASI responses was assessed through week 24.

Skin biopsy specimens

Two adjacent 4-mm punch biopsy specimens of lesional and nonlesional skin were obtained at baseline and at weeks 1 and 12 after treatment with guselkumab or placebo. One biopsy specimen from each site was embedded in OCT for cryosections, and the other was immediately snap-frozen in the dry ice/methanol slurry for RNA extraction. Both were stored at -80°C until analysis was performed.

Histology

Frozen skin tissue sections were prepared and analyzed by using methodology described previously.⁶

Gene expression

Skin biopsy specimens were processed and RT-PCR data were generated, as previously described.⁴ For microarray, RNA was hybridized to the GeneChip HT HG-U133+ PM Array (Affymetrix, Santa Clara, Calif). Expression measures were obtained by using the Robust Multi-array Average (RMA) algorithm.¹⁵ High-dose guselkumab was defined by combining samples from the 100- and 300-mg groups to increase analytic power. Comparison between baseline and posttreatment gene expression was also analyzed for each treatment group, excluding the 30-mg group because of smaller sample size (n < 5), to evaluate dose-associated trend. Raw data have been deposited in the National Center for Biotechnology Information's Gene Expression Omnibus (accession no. GSE51440).

Serum cytokine analysis

Serum was collected from patients receiving guselkumab or placebo at baseline and weeks 1 and 12 after treatment. IL-17A levels were measured with Singulex (Alameda, Calif) immunoassay kits. IFN- γ , IL-1 β , IL-6, TNF- α , IL-12p40, and IL-12p70 levels were measured with Meso Scale Discovery (Rockville, Md) kits. IL-8, IL-23p19, and CCL22 levels were measured with R&D Systems (Minneapolis, Minn) kits, and C-reactive protein levels were measured with a Life Diagnostics (West Chester, Pa) kit.

Statistical analysis

The number of patients was chosen to provide a preliminary safety and efficacy assessment of guselkumab. No formal sample size determination was undertaken. Only descriptive statistical methods were used to summarize the data (no formal hypothesis testing); however, a *post hoc* trend analysis using asymptotic and exact Cochran-Armitage trend tests were performed. Demographics, baseline disease characteristics, and the proportion of patients achieving 75% improvement in PASI scores from baseline (PASI 75) and 90% improvement in PASI scores from baseline (PASI 90) responses at each visit were summarized by treatment group.

RESULTS

Study population

Overall, the demographics and disease characteristics of guselkumab-treated patients were generally comparable among treatment groups and with those of placebo-treated patients (see [Table E1](#) in this article's Online Repository at www.jacionline.org); they were typical of patients with moderate-to-severe psoriasis and consistent with other studies of this patient population.

Neutralization of IL-23 improves clinical manifestations of psoriasis

Patients with psoriasis (n = 24) received a single subcutaneous injection of placebo or 10, 30, 100, or 300 mg of guselkumab.

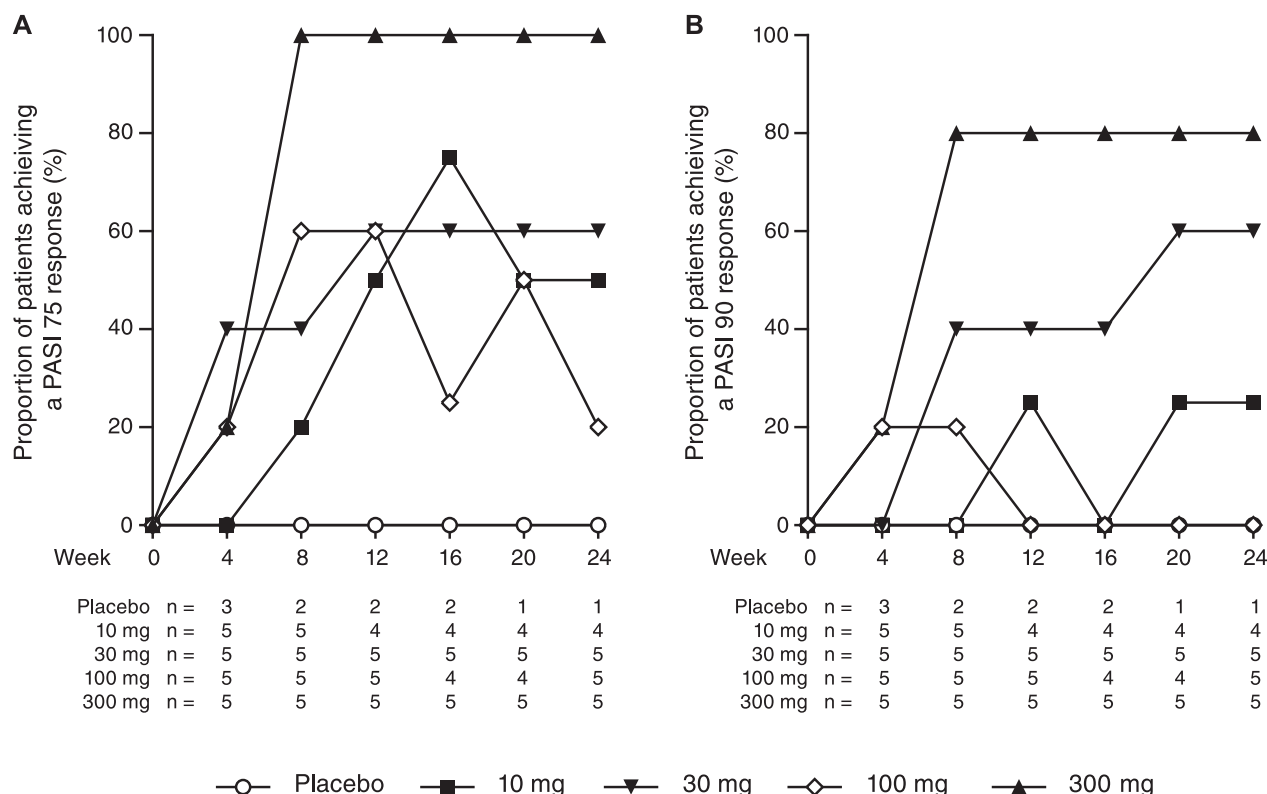


FIG 1. Proportion of patients achieving at least a 75% improvement in Psoriasis Area and Severity Index (PASI 75) response (**A**) or a PASI 90 response (**B**) from baseline to week 24.

Clinical response, as measured based on PASI response, was assessed through week 24. **Fig 1, A**, displays the proportion of patients achieving a PASI 75 response through week 24. At week 12, 50.0% (2/4) of patients in the 10-mg group, 60.0% (3/5) of patients in both the 30- and 100-mg groups, and 100% of patients (5/5) in the 300-mg group achieved PASI 75 responses (**Fig 1, A**). A *post hoc* trend analysis using the asymptotic or exact Cochran-Armitage trend test ($P = .0197$ and $P = .0241$, respectively) showed significant linear trend in the proportion of PASI 75 responses at week 12 with increasing dose levels. No patients in the placebo group achieved PASI 75 responses at any time point.

The proportion of patients achieving PASI 90 responses is displayed in **Fig 1, B**. At week 12, 25.0% of patients (1/4) in the 10-mg, 40.0% (2/5) in the 30-mg, 0.0% in the 100-mg, and 80.0% (4/5) in the 300-mg groups achieved PASI 90 responses compared with 0.0% in the placebo group. PASI responses were generally maintained through week 24, with the exception of the 100-mg dose group, in which initial high levels of response were lost over longer-term follow-up. Physician's global assessment scores were generally consistent with PASI responses over time (data not shown).

Clinical improvement in psoriatic lesions after guselkumab treatment is depicted in **Fig 2**. Two patients with comparable disease severity were treated with 2 different single doses of guselkumab, a lower dose (10 mg; **Fig 2, A**) and a higher dose (300 mg; **Fig 2, B**), and both patients achieved PASI 90 responses at week 12.

In general, guselkumab was well tolerated. Through week 24, 65.0% (13/20) of patients in the combined guselkumab groups

and 50% (2/4) in the placebo group experienced at least 1 AE (see **Table E2** in this article's Online Repository at www.jacionline.org). The most common AE was infection, with 6 patients experiencing a total of 9 infections. The infections were 2 events of upper respiratory tract infection and 1 report each of bronchitis, folliculitis, viral gastroenteritis, herpes simplex infection, lower respiratory tract infection, vaginal infection, and nasopharyngitis (data not shown). Although it is not possible to draw conclusions about the risk of infection associated with guselkumab based on this one small study, infections are a theoretic risk for any immunomodulating agent and will therefore continue to be monitored in future guselkumab studies.

No serious infections, malignancies, major adverse cardiovascular events, serious hypersensitivity reactions, or deaths were reported through week 24. This AE profile and overall comprehensive safety data suggest that guselkumab, when administered as a single subcutaneous injection, was well-tolerated.

Guselkumab eliminates pathologic cellular skin infiltrates in patients with psoriasis

Serum and skin biopsy specimens were collected before initiation of treatment (baseline) and at weeks 1 and 12 for analysis of disease-related biomarkers and histopathology. Changes in keratinocyte proliferation and leukocyte infiltration were measured to evaluate the extent to which IL-23 regulates psoriasis-specific disease features.

Immunohistochemistry was performed to determine the cellular composition of the biopsied skin tissue. At baseline, increases in T-cell counts (CD3), myeloid DC counts (CD11c),

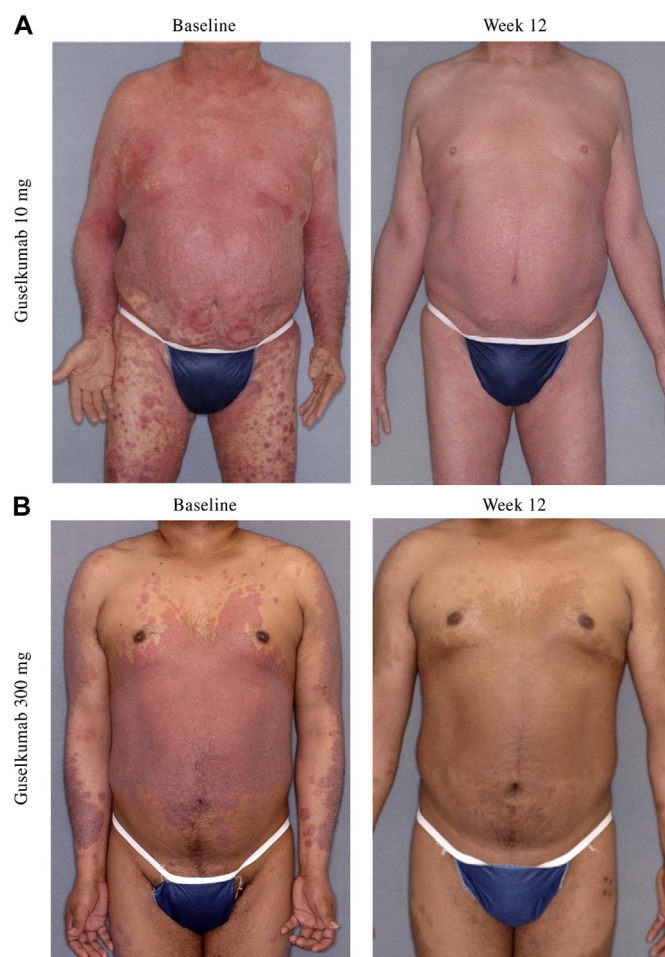


FIG 2. A, Clinical response to a single dose of 10 mg of guselkumab administered at baseline. B, Clinical response to a single dose of 300 mg of guselkumab administered at baseline.

and epidermal hyperplasia (hematoxylin and eosin and keratin 16 [KRT16]) were observed in lesional skin compared with values in nonlesional skin (Fig 3). At week 1, modest improvement was observed from baseline in epidermal thickness and in numbers of CD3⁺ or CD11c⁺ immune cells (Fig 4). At week 12, statistically significant reductions in epidermal thickness and T-cell and inflammatory CD11c⁺ DC counts were observed for each guselkumab dose group compared with baseline ($P < .05$ each), with the exception of DC counts in the 10-mg group ($P = .0723$, Fig 4). Langerhans cells, which are displaced in active psoriatic lesions, resumed a normal panepidermal pattern in guselkumab-treated biopsy specimens at week 12 (Fig 3). No reduction was observed in epidermal thickness or T-cell density in placebo-treated patients; however, a significant reduction from baseline in DC counts was observed for placebo at week 12 ($P = .0284$).

Guselkumab attenuates T_H17 molecular biomarkers in psoriatic skin

Skin tissue biopsy specimens were also evaluated for gene expression by using quantitative RT-PCR and microarray analysis (Fig 5). Fig 5, A, shows expression of KRT16, IFN- γ , IL-17F, and

lipocalin 2 (LCN2) mRNAs at baseline and week 12 from biopsy specimens of patients receiving placebo or high-dose guselkumab (100- and 300-mg groups combined). KRT16 expression was significantly decreased with guselkumab treatment to levels less than those observed in nonlesional skin. IFN- γ mRNA levels increased slightly with guselkumab treatment, as might be predicted from specific IL-23 blockade. Although not statistically significant, there was a marked reduction in expression of IL-17F (mean reduction, 26-fold; $P = .057$) and a modest (2-fold) reduction in IL-17A mRNA expression after guselkumab treatment (data not shown). The expression of LCN2, CXCL1 (Table I), and S100A7 (S100A15), which are strongly induced by IL-17 in psoriatic lesions, was significantly decreased after guselkumab treatment. CXCL10 (regulated by type I and type II interferons) and IL-22 expression was reduced at week 12, although less consistently (mean of 8- and 10-fold; $P = .15$ and $P = .11$, respectively) than expression of IL-17-targeted genes (data not shown). These data suggest that IL-23 regulates expression of IL-17 and IL-17 pathway gene targets in psoriasis lesions, with limited effect on T_H1 pathway gene targets (IFN- γ producing).

Affymetrix microarrays were used to define the transcriptome of lesional and nonlesional skin at baseline and weeks 1 and 12 after guselkumab treatment to assess the overall effect of guselkumab on the molecular disease profile (Fig 5, B; see Table E3 in this article's Online Repository at www.jacionline.org). The disease profile was defined as 1224 transcripts (891 unique ENTREZ-annotated genes) with significant modulations in gene expression when comparing lesional with nonlesional biopsy specimens at baseline. These genes are highly characteristic of the psoriasis disease profile reported recently.⁴ Of the 1224 disease-profile genes described here, 1170 were normalized by 70% or greater in week-12 biopsy specimens of psoriatic lesions treated with high-dose guselkumab (data not shown). Some improvement in the disease profile was evident at week 1, but the week-12 response was much stronger because the overall gene expression pattern is very similar to that of nonlesional skin at baseline. Significant reductions, with a smaller magnitude of change, were observed in the 10- and 30-mg groups (data not shown). Expression of KRT6A and KRT16 was significantly reduced by high-dose guselkumab from baseline to week 12 (21- and 19-fold, respectively), indicating a strong reduction in regenerative epidermal growth. Similar significant downregulation (>15-fold) was observed for S100A7A (S100A15), S100A7 (psoriasin), S100A8, and S100A9 (see Table E3). Interestingly, expression levels of KRT6 and KRT16, as well as levels of the S100 proteins, were modulated to levels less than the starting values in nonlesional skin at baseline. Additionally, a dose-dependent reduction in the expression of S100A proteins, KRT6A, KRT16, and LCN2 was observed (data not shown).

Microarray analysis also detected significant modulations in 694 genes by guselkumab (see Table E3), which were not classified as "disease-related" in this study. Approximately half of these genes (310 probes), however, were identified as a part of the psoriasis transcriptome in another recent study with a much larger patient cohort,⁴ and many of the 384 remaining genes are related to cell growth or inflammation pathways. The effects of high-dose guselkumab on genes involved in the IL-17 pathway, epidermal hyperplasia, and additional immune pathways are shown in Table I.

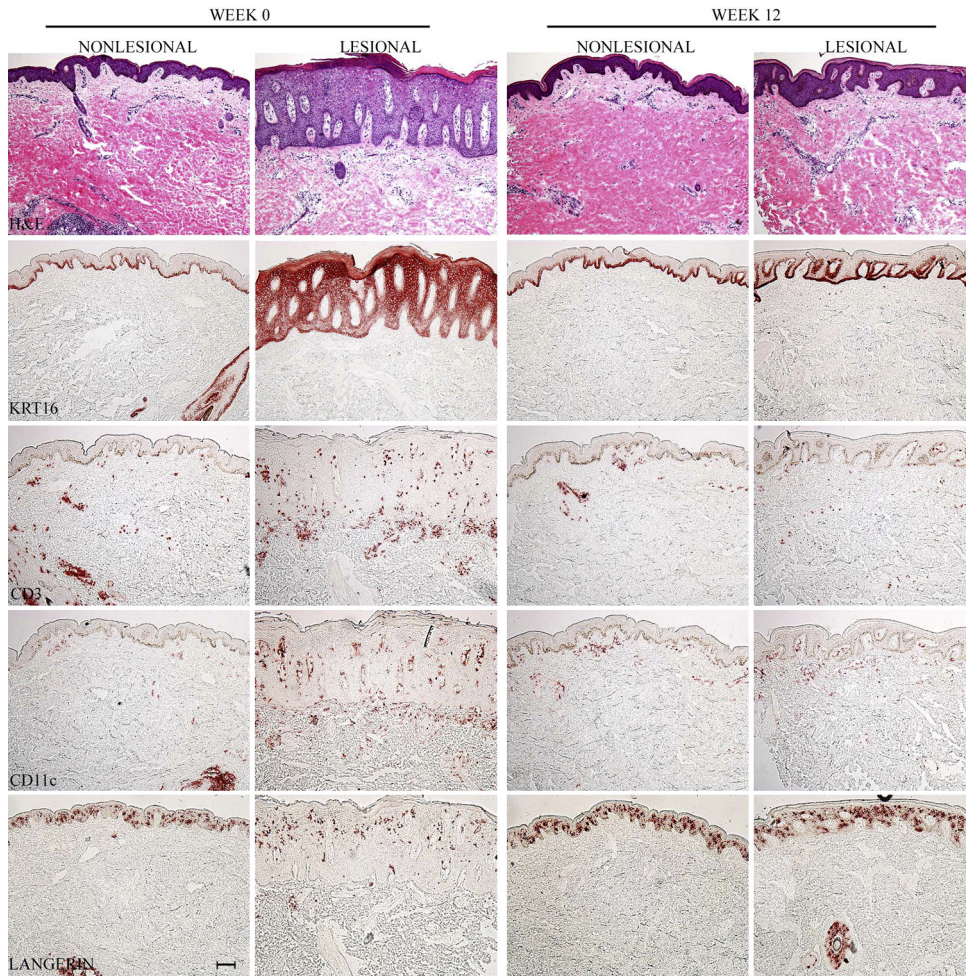


FIG 3. Histologic evaluation of nonlesional and lesional skin at baseline and week 12 after subcutaneous injection of 300 mg of guselkumab. *CD3*, T cell; *CD11c*, myeloid DC; *H&E*, hematoxylin and eosin; *KRT16*, keratin 16.

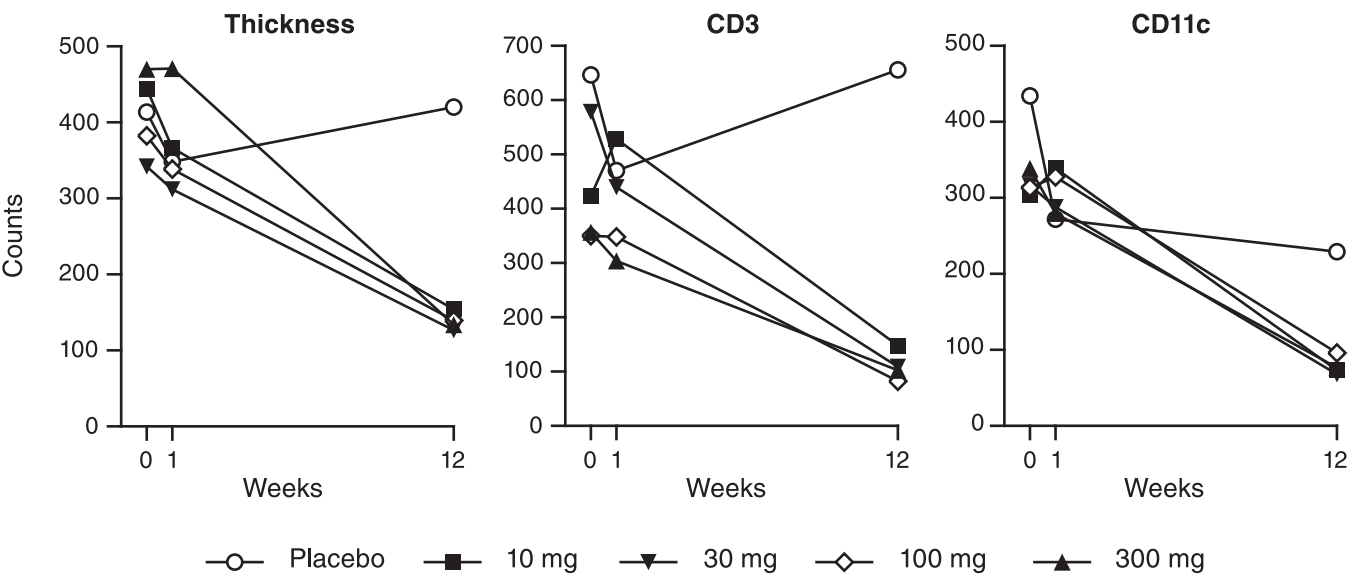


FIG 4. Evaluation of mean epidermal thickness and T-cell (*CD3*) and myeloid DC (*CD11c*) expression from lesional skin biopsy specimens at baseline and after guselkumab or placebo treatment at weeks 1 and 12.

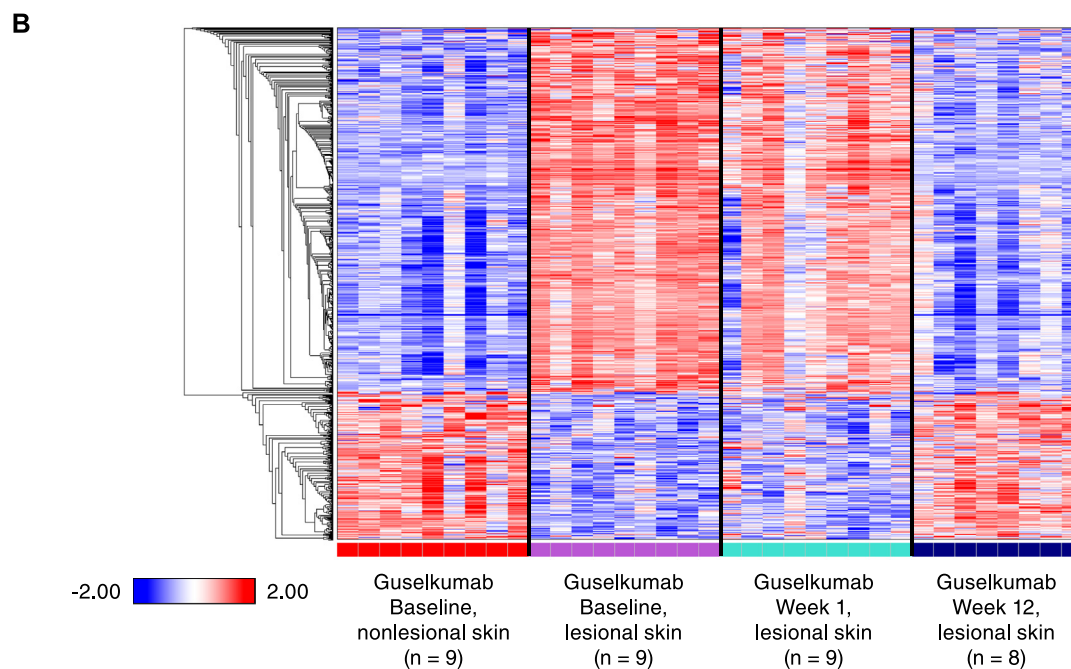
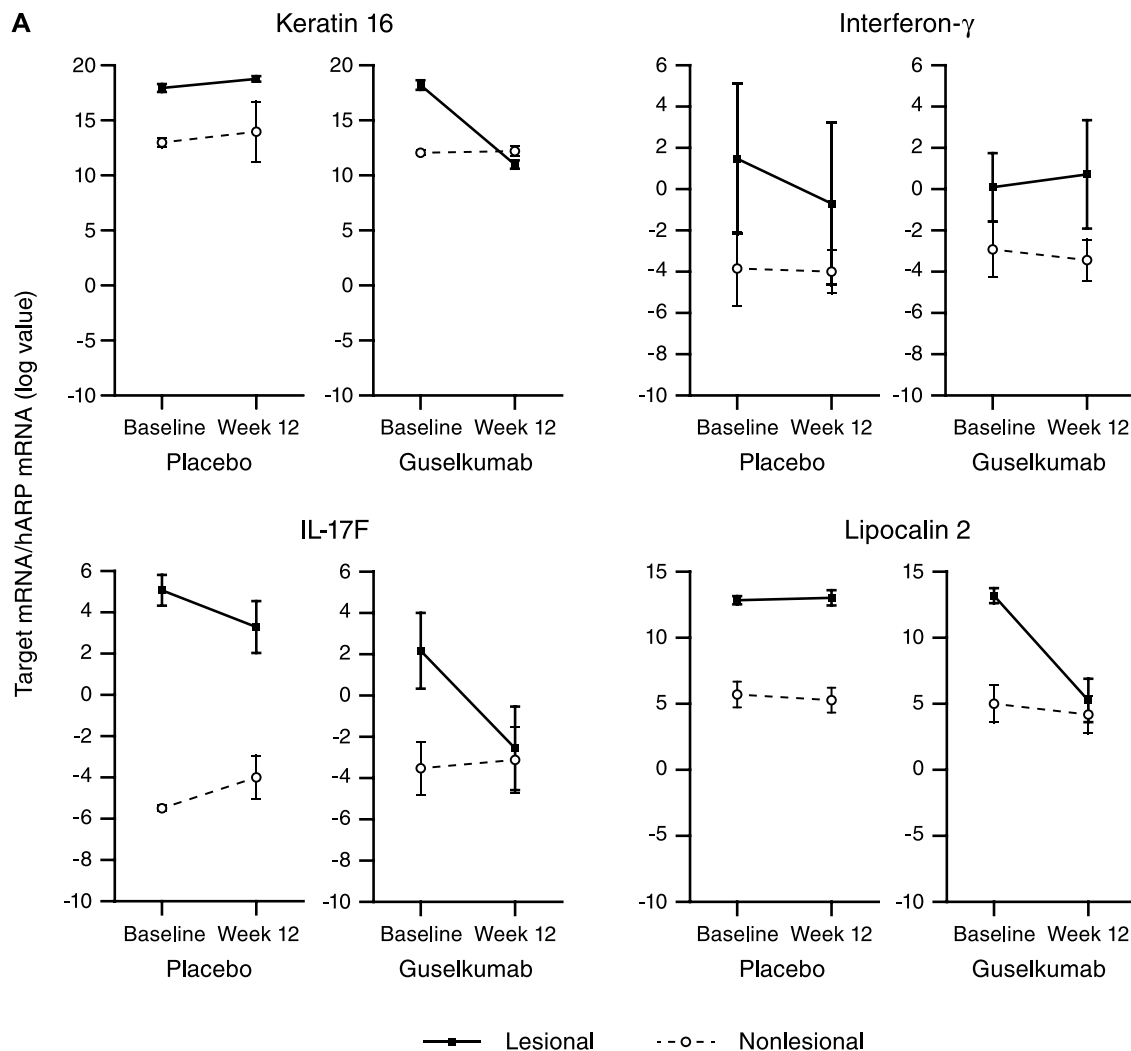


FIG 5. A, Expression of KRT16, IFN- γ , IL-17F, and LCN2 mRNA at baseline and week 12 in lesional and nonlesional biopsy specimens from patients treated with high-dose (100 mg + 300 mg) guselkumab compared with placebo. **B**, Microarray expression of 1224 transcripts of nonlesional skin at baseline versus lesional skin at baseline and at weeks 1 and 12 after guselkumab treatment.

TABLE I. Real-time reverse transcriptase PCR

		High-dose guselkumab responders*		Placebo-treated	
		Fold-change		Fold-change	
Differentially expressed genes	Gene name	(wk 12 vs baseline)	P value	(wk 12 vs baseline)	P value
IL-17 pathway related					
S100A7A	S100 calcium-binding protein A7A	<−1000	4.86 × 10 ^{−7}	−1.31	.9492
IL-8	IL-8	−699.81	.0006	−18.42	.4561
LCN2	Lipocalin 2	−244.37	.0001	1.24	.9426
CXCL1	C-X-C motif ligand 1	−157.06	.0015	1.6	.8859
RORC	RAR-related orphan receptor C	48.05	.0173	1.41	.9208
Epidermal hyperplasia					
KRT16	Keratin 16	−149.26	3.11 × 10 ^{−10}	1.22	.8962
STAT3	Signal transducer and activator of transcription 3	−4.93	.0195	2.35	.5598
Other immune pathways					
NOS2	Nitric oxide synthase 2	−145.48	.0059	−1.12	.9762
MX1	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	−17.45	.0006	2.2	.6541
GBP1	Guanylate-binding protein 1, interferon-inducible	−6.42	.0139	1.07	.9677
STAT5A	Signal transducer and activator of transcript 5A	19.25	.0497	−3.86	.6775
MUC7	Mucin 7	157.52	.0379	−1.63	.926

*Patients treated with 100 and 300 mg of guselkumab were grouped (high dose) for this analysis. Responders were defined as patients reporting at least a 50% improvement in PASI response (PASI 50) from baseline to week 12.

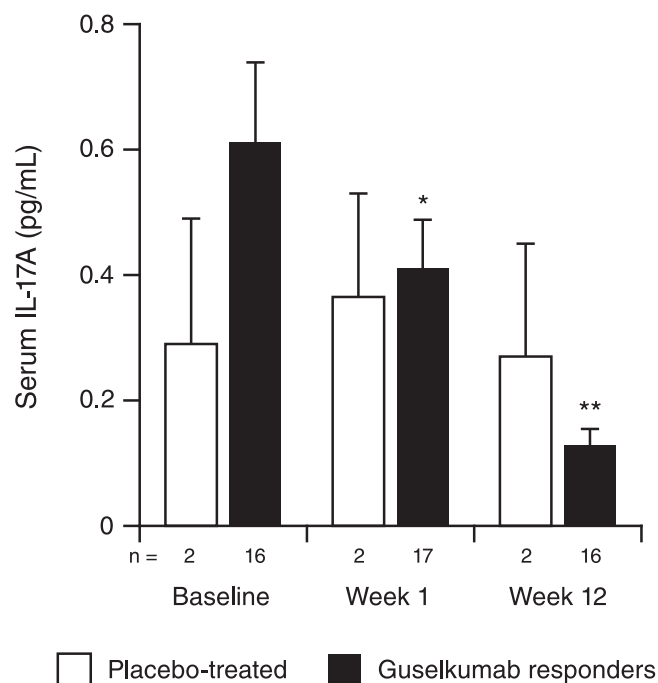


FIG 6. Serum analyses of circulating IL-17A levels in guselkumab-treated responders (PASI 50 response at week 12) at baseline and at weeks 1 and 12 compared with the placebo-treated group. *P* values measure the significant difference in posttreatment compared with baseline values. **P* = .031 and ***P* = .0015.

Serum IL-17A levels are reduced in patients responding to guselkumab

IL-17 levels are increased in the lesional skin and blood of patients with psoriasis^{3,16-18} and correlate with disease severity.¹⁹ One of the most direct pharmacodynamic measures of IL-23 inhibition in serum is a reduction of downstream IL-17A levels. IL-17A levels were analyzed at baseline and weeks 1 and 12 in

guselkumab responders (guselkumab-treated patients with ≥PASI 50 at week 12) compared with placebo-treated patients to explore whether serum IL-17A levels could be used to monitor response (Fig 6). Significant reductions from baseline in circulating IL-17A levels were observed at week 1 (*P* = .031) and week 12 (*P* = .0015) in guselkumab responders (*n* = 17), and no changes were observed in the placebo group. Although expression of genes pertinent to the IL-17A pathway was reduced in a dose-dependent manner, a similar dose trend was not observed with serum IL-17A levels (data not shown).

Ten other serum proteins were analyzed for changes after treatment with guselkumab, including inflammatory proteins: IFN-γ, IL-1β, IL-6, TNF-α, IL-12p40, IL-12p70, IL-8, C-reactive protein, IL-23p19, and CCL22 (MDC). CCL22 was the only analyte significantly reduced at week 12 after guselkumab treatment compared with placebo. No significant changes were noted for the other proteins (data not shown).

DISCUSSION

The results of this study establish that selective antagonism of IL-23 with guselkumab leads to clinical improvement in patients with psoriasis that is associated with reductions in cellular and molecular disease biomarkers in skin biopsy specimens. These data should be used to refine our current model of psoriasis pathogenesis. The current model involves not only the IL-23/T_H17 axis but also IFN-γ-producing T_H1/T_C1 cells and IL-22-producing T_H22/T_C22 cells. Activated DCs in the skin release IL-12¹ and IL-23,²⁰ which influence resident T cells to differentiate into T_H1/T_C1, T_H17/T_C17, and T_H22/T_C22 cells.³ In this model, cytokines released from distinct T-cell subsets cause epidermal keratinocytes to increase transcription of cytokine-specific gene products, and the psoriasis molecular phenotype is created by the collective response of keratinocytes to the array of cytokines produced in skin lesions. Our results suggest that the current working model should be revised to

indicate that IL-23 and downstream pathways controlled by this cytokine are sufficient to drive most of the disease phenotype, even if the IL-12/T_H1 axis continues to be expressed in skin lesions.

The importance of the IL-23/T_H17 T-cell axis in psoriasis pathogenesis is also suggested in recent studies with IL-17 antagonists in patients with psoriasis,^{6,21-23} but with the caveat that reductions in IL-12 and IFN- γ levels were also produced by antagonizing IL-17. The central role of IL-23 in psoriasis pathogenesis is supported by genetic links of IL-23 and IL-23R alleles to psoriasis susceptibility.^{24,25} Specifically, p19 mRNA is consistently overexpressed in psoriatic lesions,^{10,11} and the IL-23 risk allele increases T_H17 T-cell effector function *in vitro*.²⁶ Reports suggest that IL-23 can drive IL-17 production by cell populations beyond traditional CD4⁺ and CD8⁺ T cells in patients with psoriasis. Neutrophils, mast cells, and innate lymphoid cells have also been implicated as additional sources of IL-17.⁷ IL-23 can induce the formation of extracellular traps, structures involved in antimicrobial activity of neutrophils and mast cells, and these structures colocalized with IL-17 in psoriatic skin.⁷ Additionally, several groups have identified dermal $\gamma\delta$ T cells that secrete IL-17 in response to IL-23 *ex vivo*.^{27,28}

Because guselkumab can antagonize the IL-23/T_H17 pathway with limited effects on the IL-12/T_H1 arm and results in the collapse of major inflammatory circuits in patients with psoriasis, this study helps confirm that the IL-23/IL-17 pathway plays a central role in the current model of psoriasis pathogenesis. IL-17 antagonists, including ixekizumab and secukinumab (anti-IL-17A mAbs) and brodalumab (an anti-IL-17 receptor A mAb), are currently being studied in patients with psoriasis.^{6,21-23} Based on these limited published phase 1 data, the clinical efficacy of guselkumab is generally comparable with the results reported for ixekizumab²² and brodalumab.²³ Although inadequate data exist from phase 1 and 2 studies assessing the long-term safety of IL-23 or IL-17 antagonists, data for ustekinumab, which inhibits both IL-12 and IL-23, demonstrate a favorable benefit/risk profile in patients with moderate-to-severe psoriasis treated for up to 5 years.²⁹ Currently, the differences between the effects of IL-17 and IL-23 inhibition in patients are unknown. Upstream of IL-17, inhibition of IL-23 might have more pleiotropic effects than inhibition of IL-17. Although IL-17- or IL-17 receptor-specific antibodies suppress IL-17 levels, specific neutralization of IL-23 might decrease the number and activity of pathogenic T_H17 cells in the tissue. Comparative studies would be needed to evaluate whether IL-17 or IL-23 antagonism would result in differences in the maintenance of efficacy or safety.

In conclusion, this small clinical study provides evidence of clinical response, proof-of-concept, and safety of a single subcutaneous administration of guselkumab, an anti-IL-23-specific mAb, in patients with moderate-to-severe psoriasis. The range of doses of guselkumab included in this clinical study were well-tolerated, demonstrated significant dose-dependent clinical response, and modulated pathogenic T_H17 pathways, suggesting that neutralization of IL-23 alone is a valid therapeutic approach in patients with psoriasis. The benefit/risk profile of guselkumab in patients with psoriasis will be further defined in a larger study (X-PLORE, NCT01483599).

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Clinical implications: This initial study of guselkumab for plaque psoriasis demonstrates substantial clinical response. Further studies are warranted to verify this effect and characterize the safety profile.

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Supplemental Materials

Methods

Eligible patients were 18-65 years of age, weighed ≤ 130 kg, had been diagnosed with moderate-to-severe plaque-type psoriasis at least 6 months prior to administration of study agent, $\geq 10\%$ BSA involvement, had a PASI score of ≥ 12 , ≥ 2 plaques suitable for repeat biopsy/photography, and were candidates for phototherapy or systemic treatments. Patients ineligible to participate had used any therapeutic drug targeted against IL-12, IL-17, or IL-23, or experimental agent within 6 months, or any approved biologic agent 3 months prior to study administration; had received phototherapy, systemic therapies, immunosuppressants, or topical treatments within specified time frames, had any recent live vaccines; had a history of, or active/latent tuberculosis; or had a history of a severe, progressive, or uncontrolled medical condition.

Table E1. Baseline demographics and disease characteristics

	Placebo	Guselkumab 10 mg	Guselkumab 30 mg	Guselkumab 100 mg	Guselkumab 300 mg	Combined Guselkumab	Total
Treated patients, n	4	5	5	5	5	20	24
White, n (%)	3 (75.0)	3 (60.0)	4 (80.0)	5 (100.0)	5 (100.0)	17 (85.0)	20 (83.3)
Men, n (%)	3 (75.0)	3 (60.0)	2 (40.0)	4 (80.0)	3 (60.0)	12 (60.0)	15 (62.5)
Median age, years	46.5	43.0	39.0	43.0	37.0	41.0	42.5
Median weight (kg)	81.6	94.1	104.8	114.3	92.6	93.5	93.5
Median body mass index	27.0	32.7	31.7	36.1	31.5	31.6	31.6
Duration of psoriasis (years)							
Median	18.0	22.0	12.5	17.0	16.0	16.0	17.0
Range	(3, 26)	(0, 36)	(1, 25)	(10, 37)	(7, 19)	(0, 37)	(0, 37)
Body surface area involvement (%)							
Median	14.0	19.0	31.0	16.0	17.0	19.5	17.0
Range	(11, 17)	(12, 75)	(13, 70)	(12, 42)	(15, 56)	(12, 75)	(11, 75)

PASI score (0-72)

Median	13.2	15.2	16.7	15.8	16.6	16.2	14.8
Range	(13, 14)	(13, 34)	(14, 27)	(14, 23)	(12, 34)	(12, 34)	(12, 34)

PGA score, n (%)

Mild (2)	0	0	1 (20.0)	0	0	1 (5.0)	1 (4)
Moderate (3)	4 (100.0)	4 (80.0)	3 (60.0)	5 (100.0)	4 (80.0)	16 (80.0)	20 (83.3)
Marked (4)	0	1 (20.0)	1 (20.0)	0	1 (20.0)	3 (15.0)	3 (13.0)

PASI, Psoriasis Area and Severity Index; PGA, Physician's Global Assessment

Table E2. Adverse event summary through week 24

	Placebo	Guselkumab				
		10 mg	30 mg	100 mg	300 mg	Combined
Treated patients, n	4	5	5	5	5	20
Patients with adverse events by system organ class	2 (50)	5 (100)	2 (40)	4 (80)	2 (40)	13 (65)
Infections and infestations	0 (0)	1 (20)	1 (20)	2 (40)	2 (40)	6 (30)
Gastrointestinal disorders	0 (0)	3 (60)	0 (0)	0 (0)	0 (0)	3 (15)
Injury, poison, and procedural complications	0 (0)	1 (20)	0 (0)	1(20)	1 (20)	3 (15)
Musculoskeletal and connective tissue disorders	0 (0)	1 (20)	1 (20)	1 (20)	0 (0)	3 (15)
Nervous system disorders	1 (25)	1 (20)	0 (0)	0 (0)	1(20)	2 (10)
Respiratory, thoracic, and mediastinal disorders	0 (0)	1 (20)	1 (20)	0 (0)	0 (0)	2 (10)
Cardiac disorders	0 (0)	1 (20)	0 (0)	0 (0)	0 (0)	1 (5)
General disorders and administration site conditions	1 (25)	0 (0)	0 (0)	1 (20)	0 (0)	1 (5)
Investigations	0 (0)	0 (0)	1 (20)	0 (0)	0 (0)	1 (5)

Metabolism and nutrition disorders	0 (0)	0 (0)	0 (0)	1 (20)	0 (0)	1 (5)
Psychiatric disorders	0 (0)	0 (0)	1 (20)	0 (0)	0 (0)	1 (5)
Renal and urinary disorders	0 (0)	1 (20)	0 (0)	0 (0)	0 (0)	1 (5)
Skin and subcutaneous disorders	0 (0)	1 (20)	0 (0)	0 (0)	0 (0)	1 (5)

All values are listed as n (%) unless otherwise noted.

Table E3. Genes significantly modulated by guselkumab (week 12 vs. baseline) in psoriatic lesions

Probe set ID	Fold change	P-value	Disease profile?	% Recovery	Gene symbol	Gene title
207356_PM_at	-315.95	3.99E-07	+	310.91%	LOC100289462	similar to defensin, beta 4
41469_PM_at	-196.28	1.29E-07	+	302.67%	PI3	peptidase inhibitor 3, skin-derived
209719_PM_x_at	-188.31	3.23E-07	+	226.42%	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3
232170_PM_at	-160.15	1.93E-07	+	291.48%	S100A7A	S100 calcium binding protein A7A
203691_PM_at	-143.37	1.93E-07	+	263.73%	PI3	peptidase inhibitor 3, skin-derived
210413_PM_x_at	-87.52	4.91E-07	+	184.26%	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4
209720_PM_s_at	-79.8	1.16E-06	+	202.12%	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3
203535_PM_at	-67.7	4.91E-07	+	217.12%	S100A9	S100 calcium binding protein A9
211906_PM_s_at	-65.89	3.45E-07	+	208.92%	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3
220664_PM_at	-53.95	4.91E-07	+	244.45%	SPRR2C	small proline-rich protein 2C (pseudogene)
232220_PM_at	-50.04	1.93E-07	+	258.44%	S100A7A	S100 calcium binding protein A7A
205863_PM_at	-47.05	1.93E-07	+	178.65%	S100A12	S100 calcium binding protein A12
224328_PM_s_at	-44.8	0.0011	+	198.17%	LCE3D	late cornified envelope 3D
214370_PM_at	-34.63	0.0003	+	137.92%	S100A8	S100 calcium binding protein A8
213796_PM_at	-33.32	0.0007	+	154.66%	SPRR1A	small proline-rich protein 1A
202917_PM_s_at	-30.62	0.0016	+	110.03%	S100A8	S100 calcium binding protein A8
208539_PM_x_at	-30.47	0.0003	+	251.02%	SPRR2A	small proline-rich protein 2A
220322_PM_at	-27.19	4.91E-07	+	193.49%	IL1F9	interleukin 1 family, member 9
214580_PM_x_at	-25.2	1.93E-07	+	186.05%	KRT6A	keratin 6A
212531_PM_at	-23.74	6.90E-06	+	169.01%	LCN2	lipocalin 2
205783_PM_at	-22.88	7.55E-06	+	222.75%	KLK13	kallikrein-related peptidase 13
232082_PM_x_at	-20.66	5.05E-05	+	197.42%	SPRR2A	small proline-rich protein 2A
205064_PM_at	-19.24	0.01	+	95.64%	SPRR1B	small proline-rich protein 1B (cornifin)
205513_PM_at	-18.75	4.82E-06	+	151.15%	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)

209800_PM_at	-18.74	1.93E-07	+	185.78%	KRT16	keratin 16
209125_PM_at	-16.91	4.02E-06	+	155.82%	KRT6A	keratin 6A
219403_PM_s_at	-16.44	1.17E-05	+	165.83%	HPSE	heparanase
205916_PM_at	-16.38	0.0054	+	142.80%	S100A7	S100 calcium binding protein A7
227736_PM_at	-14.86	0.0006	+	118.23%	C10orf99	chromosome 10 open reading frame 99
206643_PM_at	-14.42	0.0002	+	194.91%	HAL	histidine ammonia-lyase
214549_PM_x_at	-13.64	9.74E-05	+	131.29%	SPRR1A	small proline-rich protein 1A
222223_PM_s_at	-13.54	3.28E-05	+	183.07%	IL1F5	interleukin 1 family, member 5 (delta)
211361_PM_s_at	-13.23	1.23E-06	+	131.67%	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13
213680_PM_at	-12.89	1.13E-05	+	196.81%	KRT6B	keratin 6B
231662_PM_at	-12.39	0.001	+	201.19%	ARG1	arginase, liver
204733_PM_at	-11.6	2.75E-05	+	141.46%	KLK6	kallikrein-related peptidase 6
217388_PM_s_at	-11.54	4.52E-06	+	124.67%	KYNU	kynureninase (L-kynurenine hydrolase)
227735_PM_s_at	-11.18	9.09E-05	+	127.49%	C10orf99	chromosome 10 open reading frame 99
214599_PM_at	-10.94	0.0017	+	162.50%	IVL	involucrin
224329_PM_s_at	-10.91	1.39E-05	+	171.48%	CNFN	cornifelin
219795_PM_at	-10.67	0.0004	+	176.06%	SLC6A14	solute carrier family 6 (amino acid transporter), member 14
217272_PM_s_at	-10.54	2.16E-06	+	157.44%	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13
206561_PM_s_at	-10.31	1.42E-05	+	104.68%	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)
209792_PM_s_at	-9.94	4.52E-06	+	200.99%	KLK10	kallikrein-related peptidase 10
231711_PM_at	-9.89	0.0002	+	174.41%	ACPP	acid phosphatase, prostate
209126_PM_x_at	-9.77	1.29E-07	+	162.58%	KRT6B	keratin 6B
202859_PM_x_at	-9.55	0.0006	+	219.56%	IL8	interleukin 8
211362_PM_s_at	-9.36	2.08E-05	+	137.15%	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13
216258_PM_s_at	-9.09	8.18E-06	+	144.45%	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13
1564307_PM_a_at	-8.74	0.0001	+	160.51%	A2ML1	alpha-2-macroglobulin-like 1
236119_PM_s_at	-8.69	0.0356	+	124.41%	SPRR2G	small proline-rich protein 2G
205157_PM_s_at	-8.55	0.0001	+	178.75%	KRT17	keratin 17
208650_PM_s_at	-8.53	7.37E-06	+	147.34%	CD24L4	Signal transducer CD24 precursor.
207602_PM_at	-8.5	8.58E-06	+	127.54%	TMPRSS11D	transmembrane protease, serine 11D
209772_PM_s_at	-8.46	3.93E-05	+	167.49%	CD24L4	Signal transducer CD24 precursor.
266_PM_s_at	-8.41	1.07E-05	+	166.38%	CD24	CD24 molecule

219352_PM_at	-8.28	9.36E-05	+	98.21%	HERC6	hect domain and RLD 6
206177_PM_s_at	-8.17	0.001	+	129.27%	ARG1	arginase, liver
228531_PM_at	-8.02	0.0013	+	90.84%	SAMD9	sterile alpha motif domain containing 9
223278_PM_at	-7.88	2.18E-06	+	152.11%	GJB2	gap junction protein, beta 2, 26kDa
206193_PM_s_at	-7.8	0.0267	+	127.98%	CDSN	corneodesmosin
202086_PM_at	-7.72	1.09E-05	+	138.12%	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
219630_PM_at	-7.56	3.83E-06	+	136.78%	PDZK1IP1	PDZK1 interacting protein 1
209773_PM_s_at	-7.39	0.0015	+	171.46%	RRM2	ribonucleotide reductase M2
204972_PM_at	-7.32	7.53E-05	+	103.23%	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
201890_PM_at	-7.23	4.54E-05	+	187.92%	RRM2	ribonucleotide reductase M2
206004_PM_at	-7.22	7.67E-05	+	145.20%	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
207381_PM_at	-7.1	5.69E-05	+	175.13%	ALOX12B	arachidonate 12-lipoxygenase, 12R type
231663_PM_s_at	-6.89	2.00E-05	+	191.04%	ARG1	arginase, liver
232001_PM_at	-6.76	0.0004	+	76.85%	LOC439949	hypothetical protein LOC439949
210663_PM_s_at	-6.75	2.69E-05	+	106.65%	KYNU	kynureninase (L-kynurenine hydrolase)
223484_PM_at	-6.68	0.0025	+	124.93%	C15orf48	chromosome 15 open reading frame 48
214710_PM_s_at	-6.66	0.0002	+	166.42%	CCNB1	cyclin B1
205014_PM_at	-6.6	0.0006	+	169.71%	FGFBP1	fibroblast growth factor binding protein 1
204415_PM_at	-6.5	2.43E-06	+	121.20%	IFI6	interferon, alpha-inducible protein 6
230323_PM_s_at	-6.49	0.0001	+	145.21%	TMEM45B	transmembrane protein 45B
216379_PM_x_at	-6.48	4.70E-05	+	169.90%	CD24	CD24 molecule
226817_PM_at	-6.46	8.52E-06	+	125.35%	DSC2	desmocollin 2
217315_PM_s_at	-6.38	5.75E-06	+	139.60%	KLK13	kallikrein-related peptidase 13
202411_PM_at	-6.14	0.0004	+	82.81%	IFI27	interferon, alpha-inducible protein 27
205569_PM_at	-6.08	6.16E-05	+	132.56%	LAMP3	lysosomal-associated membrane protein 3
204393_PM_s_at	-6.03	0.0023	+	128.25%	ACPP	acid phosphatase, prostate
226702_PM_at	-6.02	0.0009	+	85.79%	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
209771_PM_x_at	-6.01	1.07E-05	+	150.96%	CD24	CD24 molecule
231771_PM_at	-6	9.83E-06	+	140.06%	GJB6	gap junction protein, beta 6, 30kDa
220620_PM_at	-5.99	0.0052	+	158.79%	CRCT1	cysteine-rich C-terminal 1
1556409_PM_a_at	-5.99	0.0005	+	145.82%	PANX1	pannexin 1
204751_PM_x_at	-5.9	7.12E-05	+	123.17%	DSC2	desmocollin 2

219209_PM_at	-5.85	0.0006	+	121.92%	IFIH1	interferon induced with helicase C domain 1
204170_PM_s_at	-5.74	0.0002	+	162.52%	CKS2	CDC28 protein kinase regulatory subunit 2
228273_PM_at	-5.73	0.001	+	168.16%	PRR11	proline rich 11
1553589_PM_a_at	-5.7	1.39E-05	+	118.91%	PDZK1IP1	PDZK1 interacting protein 1
212236_PM_x_at	-5.66	7.24E-05	+	161.82%	KRT17	keratin 17
203779_PM_s_at	-5.64	2.13E-05	+	146.05%	MPZL2	myelin protein zero-like 2
237563_PM_s_at	-5.62	0.0002	+	157.10%	LOC440731	similar to hCG1817424
206421_PM_s_at	-5.49	0.0083	+	181.14%	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7
205767_PM_at	-5.43	0.0022	+	147.98%	EREG	epiregulin
204532_PM_x_at	-5.41	0.0004	+	148.09%	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6
228303_PM_at	-5.37	8.85E-06	+	180.27%	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
235075_PM_at	-5.36	2.77E-05	+	163.17%	DSG3	desmoglein 3 (pemphigus vulgaris antigen)
215125_PM_s_at	-5.35	0.0009	+	137.25%	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6
219554_PM_at	-5.34	4.31E-06	+	141.36%	RHCG	Rh family, C glycoprotein
203153_PM_at	-5.29	0.0032	+	75.25%	IFIT1	interferon-induced protein with tetratricopeptide repeats 1
202503_PM_s_at	-5.18	0.0003	+	122.09%	KIAA0101	KIAA0101
208651_PM_x_at	-5.15	9.60E-06	+	137.52%	CD24L4	Signal transducer CD24 precursor.
202018_PM_s_at	-5.13	0.0037	+	103.32%	LTF	lactotransferrin
203780_PM_at	-5.11	6.02E-05	+	117.88%	MPZL2	myelin protein zero-like 2
206008_PM_at	-5.1	1.29E-07	+	136.60%	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)
206553_PM_at	-5.1	1.53E-05	+	117.98%	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
204750_PM_s_at	-5.05	8.26E-06	+	118.66%	DSC2	desmocollin 2
207126_PM_x_at	-5.04	0.0006	+	153.23%	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6
202345_PM_s_at	-5.03	0.0001	+	93.68%	FABP5	fatty acid binding protein 5 (psoriasis-associated)
203560_PM_at	-5.02	0.0049	+	97.42%	GGH	gamma-glutamyl hydrolase (conjugase, folylpolyglutamyglutamyl hydrolase)
218384_PM_at	-5.01	2.36E-06	+	136.70%	CARHSP1	calcium regulated heat stable protein 1, 24kDa
214070_PM_s_at	-5	0.0018	+	117.03%	ATP10B	ATPase, class V, type 10B
238973_PM_s_at	-4.99	0.0002	+	145.44%	LOC440731	Similar to hCG1817424
204385_PM_at	-4.96	3.93E-05	+	106.74%	KYNU	kynureninase (L-kynurenine hydrolase)

202095_PM_s_at	-4.94	9.36E-05	+	157.85%	BIRC5	baculoviral IAP repeat-containing 5
224204_PM_x_at	-4.94	5.33E-05	+	134.33%	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2
220655_PM_at	-4.9	0.001	+	109.45%	TNIP3	TNFAIP3 interacting protein 3
234699_PM_at	-4.87	0.0016	+	152.61%	RNASE7	ribonuclease, RNase A family, 7
219956_PM_at	-4.85	0.0052	+	156.80%	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
216670_PM_at	-4.85	1.42E-05	+	133.45%	KLK13	kallikrein-related peptidase 13
206628_PM_at	-4.85	0.0014	+	128.71%	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1
224209_PM_s_at	-4.85	0.0211	+	53.95%	GDA	guanine deaminase
225100_PM_at	-4.84	0.0059	+	121.62%	FBXO45	F-box protein 45
213797_PM_at	-4.83	0.0012	+	107.58%	RSAD2	radical S-adenosyl methionine domain containing 2
239196_PM_at	-4.81	0.0051	+	150.71%	ANKRD22	ankyrin repeat domain 22
227609_PM_at	-4.81	1.38E-05	+	85.27%	EPSTI1	epithelial stromal interaction 1 (breast)
1558525_PM_at	-4.79	3.11E-05	+	147.06%	1558525_PM_at	---
214453_PM_s_at	-4.75	0.0011	+	67.40%	IFI44	interferon-induced protein 44
215817_PM_at	-4.72	0.0004	+	160.36%	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13
204162_PM_at	-4.7	4.98E-06	+	164.39%	NDC80	NDC80 homolog, kinetochore complex component (<i>S. cerevisiae</i>)
213572_PM_s_at	-4.7	0.0004	+	127.56%	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
219799_PM_s_at	-4.68	0.0002	+	183.54%	DHRS9	dehydrogenase/reductase (SDR family) member 9
204092_PM_s_at	-4.68	0.0004	+	160.73%	AURKA	aurora kinase A
208079_PM_s_at	-4.66	0.0016	+	153.75%	AURKA	aurora kinase A
204439_PM_at	-4.64	0.0007	+	100.03%	IFI44L	interferon-induced protein 44-like
225787_PM_at	-4.63	0.0002	+	132.88%	UBE2F	ubiquitin-conjugating enzyme E2F (putative)
201489_PM_at	-4.61	4.54E-05	+	118.20%	PPIF	peptidylprolyl isomerase F
AFFX-HUMISGF3A/M97935_3_at	-4.61	0.0002	+	108.09%	STAT1	signal transducer and activator of transcription 1, 91kDa
218542_PM_at	-4.6	0.0003	+	176.51%	CEP55	centrosomal protein 55kDa
232116_PM_at	-4.55	3.56E-05	+	153.49%	GRHL3	grainyhead-like 3 (<i>Drosophila</i>)
1557389_PM_at	-4.55	3.93E-05	+	144.59%	1557389_PM_at	---

214490_PM_at	-4.52	4.01E-05	+	145.44%	ARSF	arylsulfatase F
32128_PM_at	-4.52	0.0025	+	142.94%	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
1554914_PM_at	-4.52	8.14E-06	+	125.93%	PLA2G4D	phospholipase A2, group IVD (cytosolic)
220414_PM_at	-4.5	0.0068	+	140.59%	CALML5	calmodulin-like 5
227570_PM_at	-4.48	3.87E-06	+	161.85%	TMEM86A	transmembrane protein 86A
1555826_PM_at	-4.48	0.0017	+	128.78%	BIRC5	baculoviral IAP repeat- containing 5
217739_PM_s_at	-4.48	0.0018	+	123.79%	NAMPT	nicotinamide phosphoribosyltransferase
242271_PM_at	-4.47	0.0001	+	122.63%	SLC26A9	solute carrier family 26, member 9
1554283_PM_at	-4.42	9.36E-05	+	153.20%	CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)
225367_PM_at	-4.41	0.0015	+	115.60%	PGM2	phosphoglucomutase 2
228846_PM_at	-4.39	0.0002	+	113.05%	MXD1	MAX dimerization protein 1
220013_PM_at	-4.38	0.0005	+	153.67%	EPHX3	epoxide hydrolase 3
240304_PM_s_at	-4.38	0.0047	+	121.47%	TMC5	transmembrane channel-like 5
214382_PM_at	-4.35	0.0144	+	165.96%	UNC93A	unc-93 homolog A (C. elegans)
239381_PM_at	-4.35	0.0071	+	141.05%	KLK7	kallikrein-related peptidase 7
204470_PM_at	-4.35	0.0065	+	108.89%	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
1555758_PM_a_at	-4.31	0.0142	-	200.59%	CDKN3	cyclin-dependent kinase inhibitor 3
206125_PM_s_at	-4.3	0.0002	+	143.50%	KLK8	kallikrein-related peptidase 8
228617_PM_at	-4.3	8.86E-05	+	110.66%	XAF1	XIAP associated factor 1
231779_PM_at	-4.29	6.90E-06	+	115.05%	IRAK2	interleukin-1 receptor- associated kinase 2
229450_PM_at	-4.29	0.0117	+	78.38%	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
202575_PM_at	-4.28	4.63E-06	+	141.84%	CRABP2	cellular retinoic acid binding protein 2
217521_PM_at	-4.28	0.0026	+	116.51%	HAL	histidine ammonia-lyase
228066_PM_at	-4.27	0.0021	+	117.06%	C17orf96	chromosome 17 open reading frame 96
205990_PM_s_at	-4.27	0.0008	+	78.19%	WNT5A	wingless-type MMTV integration site family, member 5A
211368_PM_s_at	-4.26	0.0004	+	96.90%	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
224050_PM_s_at	-4.24	0.0007	+	156.27%	YOD1	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)
32069_PM_at	-4.22	0.0009	+	125.75%	N4BP1	NEDD4 binding protein 1
204971_PM_at	-4.22	0.0118	+	116.24%	CSTA	cystatin A (stefin A)

205660_PM_at	-4.21	0.001	+	100.49%	OASL	2'-5'-oligoadenylate synthetase-like
231577_PM_s_at	-4.21	0.0009	+	94.51%	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
200887_PM_s_at	-4.19	0.0015	+	95.29%	STAT1	signal transducer and activator of transcription 1, 91kDa
223220_PM_s_at	-4.19	0.0005	+	89.76%	PARP9	poly (ADP-ribose) polymerase family, member 9
222608_PM_s_at	-4.18	0.0008	+	202.52%	ANLN	anillin, actin binding protein
218400_PM_at	-4.15	0.0005	+	93.55%	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa
60474_PM_at	-4.14	0.0008	+	149.90%	FERMT1	fermitin family homolog 1 (Drosophila)
203234_PM_at	-4.14	0.0002	+	96.61%	UPP1	uridine phosphorylase 1
224051_PM_at	-4.13	0.0081	+	163.35%	YOD1	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)
204026_PM_s_at	-4.13	0.0006	+	148.81%	ZWINT	ZW10 interactor
219722_PM_s_at	-4.12	1.42E-05	+	128.32%	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3
204614_PM_at	-4.11	0.0159	-	175.36%	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2
227410_PM_at	-4.1	0.001	+	106.01%	FAM43A	family with sequence similarity 43, member A
222383_PM_s_at	-4.08	0.0021	+	177.99%	ALOXE3	arachidonate lipoxygenase 3
231665_PM_at	-4.07	8.21E-05	+	151.54%	ARG1	arginase, liver
227309_PM_at	-4.06	0.0081	+	111.57%	YOD1	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)
224917_PM_at	-4.05	0.0015	+	138.91%	MIR21	microRNA 21
220413_PM_at	-4.05	0.022	+	123.38%	SLC39A2	solute carrier family 39 (zinc transporter), member 2
201860_PM_s_at	-4.04	0.001	+	141.17%	PLAT	plasminogen activator, tissue
219148_PM_at	-4.04	3.05E-05	+	140.02%	PBK	PDZ binding kinase
226226_PM_at	-4.04	2.16E-06	+	132.43%	TMEM45B	transmembrane protein 45B
218254_PM_s_at	-4.03	0.0015	+	132.57%	SAR1B	SAR1 homolog B (S. cerevisiae)
213421_PM_x_at	-4.03	0.0009	+	127.71%	PRSS3	protease, serine, 3
219358_PM_s_at	-4.02	5.15E-05	+	136.76%	ADAP2	ArfGAP with dual PH domains 2
206165_PM_s_at	-4.02	0.0048	+	130.10%	CLCA2	chloride channel accessory 2
213425_PM_at	-4.01	4.54E-05	+	107.90%	WNT5A	wingless-type MMTV integration site family, member 5A
214509_PM_at	-3.97	0.0019	+	164.33%	HIST1H3I	histone cluster 1, H3i
227747_PM_at	-3.97	0.0014	+	143.18%	MPZL3	myelin protein zero-like 3
202869_PM_at	-3.97	0.0016	+	100.12%	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa
209727_PM_at	-3.96	0.0025	+	113.60%	GM2A	GM2 ganglioside activator

235272_PM_at	-3.93	0.0234	+	151.19%	SBSN	suprabasin
206753_PM_at	-3.93	5.58E-05	+	137.29%	RDH16	retinol dehydrogenase 16 (all-trans)
225099_PM_at	-3.92	0.0112	+	100.99%	FBXO45	F-box protein 45
242998_PM_at	-3.89	0.0014	+	136.58%	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)
242773_PM_at	-3.89	0.0183	+	89.42%	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1
229097_PM_at	-3.88	0.0019	+	134.37%	DIAPH3	diaphanous homolog 3 (Drosophila)
213060_PM_s_at	-3.88	0.0005	+	104.84%	CHI3L2	chitinase 3-like 2
205778_PM_at	-3.85	0.0129	+	125.08%	KLK7	kallikrein-related peptidase 7
218454_PM_at	-3.85	0.0007	+	100.47%	PLBD1	phospholipase B domain containing 1
213975_PM_s_at	-3.85	0.0194	+	74.59%	LYZ	lysozyme (renal amyloidosis)
210058_PM_at	-3.84	0.0032	+	146.60%	MAPK13	mitogen-activated protein kinase 13
209093_PM_s_at	-3.83	5.29E-05	+	153.67%	GBA	glucosidase, beta; acid (includes glucosylceramidase)
226698_PM_at	-3.83	1.39E-06	+	130.42%	FCHSD1	FCH and double SH3 domains 1
1554912_PM_at	-3.82	5.14E-05	+	136.78%	ESYT3	extended synaptotagmin-like protein 3
209218_PM_at	-3.82	0.0012	+	110.06%	SQLE	squalene epoxidase
215891_PM_s_at	-3.82	0.0035	+	104.45%	GM2A	GM2 ganglioside activator
218986_PM_s_at	-3.82	0.0011	+	87.53%	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
218951_PM_s_at	-3.81	2.26E-05	+	152.63%	PLCXD1	phosphatidylinositol-specific phospholipase C, X domain containing 1
1555680_PM_a_at	-3.8	5.29E-05	+	162.65%	SMOX	spermine oxidase
230188_PM_at	-3.79	0.0002	+	147.86%	NIPAL4	NIPA-like domain containing 4
203021_PM_at	-3.79	0.001	+	126.50%	SLPI	secretory leukocyte peptidase inhibitor
205552_PM_s_at	-3.77	4.28E-05	+	109.61%	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa
239430_PM_at	-3.76	0.0002	+	137.37%	IGFL1	IGF-like family member 1
214536_PM_at	-3.76	0.0033	+	134.31%	SLURP1	secreted LY6/PLAUR domain containing 1
33646_PM_g_at	-3.76	0.0016	+	98.57%	GM2A	GM2 ganglioside activator
209714_PM_s_at	-3.76	0.0046	-	182.21%	CDKN3	cyclin-dependent kinase inhibitor 3
209891_PM_at	-3.75	0.0026	+	131.38%	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)
222892_PM_s_at	-3.75	7.20E-05	+	121.44%	TMEM40	transmembrane protein 40
204952_PM_at	-3.74	0.0096	+	148.98%	LYPD3	LY6/PLAUR domain containing 3
203127_PM_s_at	-3.74	0.0025	+	139.57%	SPTLC2	serine palmitoyltransferase, long chain base subunit 2

215465_PM_at	-3.74	0.0042	+	100.78%	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12
229373_PM_at	-3.73	0.0002	+	119.65%	229373_PM_at	---
234700_PM_s_at	-3.72	0.0012	+	155.96%	RNASE7	ribonuclease, RNase A family, 7
241382_PM_at	-3.72	0.0054	+	98.27%	PCP4L1	Purkinje cell protein 4 like 1
206605_PM_at	-3.71	0.0075	+	145.88%	P11	26 serine protease
244692_PM_at	-3.71	0.0008	+	140.96%	CYP4F22	cytochrome P450, family 4, subfamily F, polypeptide 22
225195_PM_at	-3.71	0.0182	+	123.41%	DPH3	DPH3, KTI11 homolog (S. cerevisiae)
35820_PM_at	-3.71	0.0003	+	116.92%	GM2A	GM2 ganglioside activator
239586_PM_at	-3.7	2.59E-05	+	139.43%	FAM83A	family with sequence similarity 83, member A
222878_PM_s_at	-3.7	0.0007	-	188.24%	OTUB2	OTU domain, ubiquitin aldehyde binding 2
207463_PM_x_at	-3.69	0.0003	+	114.36%	PRSS3	protease, serine, 3
223658_PM_at	-3.68	0.0008	+	132.81%	KCNK6	potassium channel, subfamily K, member 6
238654_PM_at	-3.67	0.0114	+	154.20%	VSIG10L	V-set and immunoglobulin domain containing 10 like
208515_PM_at	-3.67	0.0082	+	151.30%	HIST1H2BM	histone cluster 1, H2bm
221765_PM_at	-3.67	0.0039	+	139.43%	UGCG	UDP-glucose ceramide glucosyltransferase
209921_PM_at	-3.67	0.0012	+	108.27%	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
242204_PM_at	-3.66	0.0022	-	190.39%	WFDC5	WAP four-disulfide core domain 5
227180_PM_at	-3.65	0.0048	+	109.19%	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)
216243_PM_s_at	-3.64	0.0044	+	131.18%	IL1RN	interleukin 1 receptor antagonist
210951_PM_x_at	-3.64	0.0006	+	120.15%	RAB27A	RAB27A, member RAS oncogene family
204994_PM_at	-3.64	0.0055	+	100.46%	MX2	myxovirus (influenza virus) resistance 2 (mouse)
202831_PM_at	-3.63	0.0001	+	138.87%	GPX2	glutathione peroxidase 2 (gastrointestinal)
203740_PM_at	-3.63	0.0004	+	116.33%	MPHOSPH6	M-phase phosphoprotein 6
218810_PM_at	-3.62	0.0004	+	122.86%	ZC3H12A	zinc finger CCCH-type containing 12A
203213_PM_at	-3.62	6.02E-05	+	121.78%	CDC2	cell division cycle 2, G1 to S and G2 to M
235651_PM_at	-3.61	0.0029	+	142.65%	TTC22	tetratricopeptide repeat domain 22
222361_PM_at	-3.61	0.0007	+	129.88%	TUBBP5	tubulin, beta pseudogene 5
220249_PM_at	-3.6	2.20E-05	+	155.31%	HYAL4	hyaluronoglucosaminidase 4
216245_PM_at	-3.59	0.0023	+	137.48%	IL1RN	interleukin 1 receptor antagonist
219532_PM_at	-3.59	0.0188	+	120.10%	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2,

						SUR4/Elo3, yeast)-like 4
212737_PM_at	-3.59	0.0006	+	111.34%	GM2A	GM2 ganglioside activator
223541_PM_at	-3.58	0.0003	+	149.60%	HAS3	hyaluronan synthase 3
228964_PM_at	-3.58	0.0103	+	112.59%	PRDM1	PR domain containing 1, with ZNF domain
222039_PM_at	-3.57	0.0012	+	139.52%	KIF18B	kinesin family member 18B
221698_PM_s_at	-3.56	0.0002	+	65.25%	CLEC7A	C-type lectin domain family 7, member A
55081_PM_at	-3.55	0.001	+	135.78%	MICALL1	MICAL-like 1
212449_PM_s_at	-3.55	0.0125	+	117.23%	LYPLA1	lysophospholipase I
222939_PM_s_at	-3.54	0.0062	+	141.82%	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)
220780_PM_at	-3.53	4.73E-05	+	151.61%	PLA2G3	phospholipase A2, group III
209924_PM_at	-3.53	0.0073	+	142.97%	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
203554_PM_x_at	-3.52	0.0001	+	144.24%	PTTG1	pituitary tumor-transforming 1
204420_PM_at	-3.52	0.0109	+	140.79%	FOSL1	FOS-like antigen 1
206276_PM_at	-3.52	0.0067	+	118.56%	LY6D	lymphocyte antigen 6 complex, locus D
238017_PM_at	-3.5	0.0227	+	134.74%	SDR16C5	short chain dehydrogenase/reductase family 16C, member 5
219716_PM_at	-3.5	0.0004	+	121.41%	APOL6	apolipoprotein L, 6
219267_PM_at	-3.49	0.0151	+	121.89%	GLTP	glycolipid transfer protein
1569886_PM_a_at	-3.48	3.93E-05	+	150.51%	GLB1L3	galactosidase, beta 1-like 3
223694_PM_at	-3.48	0.0153	+	139.49%	TRIM7	tripartite motif-containing 7
1553077_PM_at	-3.48	3.17E-05	+	136.88%	SDR9C7	short chain dehydrogenase/reductase family 9C, member 7
227998_PM_at	-3.47	0.0003	+	124.73%	S100A16	S100 calcium binding protein A16
232361_PM_s_at	-3.47	0.0013	+	124.60%	EHF	ets homologous factor
1555756_PM_a_at	-3.47	0.003	+	64.21%	CLEC7A	C-type lectin domain family 7, member A
220635_PM_at	-3.47	0.0117	-	176.17%	PSORS1C2	psoriasis susceptibility 1 candidate 2
203767_PM_s_at	-3.46	0.0001	+	146.76%	STS	steroid sulfatase (microsomal), isozyme S
201649_PM_at	-3.46	3.71E-05	+	126.15%	UBE2L6	ubiquitin-conjugating enzyme E2L 6
1568592_PM_at	-3.45	0.0016	+	136.05%	TRIM69	tripartite motif-containing 69
216244_PM_at	-3.44	0.0008	+	147.52%	IL1RN	interleukin 1 receptor antagonist
AFFX-HUMISGF3A/M97935_5_at	-3.41	0.0002	+	115.27%	STAT1	signal transducer and activator of transcription 1, 91kDa
222077_PM_s_at	-3.4	0.0018	+	158.79%	RACGAP1	Rac GTPase activating protein 1
225783_PM_at	-3.39	0.0035	+	118.02%	UBE2F	ubiquitin-conjugating enzyme E2F (putative)

212460_PM_at	-3.38	0.0011	+	114.19%	C14orf147	chromosome 14 open reading frame 147
1552777_PM_a_at	-3.38	0.0011	-	193.26%	RAET1E	retinoic acid early transcript 1E
201291_PM_s_at	-3.37	0.0012	+	153.95%	TOP2A	topoisomerase (DNA) II alpha 170kDa
201195_PM_s_at	-3.37	9.55E-06	+	128.69%	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
219099_PM_at	-3.37	0.0094	+	115.86%	C12orf5	chromosome 12 open reading frame 5
230748_PM_at	-3.37	0.0023	+	104.71%	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)
226177_PM_at	-3.34	0.0061	+	118.12%	GLTP	glycolipid transfer protein
210020_PM_x_at	-3.34	0.0002	+	102.92%	CALML3	calmodulin-like 3
240303_PM_at	-3.34	0.0001	-	178.52%	TMC5	transmembrane channel-like 5
1558152_PM_at	-3.33	0.0001	+	132.48%	LOC100131262	hypothetical LOC100131262
231733_PM_at	-3.33	0.0472	+	100.85%	CARD18	caspase recruitment domain family, member 18
212657_PM_s_at	-3.32	0.0008	+	127.86%	IL1RN	interleukin 1 receptor antagonist
242951_PM_at	-3.32	0.0043	+	108.12%	IGSF22	immunoglobulin superfamily, member 22
1552682_PM_a_at	-3.31	0.0064	+	143.48%	CASC5	cancer susceptibility candidate 5
231948_PM_s_at	-3.31	0.0011	+	110.64%	UBE2F	ubiquitin-conjugating enzyme E2F (putative)
209969_PM_s_at	-3.31	0.0008	+	108.94%	STAT1	signal transducer and activator of transcription 1, 91kDa
222838_PM_at	-3.31	0.0045	+	74.55%	SLAMF7	SLAM family member 7
1554253_PM_a_at	-3.3	0.0009	+	144.33%	LASS3	LAG1 homolog, ceramide synthase 3
37152_PM_at	-3.3	0.0004	+	129.28%	PPARD	peroxisome proliferator-activated receptor delta
201292_PM_at	-3.3	0.0044	+	113.37%	TOP2A	topoisomerase (DNA) II alpha 170kDa
202236_PM_s_at	-3.29	0.0046	+	104.92%	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
223946_PM_at	-3.28	0.0009	+	148.49%	MED23	mediator complex subunit 23
217738_PM_at	-3.28	0.0286	+	105.99%	NAMPT	nicotinamide phosphoribosyltransferase
220658_PM_s_at	-3.28	0.0018	+	104.34%	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2
45633_PM_at	-3.27	0.0006	+	118.38%	GINS3	GINS complex subunit 3 (Psf3 homolog)
1560756_PM_at	-3.27	0.0309	+	102.67%	FLJ39005	hypothetical protein FLJ39005
209944_PM_at	-3.26	0.0007	+	142.58%	ZNF410	zinc finger protein 410
231755_PM_at	-3.25	0.0012	+	146.75%	IL1F8	interleukin 1 family, member

						8 (eta)
224376_PM_s_at	-3.25	0.0015	+	120.80%	C20orf24	chromosome 20 open reading frame 24
203665_PM_at	-3.25	0.0005	+	114.32%	HMOX1	heme oxygenase (decycling) 1
216202_PM_s_at	-3.24	0.0064	+	139.75%	SPTLC2	serine palmitoyltransferase, long chain base subunit 2
241985_PM_at	-3.24	0.0059	+	105.96%	JMY	junction mediating and regulatory protein, p53 cofactor
225095_PM_at	-3.23	0.0103	+	116.71%	SPTLC2	serine palmitoyltransferase, long chain base subunit 2
217528_PM_at	-3.23	0.0025	+	113.32%	CLCA2	chloride channel accessory 2
204995_PM_at	-3.23	8.30E-05	+	112.75%	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
201202_PM_at	-3.23	0.0062	+	97.97%	PCNA	proliferating cell nuclear antigen
207121_PM_s_at	-3.22	0.0002	+	118.47%	MAPK6	mitogen-activated protein kinase 6
209015_PM_s_at	-3.22	0.0005	-	169.28%	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6
207213_PM_s_at	-3.21	0.0022	+	151.15%	USP2	ubiquitin specific peptidase 2
226936_PM_at	-3.21	0.0015	+	131.46%	C6orf173	chromosome 6 open reading frame 173
213562_PM_s_at	-3.21	0.0013	+	128.32%	SQLE	squalene epoxidase
224967_PM_at	-3.21	0.015	+	119.17%	UGCG	UDP-glucose ceramide glucosyltransferase
228323_PM_at	-3.2	0.0005	+	149.15%	CASC5	cancer susceptibility candidate 5
210052_PM_s_at	-3.2	0.0021	+	144.96%	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
213927_PM_at	-3.18	0.0007	+	150.99%	MAP3K9	mitogen-activated protein kinase kinase kinase 9
203764_PM_at	-3.18	0.0015	+	132.25%	DLGAP5	discs, large (Drosophila) homolog-associated protein 5
228729_PM_at	-3.17	0.0018	+	98.14%	CCNB1	cyclin B1
205220_PM_at	-3.17	0.0176	-	159.30%	GPR109B	G protein-coupled receptor 109B
207008_PM_at	-3.16	0.0005	+	107.58%	IL8RB	interleukin 8 receptor, beta
230518_PM_at	-3.16	0.015	+	89.22%	MPZL2	myelin protein zero-like 2
210589_PM_s_at	-3.15	2.35E-06	+	133.79%	GBAP	glucosidase, beta; acid, pseudogene
204268_PM_at	-3.15	0.0003	+	129.32%	S100A2	S100 calcium binding protein A2
1563659_PM_at	-3.14	0.0237	+	135.53%	HERC6	hect domain and RLD 6
211080_PM_s_at	-3.14	0.0157	+	120.31%	NEK2	NIMA (never in mitosis gene a)-related kinase 2
202068_PM_s_at	-3.14	0.0043	+	117.49%	LDLR	low density lipoprotein receptor
209679_PM_s_at	-3.13	0.0043	+	127.57%	SMAGP	small cell adhesion glycoprotein
223895_PM_s_at	-3.13	0.0316	-	163.81%	EPN3	epsin 3

205595_PM_at	-3.12	0.0008	+	118.58%	DSG3	desmoglein 3 (pemphigus vulgaris antigen)
1559607_PM_s_at	-3.12	0.0175	+	102.49%	GBP6	guanylate binding protein family, member 6
1569144_PM_a_at	-3.11	0.0042	+	125.84%	C9orf169	chromosome 9 open reading frame 169
204698_PM_at	-3.11	0.0041	+	120.27%	ISG20	interferon stimulated exonuclease gene 20kDa
206102_PM_at	-3.1	0.0025	+	127.89%	GINS1	GINS complex subunit 1 (Psf1 homolog)
235668_PM_at	-3.1	0.0015	+	115.44%	PRDM1	PR domain containing 1, with ZNF domain
201303_PM_at	-3.1	0.0026	+	108.93%	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3
209514_PM_s_at	-3.1	0.0019	+	106.42%	RAB27A	RAB27A, member RAS oncogene family
203276_PM_at	-3.09	0.0003	+	149.10%	LMNB1	lamin B1
200750_PM_s_at	-3.09	0.0017	+	127.68%	RAN	RAN, member RAS oncogene family
206034_PM_at	-3.08	0.0114	+	142.78%	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8
203888_PM_at	-3.08	0.0062	+	139.07%	THBD	thrombomodulin
205185_PM_at	-3.08	0.0219	+	133.05%	SPINK5	serine peptidase inhibitor, Kazal type 5
241946_PM_at	-3.08	0.0011	+	123.61%	ZDHHC21	zinc finger, DHHC-type containing 21
223880_PM_x_at	-3.08	0.0023	+	111.16%	C20orf24	chromosome 20 open reading frame 24
231227_PM_at	-3.08	0.0022	+	81.76%	WNT5A	wingless-type MMTV integration site family, member 5A
219920_PM_s_at	-3.08	0.0002	-	171.75%	GMPPB	GDP-mannose pyrophosphorylase B
224189_PM_x_at	-3.07	0.0001	+	132.93%	EHF	ets homologous factor
208074_PM_s_at	-3.07	0.0007	+	127.02%	AP2S1	adaptor-related protein complex 2, sigma 1 subunit
209373_PM_at	-3.07	0.03	+	125.82%	LOC100293791	hypothetical protein LOC100293791
205759_PM_s_at	-3.07	0.0016	+	123.86%	SULT2B1	sulfotransferase family, cytosolic, 2B, member 1
226275_PM_at	-3.07	0.0373	+	116.87%	MXD1	MAX dimerization protein 1
201695_PM_s_at	-3.07	0.0007	+	106.68%	NP	nucleoside phosphorylase
1554556_PM_a_at	-3.07	0.0003	+	98.52%	ATP11B	ATPase, class VI, type 11B
218662_PM_s_at	-3.06	0.0002	+	152.47%	NCAPG	non-SMC condensin I complex, subunit G
201490_PM_s_at	-3.06	0.0009	+	142.29%	PPIF	peptidylprolyl isomerase F
224511_PM_s_at	-3.06	0.0001	+	114.65%	TXNDC17	thioredoxin domain containing 17
212769_PM_at	-3.06	0.0118	-	145.94%	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
214059_PM_at	-3.05	0.0105	+	94.45%	IFI44	interferon-induced protein 44
219787_PM_s_at	-3.04	0.0007	+	112.51%	ECT2	epithelial cell transforming

						sequence 2 oncogene
225655_PM_at	-3.03	9.74E-05	+	128.86%	UHRF1	ubiquitin-like with PHD and ring finger domains 1
226661_PM_at	-3.03	0.0015	+	100.44%	CDCA2	cell division cycle associated 2
203023_PM_at	-3.02	0.0087	+	121.07%	NOP16	NOP16 nucleolar protein homolog (yeast)
203797_PM_at	-3.02	0.0012	+	117.62%	VSNL1	visinin-like 1
202705_PM_at	-3.02	6.02E-05	-	162.07%	CCNB2	cyclin B2
235068_PM_at	-3.01	0.0103	+	118.78%	ZDHHC21	zinc finger, DHHC-type containing 21
209709_PM_s_at	-3.01	0.0007	+	117.87%	HMMR	hyaluronan-mediated motility receptor (RHAMM)
202539_PM_s_at	-3.01	0.0254	+	111.94%	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
224013_PM_s_at	-3.01	0.0023	+	102.52%	SOX7	SRY (sex determining region Y)-box 7
214681_PM_at	-2.99	0.002	+	116.67%	GK	glycerol kinase
236341_PM_at	-2.99	0.006	+	103.56%	CTLA4	cytotoxic T-lymphocyte-associated protein 4
219366_PM_at	-2.99	2.59E-05	-	188.64%	AVEN	apoptosis, caspase activation inhibitor
207367_PM_at	-2.98	0.0007	+	132.01%	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
229390_PM_at	-2.98	0.0255	+	113.23%	FAM26F	family with sequence similarity 26, member F
219850_PM_s_at	-2.97	0.0002	+	136.35%	EHF	ets homologous factor
220831_PM_at	-2.97	0.0026	+	118.82%	GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase)
206166_PM_s_at	-2.97	0.0015	+	106.70%	CLCA2	chloride channel accessory 2
200734_PM_s_at	-2.96	0.0064	+	127.12%	LOC100131446	hypothetical protein LOC100131446
205194_PM_at	-2.96	0.0023	+	105.51%	PSPH	phosphoserine phosphatase
218856_PM_at	-2.96	0.0014	+	91.70%	TNFRSF21	tumor necrosis factor receptor superfamily, member 21
207387_PM_s_at	-2.95	0.0004	+	130.83%	GK	glycerol kinase
218796_PM_at	-2.95	0.0011	+	130.08%	FERMT1	fermitin family homolog 1 (Drosophila)
215011_PM_at	-2.95	0.0079	+	125.65%	ENSG0000020087	ENSG0000020087:snoRNA
219369_PM_s_at	-2.95	0.0023	+	113.71%	OTUB2	OTU domain, ubiquitin aldehyde binding 2
204580_PM_at	-2.95	0.0007	-	126.56%	MMP12	matrix metalloproteinase 12 (macrophage elastase)
218755_PM_at	-2.94	2.97E-05	+	135.37%	KIF20A	kinesin family member 20A
231849_PM_at	-2.93	0.0214	+	139.05%	KRT80	keratin 80
214214_PM_s_at	-2.92	0.0061	+	131.90%	C1QBP	complement component 1, q subcomponent binding protein
217835_PM_x_at	-2.92	0.0038	+	115.91%	C20orf24	chromosome 20 open reading

						frame 24
203770_PM_s_at	-2.92	0.0129	+	110.24%	STS	steroid sulfatase (microsomal), isozyme S
203147_PM_s_at	-2.91	4.63E-06	-	146.08%	TRIM14	tripartite motif-containing 14
227697_PM_at	-2.9	0.0482	-	171.78%	SOCS3	suppressor of cytokine signaling 3
205832_PM_at	-2.88	0.0044	+	138.22%	CPA4	carboxypeptidase A4
206094_PM_x_at	-2.88	0.0033	+	116.53%	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6
1555167_PM_s_at	-2.87	0.0013	+	134.74%	NAMPT	nicotinamide phosphoribosyltransferase
236039_PM_at	-2.87	0.0074	+	131.61%	LYPD5	LY6/PLAUR domain containing 5
240237_PM_at	-2.87	0.0021	-	131.28%	CLCN3	chloride channel 3
1553212_PM_at	-2.86	0.0005	+	132.57%	KRT78	keratin 78
222876_PM_s_at	-2.86	0.0013	+	126.94%	ADAP2	ArfGAP with dual PH domains 2
221666_PM_s_at	-2.86	0.0046	+	114.44%	PYCARD	PYD and CARD domain containing
AFFX-HUMISGF3A/M97935_MB_at	-2.86	0.0011	+	104.85%	STAT1	signal transducer and activator of transcription 1, 91kDa
203964_PM_at	-2.86	0.0011	+	100.26%	NMI	N-myc (and STAT) interactor
227458_PM_at	-2.86	0.0069	+	98.55%	CD274	CD274 molecule
222932_PM_at	-2.86	0.0032	+	95.05%	EHF	ets homologous factor
1557863_PM_at	-2.84	0.0044	+	139.61%	LOC100129266	Hypothetical protein LOC100129266
219648_PM_at	-2.84	0.0074	+	109.12%	MREG	melanoregulin
218349_PM_s_at	-2.84	0.0016	-	170.02%	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)
232667_PM_at	-2.84	0.0302	-	185.83%	232667_PM_at	---
218039_PM_at	-2.83	0.0145	+	111.68%	NUSAP1	nucleolar and spindle associated protein 1
204881_PM_s_at	-2.82	0.0352	+	118.98%	UGCG	UDP-glucose ceramide glucosyltransferase
222981_PM_s_at	-2.82	0.0055	+	117.95%	RAB10	RAB10, member RAS oncogene family
217845_PM_x_at	-2.82	0.0004	+	114.38%	HIGD1A	HIG1 hypoxia inducible domain family, member 1A
213793_PM_s_at	-2.82	0.0019	+	106.40%	HOMER1	homer homolog 1 (Drosophila)
224414_PM_s_at	-2.82	0.0466	+	82.99%	CARD6	caspase recruitment domain family, member 6
208546_PM_x_at	-2.82	0.0011	-	143.14%	HIST1H2BH	histone cluster 1, H2bh
208126_PM_s_at	-2.81	0.0202	+	123.62%	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18
216841_PM_s_at	-2.81	0.0088	+	119.56%	SOD2	superoxide dismutase 2, mitochondrial
229543_PM_at	-2.81	0.0387	+	119.18%	FAM26F	Family with sequence similarity 26, member F
214512_PM_s_at	-2.8	0.0003	+	135.88%	SUB1	SUB1 homolog (S. cerevisiae)

218186_PM_at	-2.8	0.0155	+	127.06%	RAB25	RAB25, member RAS oncogene family
207655_PM_s_at	-2.8	0.0011	+	101.17%	BLNK	B-cell linker
220066_PM_at	-2.8	0.0009	+	90.08%	NOD2	nucleotide-binding oligomerization domain containing 2
1555773_PM_at	-2.8	0.0103	-	140.62%	BPIL2	bactericidal/permeability-increasing protein-like 2
207114_PM_at	-2.8	0.0459	-	165.53%	LY6G6C	lymphocyte antigen 6 complex, locus G6C
212004_PM_at	-2.8	0.0053	-	159.17%	C1orf144	chromosome 1 open reading frame 144
210608_PM_s_at	-2.79	4.79E-05	+	124.98%	FUT2	fucosyltransferase 2 (secretor status included)
238513_PM_at	-2.79	0.0057	+	117.32%	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)
241355_PM_at	-2.79	4.02E-06	-	174.67%	HR	hairless homolog (mouse)
202712_PM_s_at	-2.78	2.18E-06	+	133.59%	CKMT1B	creatine kinase, mitochondrial 1B
243955_PM_at	-2.78	0.0004	+	129.73%	243955_PM_at	---
201530_PM_x_at	-2.78	0.0005	+	128.50%	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1
1563357_PM_at	-2.78	0.0158	+	115.81%	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9
205483_PM_s_at	-2.78	0.0002	+	115.25%	ISG15	ISG15 ubiquitin-like modifier
212021_PM_s_at	-2.77	0.0015	+	138.13%	MKI67	antigen identified by monoclonal antibody Ki-67
233565_PM_s_at	-2.77	0.0046	+	136.75%	SDCBP2	syndecan binding protein (syntenin) 2
202934_PM_at	-2.77	0.0004	+	125.79%	HK2	hexokinase 2
223298_PM_s_at	-2.77	0.0062	+	98.51%	NT5C3	5'-nucleotidase, cytosolic III
218355_PM_at	-2.77	0.0028	-	161.19%	KIF4A	kinesin family member 4A
214581_PM_x_at	-2.76	0.0005	+	114.74%	TNFRSF21	tumor necrosis factor receptor superfamily, member 21
202589_PM_at	-2.76	0.0026	-	147.92%	TYMS	thymidylate synthetase
204818_PM_at	-2.76	0.0085	-	141.00%	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2
211715_PM_s_at	-2.75	0.0005	+	131.21%	BDH1	3-hydroxybutyrate dehydrogenase, type 1
211712_PM_s_at	-2.75	0.0419	-	157.98%	ANXA9	annexin A9
226099_PM_at	-2.74	0.0135	+	92.19%	ELL2	elongation factor, RNA polymerase II, 2
226863_PM_at	-2.74	0.0313	+	89.62%	FAM110C	family with sequence similarity 110, member C
211796_PM_s_at	-2.74	0.0173	+	75.36%	TRBV19	T cell receptor beta variable 19
200798_PM_x_at	-2.72	0.0027	+	124.05%	LOC100131311	hypothetical LOC100131311
231697_PM_s_at	-2.72	0.0059	+	101.35%	231697_PM_s_at	---
208649_PM_s_at	-2.72	0.0002	-	141.39%	VCP	valosin-containing protein

242103_PM_at	-2.72	0.0004	-	163.24%	TMEM86A	transmembrane protein 86A
222639_PM_s_at	-2.71	0.0021	+	119.65%	PLBD1	phospholipase B domain containing 1
204616_PM_at	-2.71	0.0067	+	115.41%	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
221896_PM_s_at	-2.71	0.0025	+	112.24%	HIGD1A	HIG1 hypoxia inducible domain family, member 1A
202270_PM_at	-2.71	0.006	+	89.00%	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
1558195_PM_at	-2.71	0.0286	-	151.01%	LOC283404	hypothetical LOC283404
211762_PM_s_at	-2.71	0.0002	-	135.85%	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
211787_PM_s_at	-2.7	0.0005	+	122.79%	CD68	CD68 molecule
213293_PM_s_at	-2.7	0.0092	+	75.86%	TRIM22	tripartite motif-containing 22
218556_PM_at	-2.7	0.0137	-	141.32%	ORMDL2	ORM1-like 2 (S. cerevisiae)
225436_PM_at	-2.69	0.0087	+	109.98%	FAM108C1	family with sequence similarity 108, member C1
223193_PM_x_at	-2.69	0.0123	+	99.68%	FAM162A	family with sequence similarity 162, member A
200776_PM_s_at	-2.69	0.0023	+	96.78%	BZW1	basic leucine zipper and W2 domains 1
205402_PM_x_at	-2.69	1.18E-05	-	147.46%	TRY6	trypsinogen C
238710_PM_at	-2.68	0.0167	+	120.45%	TMEM86A	transmembrane protein 86A
218150_PM_at	-2.68	0.0322	+	106.85%	ARL5A	ADP-ribosylation factor-like 5A
225647_PM_s_at	-2.68	0.0141	+	103.59%	CTSC	cathepsin C
204351_PM_at	-2.68	0.008	-	206.20%	S100P	S100 calcium binding protein P
238996_PM_x_at	-2.68	0.0022	-	146.44%	ALDOA	aldolase A, fructose-bisphosphate
200824_PM_at	-2.67	4.65E-05	+	126.51%	GSTP1	glutathione S-transferase pi 1
205016_PM_at	-2.67	0.0019	+	116.68%	TGFA	transforming growth factor, alpha
1555745_PM_a_at	-2.67	0.008	+	70.78%	LYZ	lysozyme (renal amyloidosis)
204679_PM_at	-2.67	0.0005	-	148.25%	KCNK1	potassium channel, subfamily K, member 1
215779_PM_s_at	-2.67	0.0004	-	135.57%	HIST1H2BG	histone cluster 1, H2bg
228559_PM_at	-2.66	0.0113	+	121.66%	CENPN	centromere protein N
226276_PM_at	-2.66	0.0164	+	102.75%	TMEM167A	transmembrane protein 167A
202430_PM_s_at	-2.66	0.0151	+	91.95%	PLSCR1	phospholipid scramblase 1
1557864_PM_x_at	-2.66	0.0037	-	148.89%	LOC100129266	Hypothetical protein LOC100129266
203367_PM_at	-2.65	0.0006	+	127.85%	DUSP14	dual specificity phosphatase 14
227960_PM_s_at	-2.65	0.0153	+	114.28%	FAHD1	fumarylacetoacetate hydrolase domain containing 1
1569555_PM_at	-2.65	0.0047	+	112.86%	GDA	guanine deaminase
205476_PM_at	-2.65	0.0068	-	142.80%	CCL20	chemokine (C-C motif) ligand 20
208506_PM_at	-2.65	0.0174	-	133.85%	HIST1H3F	histone cluster 1, H3f

232074_PM_at	-2.64	5.29E-05	+	129.74%	PRSS27	protease, serine 27
211429_PM_s_at	-2.64	0.0036	+	114.09%	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
1563101_PM_at	-2.64	0.0006	+	112.48%	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2
224586_PM_x_at	-2.64	0.0007	+	106.72%	SUB1	SUB1 homolog (S. cerevisiae)
225541_PM_at	-2.64	0.0197	+	106.49%	RPL22L1	ribosomal protein L22-like 1
209761_PM_s_at	-2.64	0.0171	-	149.19%	SP110	SP110 nuclear body protein
216470_PM_x_at	-2.64	1.91E-06	-	139.07%	PRSS3	protease, serine, 3
221081_PM_s_at	-2.64	0.0003	-	148.28%	DENND2D	DENN/MADD domain containing 2D
229764_PM_at	-2.64	0.0305	-	147.44%	TPRG1	tumor protein p63 regulated 1
202788_PM_at	-2.63	0.0027	+	124.57%	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3
219978_PM_s_at	-2.63	0.0065	+	123.53%	NUSAP1	nucleolar and spindle associated protein 1
202069_PM_s_at	-2.63	0.0019	+	121.16%	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha
225645_PM_at	-2.63	0.0048	+	109.70%	EHF	ets homologous factor
203362_PM_s_at	-2.63	0.0073	+	90.57%	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
217028_PM_at	-2.63	0.0178	+	80.81%	CXCR4	chemokine (C-X-C motif) receptor 4
201584_PM_s_at	-2.62	0.0001	+	129.93%	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
224480_PM_s_at	-2.62	0.0031	+	115.08%	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9
228698_PM_at	-2.62	0.0036	+	93.03%	SOX7	SRY (sex determining region Y)-box 7
1564063_PM_a_at	-2.62	0.0027	+	92.06%	ATP11B	ATPase, class VI, type 11B
226649_PM_at	-2.61	0.0249	+	130.40%	PANK1	pantothenate kinase 1
223544_PM_at	-2.61	0.0009	+	113.87%	TMEM79	transmembrane protein 79
205241_PM_at	-2.61	0.0013	+	108.69%	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)
201088_PM_at	-2.61	0.0004	-	150.03%	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
229538_PM_s_at	-2.61	0.0182	-	159.15%	IQGAP3	IQ motif containing GTPase activating protein 3
238063_PM_at	-2.6	0.0406	+	109.07%	TMEM154	transmembrane protein 154
202582_PM_s_at	-2.6	0.0148	+	107.03%	RANBP9	RAN binding protein 9
220528_PM_at	-2.6	0.0017	+	98.42%	VNN3	vanin 3
202446_PM_s_at	-2.6	0.0076	+	90.95%	PLSCR1	phospholipid scramblase 1
1557136_PM_at	-2.6	0.0127	-	141.98%	ATP13A4	ATPase type 13A4
207861_PM_at	-2.6	0.0016	-	139.94%	CCL22	chemokine (C-C motif) ligand 22
226960_PM_at	-2.6	0.0032	-	155.41%	CXCL17	chemokine (C-X-C motif) ligand 17
205633_PM_s_at	-2.59	0.0056	+	116.33%	ALAS1	aminolevulinate, delta-, synthase 1

200886_PM_s_at	-2.59	0.0014	+	114.44%	PGAM1	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1).
208905_PM_at	-2.59	0.0099	+	103.29%	CYCS	cytochrome c, somatic
212022_PM_s_at	-2.59	0.0171	-	155.87%	MKI67	antigen identified by monoclonal antibody Ki-67
225667_PM_s_at	-2.59	0.0023	-	148.91%	FAM84A	family with sequence similarity 84, member A
226319_PM_s_at	-2.59	0.0451	-	164.51%	THOC4	THO complex 4
201118_PM_at	-2.58	0.0005	+	123.24%	PGD	phosphogluconate dehydrogenase
1569003_PM_at	-2.58	0.0042	+	121.21%	TMEM49	transmembrane protein 49
221521_PM_s_at	-2.58	0.0003	+	113.67%	GINS2	GINS complex subunit 2 (Psf2 homolog)
224345_PM_x_at	-2.58	0.0058	+	109.90%	FAM162A	family with sequence similarity 162, member A
209970_PM_x_at	-2.58	0.0004	+	92.24%	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
218982_PM_s_at	-2.57	0.0322	+	122.03%	MRPS17	mitochondrial ribosomal protein S17
203233_PM_at	-2.57	0.0011	+	118.24%	IL4R	interleukin 4 receptor
207254_PM_at	-2.57	0.0135	+	114.66%	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1
222646_PM_s_at	-2.57	0.0351	+	106.43%	ERO1L	ERO1-like (S. cerevisiae)
231240_PM_at	-2.57	0.0153	+	94.81%	DIO2	deiodinase, iodothyronine, type II
210834_PM_s_at	-2.57	0.0007	-	166.10%	PTGER3	prostaglandin E receptor 3 (subtype EP3)
231249_PM_at	-2.57	0.0335	-	228.93%	HYI	hydroxypyruvate isomerase homolog (E. coli)
202870_PM_s_at	-2.56	1.02E-05	+	125.65%	CDC20	cell division cycle 20 homolog (S. cerevisiae)
222774_PM_s_at	-2.56	0.0041	+	116.44%	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2
207165_PM_at	-2.56	0.0052	-	91.87%	HMMR	hyaluronan-mediated motility receptor (RHAMM)
208188_PM_at	-2.56	0.0132	-	133.22%	KRT9	keratin 9
220724_PM_at	-2.56	0.0113	-	130.37%	CWH43	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
227677_PM_at	-2.56	0.0005	-	144.12%	JAK3	Janus kinase 3
239061_PM_at	-2.55	0.0035	+	127.14%	TPRXL	tetra-peptide repeat homeobox-like
207828_PM_s_at	-2.55	0.0103	+	115.18%	CENPF	centromere protein F, 350/400ka (mitosin)
226617_PM_at	-2.55	0.0322	+	101.76%	ARL5A	ADP-ribosylation factor-like 5A
201209_PM_at	-2.55	0.0163	-	129.78%	HDAC1	histone deacetylase 1

1557236_PM_at	-2.54	0.0011	+	99.23%	APOL6	apolipoprotein L, 6
204976_PM_s_at	-2.54	0.0267	+	97.94%	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1
219412_PM_at	-2.54	0.0322	+	85.58%	RAB38	RAB38, member RAS oncogene family
218611_PM_at	-2.53	0.0051	+	121.28%	IER5	immediate early response 5
208827_PM_at	-2.53	0.0074	+	111.37%	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6
217192_PM_s_at	-2.53	0.0236	+	90.38%	PRDM1	PR domain containing 1, with ZNF domain
210293_PM_s_at	-2.53	0.0277	-	133.01%	SEC23B	Sec23 homolog B (<i>S. cerevisiae</i>)
223381_PM_at	-2.53	0.0004	-	115.33%	NUF2	NUF2, NDC80 kinetochore complex component, homolog (<i>S. cerevisiae</i>)
242727_PM_at	-2.52	0.0174	+	118.68%	ARL5B	ADP-ribosylation factor-like 5B
224446_PM_at	-2.52	0.0032	+	115.10%	LLPH	LLP homolog, long-term synaptic facilitation (<i>Aplysia</i>)
203798_PM_s_at	-2.52	0.0022	+	106.22%	VSNL1	visinin-like 1
223834_PM_at	-2.52	0.003	+	106.16%	CD274	CD274 molecule
203148_PM_s_at	-2.52	0.0081	+	101.86%	TRIM14	tripartite motif-containing 14
208424_PM_s_at	-2.52	0.0084	-	156.41%	CIAPIN1	cytokine induced apoptosis inhibitor 1
222500_PM_at	-2.52	0.0015	-	132.55%	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1
200863_PM_s_at	-2.51	0.0117	+	114.99%	RAB11A	RAB11A, member RAS oncogene family
228378_PM_at	-2.51	0.0287	+	110.91%	C12orf29	chromosome 12 open reading frame 29
206472_PM_s_at	-2.51	0.0081	-	132.85%	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, <i>Drosophila</i>)
224839_PM_s_at	-2.51	9.60E-06	-	129.46%	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2
235928_PM_at	-2.51	0.041	-	125.99%	235928_PM_at	---
238439_PM_at	-2.51	0.0448	-	140.04%	ANKRD22	ankyrin repeat domain 22
242477_PM_at	-2.51	0.0005	-	150.16%	TTC39B	tetratricopeptide repeat domain 39B
214011_PM_s_at	-2.5	0.0105	+	115.32%	NOP16	NOP16 nucleolar protein homolog (yeast)
235857_PM_at	-2.5	0.0229	+	107.87%	KCTD11	potassium channel tetramerisation domain containing 11
210915_PM_x_at	-2.5	0.0164	+	82.39%	TRBV19	T cell receptor beta variable 19
1555427_PM_s_at	-2.5	0.0044	-	155.40%	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
207911_PM_s_at	-2.5	0.0023	-	153.08%	TGM5	transglutaminase 5

220942_PM_x_at	-2.49	0.0068	+	108.73%	FAM162A	family with sequence similarity 162, member A
221923_PM_s_at	-2.49	0.0017	+	108.53%	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
219918_PM_s_at	-2.49	0.0059	+	100.27%	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
225415_PM_at	-2.49	0.0206	+	80.67%	DTX3L	deltex 3-like (Drosophila)
204141_PM_at	-2.49	0.0222	-	123.30%	TUBB2A	tubulin, beta 2A
215380_PM_s_at	-2.48	0.0073	+	113.88%	GGCT	gamma-glutamyl cyclotransferase
209546_PM_s_at	-2.48	0.0007	+	107.31%	APOL1	apolipoprotein L, 1
218095_PM_s_at	-2.48	0.0109	+	86.69%	TMEM165	transmembrane protein 165
212041_PM_at	-2.48	0.0013	-	128.56%	ATP6V0D1	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d1
1558292_PM_s_at	-2.47	0.0221	+	104.23%	PIGW	phosphatidylinositol glycan anchor biosynthesis, class W
210833_PM_at	-2.47	0.0442	+	102.73%	PTGER3	prostaglandin E receptor 3 (subtype EP3)
242294_PM_at	-2.46	0.014	+	122.48%	FBXO45	F-box protein 45
208898_PM_at	-2.46	0.0362	+	112.23%	ATP6V1D	ATPase, H ⁺ transporting, lysosomal 34kDa, V1 subunit D
200999_PM_s_at	-2.46	0.0005	+	110.31%	LOC100130905	hypothetical LOC100130905
206632_PM_s_at	-2.46	0.0154	+	106.48%	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
206765_PM_at	-2.46	0.0172	-	149.48%	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2
209260_PM_at	-2.46	0.0014	-	127.28%	SFN	stratifin
219270_PM_at	-2.46	4.22E-05	-	123.04%	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)
243550_PM_at	-2.46	0.0005	-	127.65%	ZDHHC21	zinc finger, DHHC-type containing 21
209124_PM_at	-2.45	0.0008	+	119.09%	MYD88	myeloid differentiation primary response gene (88)
209025_PM_s_at	-2.45	0.0015	+	106.78%	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
201524_PM_x_at	-2.45	0.0016	+	105.15%	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)
217764_PM_s_at	-2.45	0.0051	+	89.73%	RAB31	RAB31, member RAS oncogene family
208490_PM_x_at	-2.45	0.0028	-	145.69%	HIST1H2BF	histone cluster 1, H2bf
235095_PM_at	-2.45	2.51E-06	-	186.94%	CCDC64B	coiled-coil domain containing 64B
1564520_PM_s_at	-2.44	0.0229	+	117.57%	PRMT5	protein arginine methyltransferase 5
207181_PM_s_at	-2.44	0.0016	+	107.89%	CASP7	caspase 7, apoptosis-related

						cysteine peptidase
1554252_PM_a_at	-2.44	0.0068	-	141.78%	LASS3	LAG1 homolog, ceramide synthase 3
204510_PM_at	-2.44	0.0035	-	131.64%	CDC7	cell division cycle 7 homolog (S. cerevisiae)
209372_PM_x_at	-2.44	0.0137	-	131.23%	TUBB2A	tubulin, beta 2A
210213_PM_s_at	-2.44	0.0005	-	131.11%	EIF6	eukaryotic translation initiation factor 6
210636_PM_at	-2.44	0.0011	-	128.90%	PPARD	peroxisome proliferator-activated receptor delta
213011_PM_s_at	-2.44	0.0004	-	133.09%	TPI1	triosephosphate isomerase 1
223518_PM_at	-2.43	0.0056	+	120.36%	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide
236471_PM_at	-2.43	0.0237	+	115.91%	NFE2L3	nuclear factor (erythroid-derived 2)-like 3
221898_PM_at	-2.43	0.0326	+	115.71%	PDPN	podoplanin
237753_PM_at	-2.43	0.0196	+	110.37%	IL21R	interleukin 21 receptor
224612_PM_s_at	-2.43	0.0095	+	108.39%	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5
202314_PM_at	-2.43	0.022	+	105.91%	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1
203046_PM_s_at	-2.43	6.02E-05	+	104.02%	TIMELESS	timeless homolog (Drosophila)
202266_PM_at	-2.43	0.0139	+	86.18%	TTRAP	TRAF and TNF receptor associated protein
210059_PM_s_at	-2.43	0.0032	-	150.77%	MAPK13	mitogen-activated protein kinase 13
223291_PM_at	-2.43	0.0005	-	148.99%	MRPS15	mitochondrial ribosomal protein S15
222607_PM_s_at	-2.42	0.0162	+	118.70%	DIS3	DIS3 mitotic control homolog (S. cerevisiae)
201437_PM_s_at	-2.42	0.0011	+	115.07%	EIF4E	eukaryotic translation initiation factor 4E
224232_PM_s_at	-2.42	0.0109	+	111.02%	PRELID1	PRELI domain containing 1
201745_PM_at	-2.42	0.0125	+	93.55%	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)
214829_PM_at	-2.42	0.0034	+	85.07%	AASS	aminoadipate-semialdehyde synthase
214088_PM_s_at	-2.42	0.0006	-	124.47%	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)
60528_PM_at	-2.42	0.0004	-	137.01%	JMJD7-PLA2G4B	JMJD7-PLA2G4B readthrough
203499_PM_at	-2.41	0.0005	+	118.04%	EPHA2	EPH receptor A2
204715_PM_at	-2.41	0.0263	+	112.82%	PANX1	pannexin 1
53720_PM_at	-2.41	0.015	+	96.06%	C19orf66	chromosome 19 open reading frame 66
204962_PM_s_at	-2.41	0.0006	-	128.61%	CENPA	centromere protein A
207206_PM_s_at	-2.41	0.0084	-	179.57%	ALOX12	arachidonate 12-lipoxygenase
209247_PM_s_at	-2.41	0.0008	-	126.72%	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2

221893_PM_s_at	-2.41	0.0386	-	185.63%	ADCK2	aarF domain containing kinase 2
223993_PM_s_at	-2.41	0.0157	-	122.62%	CNIH4	cornichon homolog 4 (Drosophila)
219459_PM_at	-2.4	0.0213	+	111.81%	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B
217752_PM_s_at	-2.4	0.0036	+	104.56%	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)
211366_PM_x_at	-2.4	0.0023	+	94.60%	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
1553213_PM_a_at	-2.4	0.0046	-	128.14%	KRT78	keratin 78
203511_PM_s_at	-2.4	0.0165	-	121.35%	TRAPPC3	trafficking protein particle complex 3
203747_PM_at	-2.4	8.46E-05	-	149.58%	AQP3	aquaporin 3 (Gill blood group)
203968_PM_s_at	-2.4	0.0043	-	136.51%	CDC6	cell division cycle 6 homolog (S. cerevisiae)
217183_PM_at	-2.4	0.0005	-	127.63%	LDLR	low density lipoprotein receptor
227103_PM_s_at	-2.4	0.0024	-	129.30%	ECE2	endothelin converting enzyme 2
225105_PM_at	-2.39	0.0137	+	112.99%	C12orf75	chromosome 12 open reading frame 75
202540_PM_s_at	-2.39	0.04	+	112.48%	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
200654_PM_at	-2.39	8.88E-05	-	122.15%	P4HB	prolyl 4-hydroxylase, beta polypeptide
200708_PM_at	-2.39	0.0016	-	126.69%	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
202284_PM_s_at	-2.39	0.0148	-	127.88%	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
205239_PM_at	-2.39	0.0316	-	120.17%	AREG	amphiregulin
217834_PM_s_at	-2.39	0.0002	-	122.90%	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
221987_PM_s_at	-2.39	0.0232	-	132.07%	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)
225822_PM_at	-2.39	0.0118	-	158.01%	TMEM125	transmembrane protein 125
234335_PM_s_at	-2.39	0.0133	-	138.37%	FAM84A	family with sequence similarity 84, member A
209191_PM_at	-2.38	0.0069	+	109.06%	TUBB6	tubulin, beta 6
217933_PM_s_at	-2.38	0.0149	+	96.93%	LAP3	leucine aminopeptidase 3
200777_PM_s_at	-2.38	0.0082	+	90.22%	BZW1	basic leucine zipper and W2 domains 1
1552487_PM_a_at	-2.38	0.0072	-	145.74%	BNC1	basonuclin 1
203616_PM_at	-2.38	0.0015	-	125.05%	POLB	polymerase (DNA directed), beta
226059_PM_at	-2.38	0.0023	-	142.86%	TOMM40L	translocase of outer mitochondrial membrane 40

						homolog (yeast)-like
244748_PM_at	-2.38	0.0428	-	168.83%	TMPRSS4	transmembrane protease, serine 4
200733_PM_s_at	-2.37	0.0045	+	113.46%	PTP4A1	protein tyrosine phosphatase type IVA, member 1
223434_PM_at	-2.37	0.0036	+	109.23%	GBP3	guanylate binding protein 3
205554_PM_s_at	-2.37	0.0014	+	94.45%	DNASE1L3	deoxyribonuclease I-like 3
217851_PM_s_at	-2.37	0.0484	+	85.19%	SLMO2	slowmo homolog 2 (Drosophila)
210119_PM_at	-2.37	0.0105	+	78.67%	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15
201251_PM_at	-2.37	7.47E-05	-	130.22%	PKM2	pyruvate kinase, muscle
205844_PM_at	-2.37	0.016	-	90.37%	VNN1	vanin 1
208496_PM_x_at	-2.37	0.0021	-	120.62%	HIST1H3G	histone cluster 1, H3g
213911_PM_s_at	-2.37	0.0039	-	139.30%	H2AFZ	H2A histone family, member Z
222866_PM_s_at	-2.37	0.0006	-	117.95%	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2
223218_PM_s_at	-2.37	0.0022	-	127.08%	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
234331_PM_s_at	-2.37	0.0014	-	182.01%	FAM84A	family with sequence similarity 84, member A
201274_PM_at	-2.36	0.0019	+	112.31%	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5
220318_PM_at	-2.36	0.0017	+	111.65%	EPN3	epsin 3
205349_PM_at	-2.36	0.0033	+	106.82%	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
200853_PM_at	-2.36	0.0016	-	144.41%	H2AFZ	H2A histone family, member Z
201245_PM_s_at	-2.36	0.0035	-	157.53%	OTUB1	OTU domain, ubiquitin aldehyde binding 1
225344_PM_at	-2.36	0.0072	-	126.47%	NCOA7	nuclear receptor coactivator 7
200693_PM_at	-2.35	0.0127	+	116.36%	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
232277_PM_at	-2.35	0.0028	+	110.83%	232277_PM_at	---
218943_PM_s_at	-2.35	0.0011	+	86.95%	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
1553505_PM_at	-2.35	0.0083	-	163.65%	A2ML1	alpha-2-macroglobulin-like 1
218009_PM_s_at	-2.35	0.0008	-	128.89%	PRC1	protein regulator of cytokinesis 1
221637_PM_s_at	-2.35	0.0006	-	138.66%	C11orf48	chromosome 11 open reading frame 48
208596_PM_s_at	-2.34	0.0178	+	115.96%	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6
1557458_PM_s_at	-2.34	0.0062	+	109.66%	SHB	Src homology 2 domain containing adaptor protein B

202120_PM_x_at	-2.34	0.0015	+	108.88%	AP2S1	adaptor-related protein complex 2, sigma 1 subunit
203700_PM_s_at	-2.34	0.0041	+	107.67%	DIO2	deiodinase, iodothyronine, type II
213101_PM_s_at	-2.34	0.0313	+	106.90%	ACTR3	ARP3 actin-related protein 3 homolog (yeast)
227928_PM_at	-2.34	0.0418	+	104.92%	C12orf48	chromosome 12 open reading frame 48
206332_PM_s_at	-2.34	0.0059	+	96.40%	IFI16	interferon, gamma-inducible protein 16
225478_PM_at	-2.34	0.0398	+	71.98%	MFHAS1	malignant fibrous histiocytoma amplified sequence 1
1554510_PM_s_at	-2.34	0.022	-	116.58%	GHITM	growth hormone inducible transmembrane protein
203746_PM_s_at	-2.34	0.0125	-	118.46%	HCCS	holocytochrome c synthase (cytochrome c heme-lyase)
213577_PM_at	-2.34	0.0062	-	118.18%	SQLE	squalene epoxidase
219806_PM_s_at	-2.34	0.0164	-	159.90%	C11orf75	chromosome 11 open reading frame 75
223478_PM_at	-2.34	0.0087	-	121.72%	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)
225687_PM_at	-2.34	0.0003	-	117.65%	FAM83D	family with sequence similarity 83, member D
227177_PM_at	-2.34	0.0041	-	148.50%	CORO2A	coronin, actin binding protein, 2A
215890_PM_at	-2.33	0.0092	+	113.71%	GM2A	GM2 ganglioside activator
201577_PM_at	-2.33	0.0013	+	110.56%	NME1-NME2	NME1-NME2 readthrough
204809_PM_at	-2.33	0.005	+	105.87%	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)
206877_PM_at	-2.33	0.0145	+	105.64%	MXD1	MAX dimerization protein 1
202195_PM_s_at	-2.33	0.0064	-	143.27%	TMED5	transmembrane emp24 protein transport domain containing 5
203145_PM_at	-2.33	4.73E-05	-	144.64%	SPAG5	sperm associated antigen 5
222811_PM_at	-2.33	0.0005	-	122.42%	FTSJD1	FtsJ methyltransferase domain containing 1
223060_PM_at	-2.33	0.0021	-	140.52%	C14orf119	chromosome 14 open reading frame 119
232751_PM_at	-2.33	0.0015	-	178.68%	RBBP9	retinoblastoma binding protein 9
1554179_PM_s_at	-2.32	0.0157	+	112.44%	LYNX1	Ly6/neurotoxin 1
222859_PM_s_at	-2.32	0.0335	+	111.59%	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides
209803_PM_s_at	-2.32	0.0302	+	111.15%	PHLDA2	pleckstrin homology-like domain, family A, member 2
229396_PM_at	-2.32	0.0199	+	108.43%	OVOL1	ovo-like 1(Drosophila)
226621_PM_at	-2.32	0.0411	+	106.72%	FGG	fibrinogen gamma chain
214056_PM_at	-2.32	0.0056	+	101.98%	LOC100131311	hypothetical LOC100131311
209853_PM_s_at	-2.32	0.0091	+	98.08%	PSME3	proteasome (prosome, macropain) activator subunit

						3 (PA28 gamma; Ki)
214329_PM_x_at	-2.32	0.0275	+	82.98%	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
213193_PM_x_at	-2.32	0.0163	+	82.10%	TRBV19	T cell receptor beta variable 19
208436_PM_s_at	-2.32	0.0001	-	125.13%	IRF7	interferon regulatory factor 7
216228_PM_s_at	-2.32	0.0221	-	120.45%	WDHD1	WD repeat and HMG-box DNA binding protein 1
222354_PM_at	-2.32	0.0025	-	149.54%	hCG_20857	hypothetical protein LOC100134860
227452_PM_at	-2.32	0.0234	-	121.64%	227452_PM_at	---
229070_PM_at	-2.32	0.0229	-	122.58%	C6orf105	chromosome 6 open reading frame 105
204444_PM_at	-2.31	0.0177	+	110.76%	KIF11	kinesin family member 11
224654_PM_at	-2.31	0.0336	+	103.02%	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
203699_PM_s_at	-2.31	0.0059	+	95.69%	DIO2	deiodinase, iodothyronine, type II
215223_PM_s_at	-2.31	0.0311	+	92.60%	SOD2	superoxide dismutase 2, mitochondrial
208992_PM_s_at	-2.31	0.0004	-	136.37%	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)
216554_PM_s_at	-2.31	0.0004	-	140.42%	ENO1	enolase 1, (alpha)
238567_PM_at	-2.3	0.0225	+	112.55%	SGPP2	sphingosine-1-phosphate phosphatase 2
218188_PM_s_at	-2.3	9.36E-05	+	111.32%	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)
203132_PM_at	-2.3	0.0083	+	105.42%	RB1	retinoblastoma 1
203887_PM_s_at	-2.3	0.0412	+	103.27%	THBD	thrombomodulin
1553364_PM_at	-2.3	0.0207	-	142.25%	PNPLA1	patatin-like phospholipase domain containing 1
213076_PM_at	-2.3	0.0062	-	133.26%	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C
217755_PM_at	-2.3	0.001	-	116.64%	HN1	hematological and neurological expressed 1
218163_PM_at	-2.3	0.0065	-	117.98%	MCTS1	malignant T cell amplified sequence 1
221269_PM_s_at	-2.3	0.0026	-	117.54%	SH3BGL3	SH3 domain binding glutamic acid-rich protein like 3
208652_PM_at	-2.29	0.0018	+	110.85%	PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
204823_PM_at	-2.29	0.0164	+	108.86%	NAV3	neuron navigator 3
228654_PM_at	-2.29	0.0194	+	107.87%	SPIN4	spindlin family, member 4
212978_PM_at	-2.29	0.0214	+	106.44%	LRRC8B	leucine rich repeat containing 8 family, member B
AFFX-HUMISGF3A/M97935_MA_at	-2.29	0.0023	+	88.98%	STAT1	signal transducer and activator of transcription 1, 91kDa
204341_PM_at	-2.29	0.0286	-	131.68%	TRIM16	tripartite motif-containing 16
208577_PM_at	-2.29	0.0003	-	125.58%	HIST1H3C	histone cluster 1, H3c

208579_PM_x_at	-2.29	0.0029	-	131.31%	H2BFS	H2B histone family, member S
212432_PM_at	-2.29	0.0125	-	116.38%	GRPEL1	GrpE-like 1, mitochondrial (E. coli)
225083_PM_at	-2.29	0.0084	-	118.70%	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa
225620_PM_at	-2.29	0.0057	-	123.85%	RAB35	RAB35, member RAS oncogene family
203128_PM_at	-2.28	0.0176	+	111.68%	SPTLC2	serine palmitoyltransferase, long chain base subunit 2
201876_PM_at	-2.28	0.0042	+	108.22%	PON2	paraoxonase 2
201735_PM_s_at	-2.28	0.0039	+	107.72%	CLCN3	chloride channel 3
224806_PM_at	-2.28	0.0184	+	101.60%	TRIM25	tripartite motif-containing 25
209585_PM_s_at	-2.28	0.0016	+	95.95%	MINPP1	multiple inositol polyphosphate histidine phosphatase, 1
217763_PM_s_at	-2.28	0.0232	+	91.99%	RAB31	RAB31, member RAS oncogene family
204023_PM_at	-2.28	0.011	-	128.48%	RFC4	replication factor C (activator 1) 4, 37kDa
205534_PM_at	-2.28	0.0277	-	125.84%	PCDH7	protocadherin 7
206023_PM_at	-2.28	0.0163	-	127.26%	NMU	neuromedin U
209558_PM_s_at	-2.28	0.0003	-	164.41%	HIP1R	huntingtin interacting protein 1 related
206109_PM_at	-2.27	0.0441	+	109.76%	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)
225536_PM_at	-2.27	0.0212	+	107.54%	TMEM54	transmembrane protein 54
201587_PM_s_at	-2.27	0.0065	+	102.72%	IRAK1	interleukin-1 receptor-associated kinase 1
212295_PM_s_at	-2.27	0.0051	+	101.25%	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
1558687_PM_a_at	-2.27	0.0277	-	124.47%	FOXN1	forkhead box N1
201732_PM_s_at	-2.27	0.0389	-	116.37%	CLCN3	chloride channel 3
213174_PM_at	-2.27	0.0303	-	114.68%	TTC9	tetratricopeptide repeat domain 9
217294_PM_s_at	-2.27	0.0178	-	130.61%	ENO1	enolase 1, (alpha)
222702_PM_x_at	-2.26	0.0477	+	111.21%	CRIP1	cysteine-rich PDZ-binding protein
234464_PM_s_at	-2.26	0.0064	+	104.65%	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)
204942_PM_s_at	-2.26	0.0114	+	104.38%	ALDH3B2	aldehyde dehydrogenase 3 family, member B2
1553059_PM_at	-2.26	0.0013	-	132.31%	PGLYRP3	peptidoglycan recognition protein 3
200822_PM_x_at	-2.26	0.0029	-	121.04%	TPI1	triosephosphate isomerase 1
219680_PM_at	-2.26	0.0042	-	120.99%	NLRX1	NLR family member X1
224813_PM_at	-2.25	0.0245	+	105.15%	WASL	Wiskott-Aldrich syndrome-

						like
220990_PM_s_at	-2.25	0.0024	+	99.49%	MIR21	microRNA 21
202357_PM_s_at	-2.25	0.0164	+	91.28%	CFB	complement factor B
1555764_PM_s_at	-2.25	0.0043	-	125.52%	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)
200052_PM_s_at	-2.25	0.0107	-	131.23%	ILF2	interleukin enhancer binding factor 2, 45kDa
200660_PM_at	-2.25	4.12E-06	-	123.18%	S100A11	S100 calcium binding protein A11
202309_PM_at	-2.25	5.69E-05	-	146.81%	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
226421_PM_at	-2.25	0.0094	-	112.64%	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1
236172_PM_at	-2.25	0.0049	-	130.38%	LTB4R	leukotriene B4 receptor
208708_PM_x_at	-2.24	0.0029	+	108.91%	EIF5	eukaryotic translation initiation factor 5
215979_PM_s_at	-2.24	0.0016	+	107.77%	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
213696_PM_s_at	-2.24	0.01	+	107.32%	MED8	mediator complex subunit 8
201475_PM_x_at	-2.24	0.0051	+	107.13%	MARS	methionyl-tRNA synthetase
223032_PM_x_at	-2.24	0.0043	+	105.07%	PRELID1	PRELI domain containing 1
200838_PM_at	-2.24	0.0218	-	119.20%	CTSB	cathepsin B
202780_PM_at	-2.24	0.0242	-	126.32%	OXCT1	3-oxoacid CoA transferase 1
207992_PM_s_at	-2.24	0.0012	-	120.49%	AMPD3	adenosine monophosphate deaminase (isoform E)
221437_PM_s_at	-2.24	0.0109	-	127.86%	MRPS15	mitochondrial ribosomal protein S15
221871_PM_s_at	-2.24	0.0093	-	156.61%	TFG	TRK-fused gene
223414_PM_s_at	-2.24	0.001	-	131.74%	LYAR	Ly1 antibody reactive homolog (mouse)
224982_PM_at	-2.24	0.019	-	122.83%	AKT1S1	AKT1 substrate 1 (proline-rich)
223738_PM_s_at	-2.23	0.0447	+	90.76%	PGM2	phosphoglucomutase 2
204058_PM_at	-2.23	0.0393	+	80.50%	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic
33304_PM_at	-2.23	0.0103	+	76.67%	ISG20	interferon stimulated exonuclease gene 20kDa
203418_PM_at	-2.23	0.0037	-	117.45%	CCNA2	cyclin A2
219347_PM_at	-2.23	0.0084	-	118.11%	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15
225404_PM_at	-2.23	0.0099	-	122.44%	C1orf212	chromosome 1 open reading frame 212

200996_PM_at	-2.22	0.0468	+	104.09%	ACTR3	ARP3 actin-related protein 3 homolog (yeast)
203476_PM_at	-2.22	0.0006	+	87.36%	TPBG	trophoblast glycoprotein
200894_PM_s_at	-2.22	0.0005	-	147.23%	FKBP4	FK506 binding protein 4, 59kDa
203755_PM_at	-2.22	0.0076	-	142.54%	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
212882_PM_at	-2.22	0.0408	-	113.60%	KLHL18	kelch-like 18 (Drosophila)
218677_PM_at	-2.22	0.001	-	119.17%	S100A14	S100 calcium binding protein A14
211506_PM_s_at	-2.21	0.0374	+	108.88%	IL8	interleukin 8
226560_PM_at	-2.21	0.0122	+	98.17%	SGPP2	sphingosine-1-phosphate phosphatase 2
215966_PM_x_at	-2.21	0.0078	+	92.53%	GK3P	glycerol kinase 3 pseudogene
202954_PM_at	-2.21	0.0067	-	128.23%	UBE2C	ubiquitin-conjugating enzyme E2C
205774_PM_at	-2.21	0.003	-	122.78%	F12	coagulation factor XII (Hageman factor)
209249_PM_s_at	-2.21	0.0188	-	126.11%	GHITM	growth hormone inducible transmembrane protein
220723_PM_s_at	-2.21	0.0084	-	114.65%	CWH43	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
225260_PM_s_at	-2.21	0.0019	-	112.44%	MRPL32	mitochondrial ribosomal protein L32
227919_PM_at	-2.21	0.0047	-	160.74%	UCA1	urothelial cancer associated 1 (non-protein coding)
208152_PM_s_at	-2.2	0.0209	+	105.13%	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
217995_PM_at	-2.2	0.0016	+	104.95%	SQRDL	sulfide quinone reductase-like (yeast)
222980_PM_at	-2.2	0.0373	+	100.73%	RAB10	RAB10, member RAS oncogene family
202154_PM_x_at	-2.2	0.0045	-	117.94%	TUBB3	tubulin, beta 3
213135_PM_at	-2.2	0.0351	-	143.13%	TIAM1	T-cell lymphoma invasion and metastasis 1
217970_PM_s_at	-2.2	0.0066	-	126.76%	CNOT6	CCR4-NOT transcription complex, subunit 6
225792_PM_at	-2.2	0.0017	-	114.78%	HOOK1	hook homolog 1 (Drosophila)
232181_PM_at	-2.19	0.0326	+	106.91%	LOC153346	hypothetical protein LOC153346
221779_PM_at	-2.19	0.0196	+	103.62%	MICALL1	MICAL-like 1
229500_PM_at	-2.19	0.0302	+	101.24%	SLC30A9	solute carrier family 30 (zinc transporter), member 9
212857_PM_x_at	-2.19	0.0031	+	99.97%	SUB1	SUB1 homolog (S. cerevisiae)
203971_PM_at	-2.19	0.0249	+	97.59%	SLC31A1	solute carrier family 31 (copper transporters), member 1
1557129_PM_a_at	-2.19	0.0074	+	96.60%	FAM111B	family with sequence similarity 111, member B
219684_PM_at	-2.19	0.0162	+	87.89%	RTP4	receptor (chemosensory) transporter protein 4

202168_PM_at	-2.19	0.0491	-	129.20%	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
202655_PM_at	-2.19	0.0038	-	115.83%	MANF	mesencephalic astrocyte-derived neurotrophic factor
204804_PM_at	-2.19	0.0012	-	132.46%	TRIM21	tripartite motif-containing 21
208374_PM_s_at	-2.19	0.0024	-	115.00%	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1
219695_PM_at	-2.19	0.0009	-	119.54%	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
227964_PM_at	-2.19	0.0011	-	115.06%	FRMD8	FERM domain containing 8
228607_PM_at	-2.19	0.0103	-	117.76%	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
229518_PM_at	-2.19	0.0426	-	126.87%	FAM46B	family with sequence similarity 46, member B
233687_PM_s_at	-2.18	7.12E-05	+	106.61%	KLK9	kallikrein-related peptidase 9
226706_PM_at	-2.18	0.0044	+	106.31%	FLJ23867	hypothetical protein FLJ23867
1553989_PM_a_at	-2.18	0.0053	-	140.10%	ATP6V1C2	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2
208900_PM_s_at	-2.18	0.0012	-	129.13%	TOP1	topoisomerase (DNA) I
210638_PM_s_at	-2.18	0.0002	-	111.90%	FBXO9	F-box protein 9
204478_PM_s_at	-2.17	0.0078	+	95.96%	RABIF	RAB interacting factor
213344_PM_s_at	-2.17	0.003	-	123.23%	H2AFX	H2A histone family, member X
219597_PM_s_at	-2.17	0.0002	-	138.58%	DUOX1	dual oxidase 1
224613_PM_s_at	-2.17	0.0015	-	130.04%	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5
228361_PM_at	-2.17	0.0007	-	126.07%	E2F2	E2F transcription factor 2
238164_PM_at	-2.17	0.0263	-	113.19%	USP6NL	USP6 N-terminal like
242722_PM_at	-2.17	0.0058	-	161.43%	LMO7	LIM domain 7
219037_PM_at	-2.16	0.0492	+	101.03%	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)
218357_PM_s_at	-2.16	0.003	+	99.80%	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)
229055_PM_at	-2.16	0.0049	+	91.31%	GPR68	G protein-coupled receptor 68
223361_PM_at	-2.16	0.044	+	84.19%	C6orf115	chromosome 6 open reading frame 115
1557866_PM_at	-2.16	0.0411	-	195.51%	C9orf117	chromosome 9 open reading frame 117
201196_PM_s_at	-2.16	0.0156	-	114.75%	AMD1	adenosylmethionine decarboxylase 1
201568_PM_at	-2.16	0.0037	-	118.96%	UQCRCQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa
204025_PM_s_at	-2.16	0.019	-	129.23%	PDCD2	programmed cell death 2
204117_PM_at	-2.16	0.0022	-	126.18%	PREP	prolyl endopeptidase

211730_PM_s_at	-2.16	0.0244	-	125.43%	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa
213945_PM_s_at	-2.16	0.0113	-	137.89%	NUP210	nucleoporin 210kDa
228648_PM_at	-2.16	0.0056	-	113.97%	LRG1	leucine-rich alpha-2-glycoprotein 1
241368_PM_at	-2.16	0.0241	-	112.16%	PLIN5	perilipin 5
39249_PM_at	-2.16	0.0011	-	146.64%	AQP3	aquaporin 3 (Gill blood group)
223335_PM_at	-2.15	0.0154	+	106.49%	TMEM69	transmembrane protein 69
201573_PM_s_at	-2.15	0.0112	+	106.44%	ETF1	eukaryotic translation termination factor 1
211047_PM_x_at	-2.15	0.0024	+	104.51%	AP2S1	adaptor-related protein complex 2, sigma 1 subunit
221840_PM_at	-2.15	0.0089	+	98.19%	PTPRE	protein tyrosine phosphatase, receptor type, E
200987_PM_x_at	-2.15	0.0267	+	87.67%	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
1553984_PM_s_at	-2.15	0.0024	-	127.85%	DTYMK	deoxythymidylate kinase (thymidylate kinase)
208523_PM_x_at	-2.15	0.0024	-	133.70%	HIST1H2BI	histone cluster 1, H2bi
213285_PM_at	-2.15	0.0415	-	114.80%	TMEM30B	transmembrane protein 30B
217173_PM_s_at	-2.15	0.0055	-	123.32%	LDLR	low density lipoprotein receptor
217786_PM_at	-2.15	0.0426	-	126.31%	PRMT5	protein arginine methyltransferase 5
201664_PM_at	-2.14	0.0226	+	103.92%	SMC4	structural maintenance of chromosomes 4
225686_PM_at	-2.14	0.0206	+	103.91%	SKA2	spindle and kinetochore associated complex subunit 2
219544_PM_at	-2.14	0.0214	+	103.11%	C13orf34	chromosome 13 open reading frame 34
212815_PM_at	-2.14	0.0476	+	95.55%	ASCC3	activating signal cointegrator 1 complex subunit 3
203256_PM_at	-2.14	0.0026	+	94.18%	CDH3	cadherin 3, type 1, P-cadherin (placental)
208966_PM_x_at	-2.14	0.0066	+	92.76%	IFI16	interferon, gamma-inducible protein 16
200658_PM_s_at	-2.14	0.0084	-	125.21%	PHB	prohibitin
205193_PM_at	-2.14	0.0189	-	130.00%	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
208478_PM_s_at	-2.14	0.0103	-	155.86%	BAX	BCL2-associated X protein
222441_PM_x_at	-2.14	0.0263	-	117.18%	SLMO2	slowmo homolog 2 (Drosophila)
230734_PM_x_at	-2.14	0.0292	-	123.55%	STRN	striatin, calmodulin binding protein
218027_PM_at	-2.13	0.0285	+	106.36%	MRPL15	mitochondrial ribosomal protein L15
225638_PM_at	-2.13	0.0176	+	105.56%	C1orf31	chromosome 1 open reading frame 31
229494_PM_s_at	-2.13	0.0094	+	104.70%	PHLDA2	pleckstrin homology-like domain, family A, member 2

208815_PM_x_at	-2.13	0.0081	+	99.60%	HSPA4	heat shock 70kDa protein 4
228053_PM_s_at	-2.13	0.0018	+	95.14%	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)
202269_PM_x_at	-2.13	0.0179	+	93.25%	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
213102_PM_at	-2.13	0.0488	+	92.34%	ACTR3	ARP3 actin-related protein 3 homolog (yeast)
200783_PM_s_at	-2.13	0.001	-	120.25%	STMN1	stathmin 1
200998_PM_s_at	-2.13	0.0035	-	109.48%	CKAP4	cytoskeleton-associated protein 4
201473_PM_at	-2.13	0.0225	-	131.28%	JUNB	jun B proto-oncogene
201884_PM_at	-2.13	0.0327	-	161.18%	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5
202199_PM_s_at	-2.13	0.0355	-	147.75%	SRPK1	SFRS protein kinase 1
204825_PM_at	-2.13	0.0008	-	125.69%	MELK	maternal embryonic leucine zipper kinase
208751_PM_at	-2.13	0.0068	-	152.33%	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha
209080_PM_x_at	-2.13	0.0001	-	110.35%	GLRX3	glutaredoxin 3
209251_PM_x_at	-2.13	0.0021	-	118.25%	TUBA1C	tubulin, alpha 1c
212861_PM_at	-2.13	0.0109	-	107.81%	MFSD5	major facilitator superfamily domain containing 5
225880_PM_at	-2.13	0.015	-	124.57%	225880_PM_at	---
201263_PM_at	-2.12	0.0024	+	105.20%	TARS	threonyl-tRNA synthetase
217745_PM_s_at	-2.12	0.0164	+	102.52%	NAT13	N-acetyltransferase 13 (GCN5-related)
205048_PM_s_at	-2.12	0.032	+	87.85%	PSPH	phosphoserine phosphatase
202088_PM_at	-2.12	0.0271	+	85.65%	SLC39A6	solute carrier family 39 (zinc transporter), member 6
1559946_PM_s_at	-2.12	0.0388	-	133.32%	RUVBL2	RuvB-like 2 (E. coli)
1566342_PM_at	-2.12	0.0099	-	108.57%	SOD2	Superoxide dismutase 2, mitochondrial
200903_PM_s_at	-2.12	0.0016	-	112.26%	AHCY	adenosylhomocysteinase
201853_PM_s_at	-2.12	0.0003	-	108.81%	CDC25B	cell division cycle 25 homolog B (S. pombe)
204695_PM_at	-2.12	0.0009	-	141.03%	CDC25A	cell division cycle 25 homolog A (S. pombe)
204761_PM_at	-2.12	0.0259	-	119.73%	USP6NL	USP6 N-terminal like
213189_PM_at	-2.12	0.0311	-	131.45%	MINA	MYC induced nuclear antigen
213933_PM_at	-2.12	0.0167	-	111.06%	PTGER3	prostaglandin E receptor 3 (subtype EP3)
226829_PM_at	-2.12	0.0055	-	118.57%	AFAP1L2	actin filament associated protein 1-like 2
202918_PM_s_at	-2.11	0.0234	+	103.61%	MOBKL3	MOB1, Mps One Binder kinase activator-like 3 (yeast)
201123_PM_s_at	-2.11	0.004	-	132.40%	EIF5A	eukaryotic translation initiation factor 5A
202263_PM_at	-2.11	0.0061	-	150.57%	CYB5R1	cytochrome b5 reductase 1
204281_PM_at	-2.11	0.0099	-	134.86%	TEAD4	TEA domain family member 4

209104_PM_s_at	-2.11	0.0127	-	113.94%	NHP2	NHP2 ribonucleoprotein homolog (yeast)
213523_PM_at	-2.11	0.0013	-	116.81%	CCNE1	cyclin E1
220966_PM_x_at	-2.11	0.0051	-	107.53%	ARPC5L	actin related protein 2/3 complex, subunit 5-like
223570_PM_at	-2.11	0.0014	-	123.04%	MCM10	minichromosome maintenance complex component 10
204440_PM_at	-2.1	0.0466	+	101.26%	CD83	CD83 molecule
217868_PM_s_at	-2.1	0.041	+	95.60%	METTL9	methyltransferase like 9
212724_PM_at	-2.1	0.0268	+	93.11%	RND3	Rho family GTPase 3
213857_PM_s_at	-2.1	0.0006	+	89.37%	CD47	CD47 molecule
206133_PM_at	-2.1	0.0099	+	89.25%	XAF1	XIAP associated factor 1
221690_PM_s_at	-2.1	0.0222	+	86.32%	NLRP2	NLR family, pyrin domain containing 2
1564521_PM_x_at	-2.1	0.0121	-	119.69%	PRMT5	protein arginine methyltransferase 5
1565836_PM_at	-2.1	0.0165	-	122.66%	1565836_PM_at	---
202626_PM_s_at	-2.1	0.0259	-	120.15%	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
205027_PM_s_at	-2.1	0.0121	-	122.38%	MAP3K8	mitogen-activated protein kinase kinase kinase 8
209040_PM_s_at	-2.1	0.0025	-	105.17%	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
211750_PM_x_at	-2.1	0.003	-	115.20%	TUBA1C	tubulin, alpha 1c
214091_PM_s_at	-2.1	0.04	-	125.63%	GPX3	glutathione peroxidase 3 (plasma)
217249_PM_x_at	-2.1	0.0092	-	130.74%	ENSG00000109238	ENSG00000109238:retrotransposed
219461_PM_at	-2.1	0.0168	-	134.26%	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6
223292_PM_s_at	-2.1	0.0084	-	147.25%	MRPS15	mitochondrial ribosomal protein S15
224587_PM_at	-2.1	0.0326	-	106.01%	SUB1	SUB1 homolog (S. cerevisiae)
225251_PM_at	-2.1	0.0007	-	126.08%	RAB24	RAB24, member RAS oncogene family
225616_PM_at	-2.1	0.0164	-	110.16%	SPRYD4	SPRY domain containing 4
228852_PM_at	-2.09	0.015	+	102.14%	ENSA	endosulfine alpha
208901_PM_s_at	-2.09	0.0381	+	95.83%	TOP1	topoisomerase (DNA) I
214838_PM_at	-2.09	0.0216	+	90.03%	SFT2D2	SFT2 domain containing 2
201252_PM_at	-2.09	0.0107	-	115.55%	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4
201930_PM_at	-2.09	0.0448	-	113.41%	MCM6	minichromosome maintenance complex component 6
217977_PM_at	-2.09	0.0044	-	121.38%	SEPX1	selenoprotein X, 1
218719_PM_s_at	-2.09	0.001	-	118.68%	GINS3	GINS complex subunit 3

						(Psf3 homolog)
226473_PM_at	-2.09	0.0015	-	109.53%	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)
241443_PM_at	-2.09	0.0155	-	115.92%	ADI1	acireductone dioxygenase 1
242873_PM_at	-2.09	0.0221	-	116.98%	KLRK1	killer cell lectin-like receptor subfamily K, member 1
39402_PM_at	-2.09	0.0259	-	133.73%	IL1B	interleukin 1, beta
226952_PM_at	-2.08	0.0253	+	102.77%	EAF1	ELL associated factor 1
1556551_PM_s_at	-2.08	0.0272	+	101.45%	SLC39A6	solute carrier family 39 (zinc transporter), member 6
213086_PM_s_at	-2.08	0.0078	+	91.52%	CSNK1A1	casein kinase 1, alpha 1
201351_PM_s_at	-2.08	0.0148	-	127.87%	YME1L1	YME1-like 1 (S. cerevisiae)
201848_PM_s_at	-2.08	0.0197	-	142.50%	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3
208576_PM_s_at	-2.08	0.0395	-	117.93%	HIST1H3B	histone cluster 1, H3b
224783_PM_at	-2.08	0.0002	-	129.59%	FAM100B	family with sequence similarity 100, member B
228869_PM_at	-2.08	0.0162	-	119.39%	NP_878274.1	selectin ligand interactor cytoplasmic-1
229037_PM_at	-2.08	0.0472	-	129.63%	TRIM69	tripartite motif-containing 69
214022_PM_s_at	-2.07	0.0172	+	86.94%	IFITM1	interferon induced transmembrane protein 1 (9-27)
201144_PM_s_at	-2.07	0.0165	-	113.95%	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
201231_PM_s_at	-2.07	0.0003	-	136.05%	ENO1	enolase 1, (alpha)
201733_PM_at	-2.07	0.0412	-	107.79%	CLCN3	chloride channel 3
213476_PM_x_at	-2.07	0.0083	-	128.88%	TUBB3	tubulin, beta 3
222752_PM_s_at	-2.07	0.0409	-	116.00%	TMEM206	transmembrane protein 206
224769_PM_at	-2.07	0.023	-	118.71%	224769_PM_at	---
225252_PM_at	-2.07	0.0105	-	105.96%	SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)
225291_PM_at	-2.07	0.0312	-	112.60%	PNPT1	polyribonucleotide nucleotidyltransferase 1
225535_PM_s_at	-2.07	0.0203	-	112.83%	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)
208648_PM_at	-2.06	0.0295	+	101.40%	VCP	valosin-containing protein
223151_PM_at	-2.06	0.0125	+	97.21%	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)
206513_PM_at	-2.06	0.0157	+	88.32%	AIM2	absent in melanoma 2
1555214_PM_a_at	-2.06	0.0221	-	113.87%	CLEC7A	C-type lectin domain family 7, member A
201805_PM_at	-2.06	0.0148	-	126.86%	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
205125_PM_at	-2.06	0.0083	-	107.10%	PLCD1	phospholipase C, delta 1
206491_PM_s_at	-2.06	0.0033	-	118.23%	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha

208505_PM_s_at	-2.06	0.0144	-	126.77%	FUT2	fucosyltransferase 2 (secretor status included)
208527_PM_x_at	-2.06	0.0036	-	137.49%	HIST1H2BE	histone cluster 1, H2be
209589_PM_s_at	-2.06	0.0367	-	111.43%	EPHB2	EPH receptor B2
213297_PM_at	-2.06	0.0208	-	121.48%	NHP2	NHP2 ribonucleoprotein homolog (yeast)
217167_PM_x_at	-2.06	0.0155	-	109.93%	GK	glycerol kinase
218028_PM_at	-2.06	0.0175	-	120.62%	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
227942_PM_s_at	-2.06	0.0449	-	107.61%	CRIP1	cysteine-rich PDZ-binding protein
236069_PM_at	-2.06	0.0015	-	129.74%	FLJ39005	hypothetical protein FLJ39005
212543_PM_at	-2.05	0.0215	+	101.28%	AIM1	absent in melanoma 1
226345_PM_at	-2.05	0.0272	+	92.36%	ARL5B	ADP-ribosylation factor-like 5B
213860_PM_x_at	-2.05	0.0151	+	91.28%	CSNK1A1	casein kinase 1, alpha 1
212268_PM_at	-2.05	0.017	+	88.24%	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
203465_PM_at	-2.05	0.0283	-	105.57%	MRPL19	mitochondrial ribosomal protein L19
207540_PM_s_at	-2.05	0.0078	-	115.85%	SYK	spleen tyrosine kinase
218728_PM_s_at	-2.05	0.003	-	126.54%	CNIH4	cornichon homolog 4 (Drosophila)
219006_PM_at	-2.05	0.012	-	106.87%	NDUFAF4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4
220608_PM_s_at	-2.05	0.0165	-	117.42%	ZNF770	zinc finger protein 770
221962_PM_s_at	-2.05	0.0302	-	126.97%	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
223982_PM_s_at	-2.05	0.0333	-	111.50%	PNPLA8	patatin-like phospholipase domain containing 8
202060_PM_at	-2.04	0.0399	+	95.79%	CTR9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
208744_PM_x_at	-2.04	0.0172	+	95.27%	HSPH1	heat shock 105kDa/110kDa protein 1
209159_PM_s_at	-2.04	0.0053	+	94.52%	NDRG4	NDRG family member 4
201762_PM_s_at	-2.04	0.0007	+	94.42%	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
208693_PM_s_at	-2.04	0.0078	+	92.80%	GARS	glycyl-tRNA synthetase
201487_PM_at	-2.04	0.0481	+	76.95%	CTSC	cathepsin C
200925_PM_at	-2.04	0.0032	-	129.03%	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1
200935_PM_at	-2.04	0.0121	-	137.40%	CALR	calreticulin
201594_PM_s_at	-2.04	0.0005	-	109.85%	PPP4R1	protein phosphatase 4, regulatory subunit 1
201614_PM_s_at	-2.04	0.0096	-	129.04%	RUVBL1	RuvB-like 1 (E. coli)
208484_PM_at	-2.04	0.0018	-	109.83%	HIST1H1A	histone cluster 1, H1a

209338_PM_at	-2.04	0.011	-	126.25%	TFCP2	transcription factor CP2
214537_PM_at	-2.04	0.0014	-	128.94%	HIST1H1D	histone cluster 1, H1d
228324_PM_at	-2.04	0.0143	-	117.13%	C9orf41	chromosome 9 open reading frame 41
228538_PM_at	-2.04	0.015	-	124.50%	ZNF662	zinc finger protein 662
201850_PM_at	-2.03	0.0012	-	125.81%	CAPG	capping protein (actin filament), gelsolin-like
203214_PM_x_at	-2.03	0.0026	-	134.95%	CDC2	cell division cycle 2, G1 to S and G2 to M
203416_PM_at	-2.03	0.0216	-	104.21%	CD53	CD53 molecule
217962_PM_at	-2.03	0.024	-	105.80%	NOP10	NOP10 ribonucleoprotein homolog (yeast)
220475_PM_at	-2.03	0.0397	-	104.80%	SLC28A3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3
223574_PM_x_at	-2.03	0.0014	-	120.84%	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform
232520_PM_s_at	-2.03	0.0269	-	126.87%	NSFL1C	NSFL1 (p97) cofactor (p47)
238025_PM_at	-2.03	0.0259	-	147.81%	MLKL	mixed lineage kinase domain-like
226726_PM_at	-2.02	0.0164	+	97.22%	MBOAT2	membrane bound O-acyltransferase domain containing 2
212290_PM_at	-2.02	0.0045	+	95.63%	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
221245_PM_s_at	-2.02	0.0308	+	85.65%	FZD5	frizzled homolog 5 (Drosophila)
200957_PM_s_at	-2.02	0.0176	-	120.84%	SSRP1	structure specific recognition protein 1
202299_PM_s_at	-2.02	0.0215	-	115.19%	HBXIP	hepatitis B virus x interacting protein
203585_PM_at	-2.02	0.0223	-	124.99%	ZNF185	zinc finger protein 185 (LIM domain)
215093_PM_at	-2.02	0.0042	-	131.80%	NSDHL	NAD(P) dependent steroid dehydrogenase-like
216041_PM_x_at	-2.02	0.0293	-	131.40%	GRN	granulin
223497_PM_at	-2.02	0.0312	-	110.35%	FAM135A	family with sequence similarity 135, member A
223515_PM_s_at	-2.02	0.0461	-	109.21%	COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)
228910_PM_at	-2.02	1.42E-05	-	117.39%	CD82	CD82 molecule
240242_PM_at	-2.02	0.04	-	147.56%	240242_PM_at	---
243645_PM_at	-2.02	0.0064	-	125.90%	NFASC	neurofascin homolog (chicken)
1552257_PM_a_at	-2.01	0.0023	-	122.94%	TTLL12	tubulin tyrosine ligase-like family, member 12
200703_PM_at	-2.01	0.0127	-	111.78%	DYNLL1	dynein, light chain, LC8-type 1
202483_PM_s_at	-2.01	0.0051	-	118.93%	RANBP1	RAN binding protein 1

208696_PM_at	-2.01	0.0095	-	112.85%	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)
214794_PM_at	-2.01	0.0379	-	115.19%	PA2G4	proliferation-associated 2G4, 38kDa
222425_PM_s_at	-2.01	0.0115	-	133.61%	POLDIP2	polymerase (DNA-directed), delta interacting protein 2
224785_PM_at	-2.01	0.0102	-	113.38%	FAM100B	family with sequence similarity 100, member B
218543_PM_s_at	-2	0.0019	+	99.48%	PARP12	poly (ADP-ribose) polymerase family, member 12
222843_PM_at	-2	0.0057	+	94.37%	FIGNL1	fidgetin-like 1
201601_PM_x_at	-2	0.0106	+	87.44%	IFITM1	interferon induced transmembrane protein 1 (9-27)
201317_PM_s_at	-2	0.0366	-	102.36%	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2
209852_PM_x_at	-2	0.0443	-	113.45%	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
217919_PM_s_at	-2	0.0254	-	107.42%	MRPL42	mitochondrial ribosomal protein L42
220104_PM_at	-2	0.0024	-	105.80%	ZC3HAV1	zinc finger CCCH-type, antiviral 1
222642_PM_s_at	-2	0.0056	-	110.19%	TMEM33	transmembrane protein 33
229545_PM_at	-2	0.0213	-	112.72%	FERMT1	fermitin family homolog 1 (Drosophila)
221957_PM_at	2	0.0142	+	91.63%	PDK3	pyruvate dehydrogenase kinase, isozyme 3
201010_PM_s_at	2	0.0005	-	112.19%	TXNIP	thioredoxin interacting protein
209867_PM_s_at	2	0.0211	-	141.73%	LPHN3	latrophilin 3
210495_PM_x_at	2	0.0059	-	168.53%	FN1	fibronectin 1
212677_PM_s_at	2	0.006	-	130.06%	CEP68	centrosomal protein 68kDa
214451_PM_at	2	0.0019	-	114.48%	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
217430_PM_x_at	2	0.0395	-	158.37%	COL1A1	collagen, type I, alpha 1
218418_PM_s_at	2	0.0037	-	131.61%	KANK2	KN motif and ankyrin repeat domains 2
225816_PM_at	2	0.0128	-	154.82%	PHF17	PHD finger protein 17
226407_PM_at	2	0.0213	-	127.06%	RCN1	reticulocalbin 1, EF-hand calcium binding domain
238658_PM_at	2.01	0.0489	+	97.42%	238658_PM_at	---
1569126_PM_at	2.01	0.0465	-	110.34%	CCNC	cyclin C
201952_PM_at	2.01	0.0041	-	117.92%	ALCAM	activated leukocyte cell adhesion molecule
202037_PM_s_at	2.01	0.0248	-	109.38%	SFRP1	secreted frizzled-related protein 1
213914_PM_s_at	2.01	0.0028	-	102.55%	SPTBN1	spectrin, beta, non-erythrocytic 1
215183_PM_at	2.01	0.0378	-	105.88%	215183_PM_at	---

215945_PM_s_at	2.01	0.0006	-	109.45%	TRIM2	tripartite motif-containing 2
222135_PM_at	2.01	0.0223	-	-190.72%	ZNF814	zinc finger protein 814
222298_PM_at	2.01	0.0193	-	115.70%	TSGA13	testis specific, 13
223623_PM_at	2.01	0.0175	-	104.40%	C2orf40	chromosome 2 open reading frame 40
232692_PM_at	2.01	0.0176	-	174.16%	TDRD6	tudor domain containing 6
236189_PM_at	2.01	0.021	-	136.28%	ANKRD50	ankyrin repeat domain 50
238408_PM_at	2.01	0.023	-	107.80%	OXR1	oxidation resistance 1
223836_PM_at	2.02	0.0144	+	98.08%	FGFBP2	fibroblast growth factor binding protein 2
205043_PM_at	2.02	0.0218	+	95.83%	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)
1570361_PM_a_at	2.02	0.0261	-	126.29%	1570361_PM_a_at	---
203414_PM_at	2.02	0.0334	-	185.90%	MMD	monocyte to macrophage differentiation-associated
215992_PM_s_at	2.02	0.0191	-	121.39%	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2
220407_PM_s_at	2.02	0.0173	-	140.31%	TGFB2	transforming growth factor, beta 2
221833_PM_at	2.02	0.0242	-	125.79%	SIAH1	seven in absentia homolog 1 (Drosophila)
221950_PM_at	2.02	0.0404	-	133.21%	EMX2	empty spiracles homeobox 2
223251_PM_s_at	2.02	0.0202	-	126.70%	ANKRD10	ankyrin repeat domain 10
225720_PM_at	2.02	0.0156	-	116.71%	SYNPO2	synaptopodin 2
225926_PM_at	2.02	0.0369	-	189.58%	ARG2	arginase, type II
226625_PM_at	2.02	0.0012	-	107.80%	TGFBR3	transforming growth factor, beta receptor III
238414_PM_at	2.03	0.0468	+	95.33%	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)
239479_PM_x_at	2.03	0.0484	+	92.23%	239479_PM_x_at	---
1559988_PM_at	2.03	0.0099	-	122.88%	ZNF483	zinc finger protein 483
204863_PM_s_at	2.03	0.0011	-	121.07%	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)
208944_PM_at	2.03	0.0178	-	163.76%	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)
214850_PM_at	2.03	0.0119	-	112.50%	LOC100170939	glucuronidase, beta pseudogene
214972_PM_at	2.03	0.0042	-	106.85%	MGEA5	meningioma expressed antigen 5 (hyaluronidase)
224098_PM_at	2.03	0.0099	-	143.24%	LOC100290874	hypothetical protein LOC100290874
236419_PM_at	2.03	0.0358	-	131.04%	236419_PM_at	---
244292_PM_at	2.03	0.0425	-	129.08%	244292_PM_at	---
219689_PM_at	2.04	0.0255	+	101.87%	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G
200696_PM_s_at	2.04	0.0005	-	118.92%	GSN	gelsolin (amyloidosis, Finnish

						type)
211347_PM_at	2.04	0.0018	-	154.93%	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
213547_PM_at	2.04	0.0242	-	126.65%	CAND2	cullin-associated and neddylation-dissociated 2 (putative)
221645_PM_s_at	2.04	0.0069	-	127.21%	ZNF83	zinc finger protein 83
224560_PM_at	2.04	0.0028	-	130.88%	TIMP2	TIMP metalloproteinase inhibitor 2
224763_PM_at	2.04	0.0005	-	118.43%	RPL37	ribosomal protein L37
232528_PM_at	2.04	0.0428	-	127.84%	232528_PM_at	---
235167_PM_at	2.05	0.0082	+	90.50%	LOC100190986	hypothetical LOC100190986
212937_PM_s_at	2.05	0.037	-	155.55%	COL6A1	collagen, type VI, alpha 1
214722_PM_at	2.05	1.02E-05	-	112.73%	NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like
216035_PM_x_at	2.05	0.0057	-	121.14%	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)
220436_PM_at	2.05	0.03	-	117.28%	CNTNAP3	contactin associated protein-like 3
229935_PM_s_at	2.05	0.0227	-	121.13%	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)
233980_PM_s_at	2.05	0.0001	-	146.01%	VWF	von Willebrand factor
238512_PM_at	2.05	0.0468	-	122.09%	ST7L	suppression of tumorigenicity 7 like
225545_PM_at	2.06	0.0044	+	92.31%	EEF2K	eukaryotic elongation factor-2 kinase
203498_PM_at	2.06	0.0169	-	116.86%	RCAN2	regulator of calcineurin 2
209220_PM_at	2.06	0.0224	-	132.34%	GPC3	glypican 3
209437_PM_s_at	2.06	0.0245	-	191.49%	SPON1	spondin 1, extracellular matrix protein
216902_PM_s_at	2.06	0.0106	-	156.51%	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene
235044_PM_at	2.06	0.0099	-	155.58%	CYYR1	cysteine/tyrosine-rich 1
40446_PM_at	2.06	0.0085	-	118.21%	PHF1	PHD finger protein 1
241673_PM_x_at	2.07	0.0481	+	99.16%	241673_PM_x_at	---
1561274_PM_at	2.07	0.0014	-	124.39%	CRYBB2P1	crystallin, beta B2 pseudogene 1
1562228_PM_s_at	2.07	0.0155	-	146.58%	PDE5A	phosphodiesterase 5A, cGMP-specific
202551_PM_s_at	2.07	0.0023	-	126.66%	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
204969_PM_s_at	2.07	0.0486	-	155.67%	RDX	radixin
205765_PM_at	2.07	0.0045	-	111.43%	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5
214454_PM_at	2.07	0.0311	-	150.02%	ADAMTS2	ADAM metalloproteinase with thrombospondin type 1 motif, 2
221986_PM_s_at	2.07	0.0162	-	122.61%	KLHL24	kelch-like 24 (Drosophila)

223378_PM_at	2.07	0.0347	-	138.61%	GLIS2	GLIS family zinc finger 2
224191_PM_x_at	2.07	0.0255	-	120.15%	ROPN1	ropporin, rhophilin associated protein 1
227662_PM_at	2.07	0.0279	-	128.33%	SYNPO2	synaptopodin 2
232991_PM_at	2.07	0.0236	-	150.55%	ARL17	ADP-ribosylation factor-like 17
1564426_PM_x_at	2.08	0.0085	+	91.83%	LOC389634	hypothetical LOC389634
203571_PM_s_at	2.08	0.0131	-	110.00%	C10orf116	chromosome 10 open reading frame 116
211890_PM_x_at	2.08	0.0381	-	132.41%	CAPN3	calpain 3, (p94)
224920_PM_x_at	2.08	0.0085	-	124.54%	MYADM	myeloid-associated differentiation marker
225915_PM_at	2.08	0.0422	-	113.15%	CAB39L	calcium binding protein 39-like
226342_PM_at	2.08	0.019	-	129.25%	SPTBN1	spectrin, beta, non-erythrocytic 1
232729_PM_at	2.08	0.0126	-	125.99%	FBXO32	F-box protein 32
235136_PM_at	2.08	0.0311	-	153.71%	ORMDL3	ORM1-like 3 (S. cerevisiae)
235267_PM_at	2.08	0.0092	-	147.21%	235267_PM_at	---
238558_PM_at	2.08	0.0085	-	109.69%	238558_PM_at	---
211388_PM_s_at	2.09	0.0346	+	91.86%	211388_PM_s_at	---
223185_PM_s_at	2.09	0.02	+	73.36%	BHLHE41	basic helix-loop-helix family, member e41
1553693_PM_s_at	2.09	0.007	-	129.95%	CBR4	carbonyl reductase 4
205559_PM_s_at	2.09	0.0065	-	165.11%	PCSK5	proprotein convertase subtilisin/kexin type 5
210198_PM_s_at	2.09	0.0176	-	119.50%	PLP1	proteolipid protein 1
211220_PM_s_at	2.09	0.0137	-	122.81%	HSF2	heat shock transcription factor 2
221747_PM_at	2.09	0.004	-	127.03%	TNS1	tensin 1
221748_PM_s_at	2.09	0.0021	-	124.69%	TNS1	tensin 1
226984_PM_at	2.09	0.041	-	159.29%	FGD5	FYVE, RhoGEF and PH domain containing 5
244308_PM_at	2.09	0.0403	-	152.70%	SYT15	Synaptotagmin XV
244581_PM_at	2.09	0.0331	-	124.27%	ZBTB20	zinc finger and BTB domain containing 20
209283_PM_at	2.1	0.0068	+	92.14%	CRYAB	crystallin, alpha B
1552646_PM_at	2.1	0.0356	-	111.21%	IL11RA	interleukin 11 receptor, alpha
1568876_PM_a_at	2.1	0.0265	-	122.03%	1568876_PM_a_at	---
202379_PM_s_at	2.1	0.0156	-	107.72%	NKTR	natural killer-tumor recognition sequence
203851_PM_at	2.1	0.0059	-	106.09%	IGFBP6	insulin-like growth factor binding protein 6
209488_PM_s_at	2.1	0.0385	-	123.10%	LOC100134188	hypothetical protein LOC100134188
225571_PM_at	2.1	0.0121	-	108.09%	LIFR	leukemia inhibitory factor receptor alpha
227550_PM_at	2.1	0.0343	-	124.45%	GFRA1	GDNF family receptor alpha 1
228885_PM_at	2.1	0.0146	-	121.18%	MAMDC2	MAM domain containing 2

236131_PM_at	2.1	0.0319	-	121.58%	TSGA13	testis specific, 13
239017_PM_at	2.11	0.0211	+	79.34%	Q6ZP57_HUMAN	CDNA FLJ26472 fis, clone KDN04506.
1557081_PM_at	2.11	0.0149	-	110.29%	RBM25	RNA binding motif protein 25
209656_PM_s_at	2.11	0.0135	-	115.25%	TMEM47	transmembrane protein 47
226326_PM_at	2.11	0.0015	-	144.26%	PCGF5	polycomb group ring finger 5
227514_PM_at	2.11	0.02	-	130.09%	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2
236649_PM_at	2.11	0.0492	-	136.49%	DTWD1	DTW domain containing 1
1552643_PM_at	2.12	0.0018	-	152.01%	ZNF626	zinc finger protein 626
209168_PM_at	2.12	0.0142	-	176.31%	GPM6B	glycoprotein M6B
209522_PM_s_at	2.12	0.0292	-	116.18%	CRAT	carnitine acetyltransferase
219179_PM_at	2.12	0.0277	-	132.57%	DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
1558802_PM_at	2.13	0.0174	-	149.12%	1558802_PM_at	---
205440_PM_s_at	2.13	0.0114	-	115.80%	NPY1R	neuropeptide Y receptor Y1
205522_PM_at	2.13	0.0308	-	205.04%	HOXD4	homeobox D4
213348_PM_at	2.13	0.043	-	138.62%	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
222316_PM_at	2.13	0.0178	-	130.03%	222316_PM_at	---
228245_PM_s_at	2.13	0.0444	-	161.00%	OVOS2	ovostatin 2
228811_PM_at	2.13	0.0063	-	116.44%	TMEM8B	transmembrane protein 8B
229879_PM_at	2.13	0.0096	-	159.05%	CLVS1	clavesin 1
235024_PM_at	2.13	0.0176	-	126.73%	PHF17	PHD finger protein 17
232417_PM_x_at	2.14	0.0065	+	94.49%	ZDHHC11	zinc finger, DHHC-type containing 11
204712_PM_at	2.14	0.0258	+	78.09%	WIF1	WNT inhibitory factor 1
204627_PM_s_at	2.14	0.0495	-	140.23%	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
205923_PM_at	2.14	0.0178	-	134.24%	RELN	reelin
213974_PM_at	2.14	0.0162	-	118.52%	ADAMTSL3	ADAMTS-like 3
228255_PM_at	2.14	0.0103	-	132.20%	ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4
241091_PM_at	2.14	0.0292	-	123.31%	241091_PM_at	---
242960_PM_at	2.14	0.0323	-	212.72%	EPC2	enhancer of polycomb homolog 2 (Drosophila)
243168_PM_at	2.14	0.0131	-	116.25%	PDZK1	PDZ domain containing 1
209909_PM_s_at	2.15	0.0092	+	104.95%	TGFB2	transforming growth factor, beta 2
206116_PM_s_at	2.15	0.0018	+	102.44%	TPM1	tropomyosin 1 (alpha)
206059_PM_at	2.15	0.0253	+	100.05%	ZNF91	zinc finger protein 91
230064_PM_at	2.15	0.0253	+	94.47%	230064_PM_at	---
201918_PM_at	2.15	0.0227	-	131.07%	SLC25A36	solute carrier family 25, member 36
203542_PM_s_at	2.15	0.0176	-	121.81%	KLF9	Kruppel-like factor 9

212732_PM_at	2.15	0.0186	-	163.82%	LOC100131839	hypothetical protein LOC100131839
220065_PM_at	2.15	0.0142	-	132.95%	TNMD	tenomodulin
229111_PM_at	2.15	0.0191	-	140.53%	MASP2	mannan-binding lectin serine peptidase 2
239475_PM_at	2.15	0.0114	-	155.83%	ACPL2	acid phosphatase-like 2
241090_PM_at	2.15	0.0497	-	112.49%	PKD1	polycystic kidney disease 1 (autosomal dominant)
243233_PM_at	2.15	0.0109	-	139.96%	243233_PM_at	---
220940_PM_at	2.16	0.0163	+	102.27%	ANKRD36B	ankyrin repeat domain 36B
1560263_PM_at	2.16	0.0442	-	129.92%	GPBP1L1	GC-rich promoter binding protein 1-like 1
224959_PM_at	2.16	0.0036	-	128.89%	SLC26A2	solute carrier family 26 (sulfate transporter), member 2
226252_PM_at	2.16	0.0014	-	139.38%	226252_PM_at	---
239577_PM_at	2.16	0.0117	-	127.07%	239577_PM_at	---
1558075_PM_at	2.17	0.0015	+	100.46%	LOC339047	Hypothetical protein LOC339047
211685_PM_s_at	2.17	0.0043	+	100.21%	NCALD	neurocalcin delta
238751_PM_at	2.17	0.0322	+	89.61%	SORBS2	sorbin and SH3 domain containing 2
215388_PM_s_at	2.17	0.0017	-	150.00%	LOC100293069	similar to complement factor H-related 1
226999_PM_at	2.17	0.0383	-	130.19%	RNPC3	RNA-binding region (RNP1, RRM) containing 3
228434_PM_at	2.17	0.0162	-	123.16%	BTNL9	butyrophilin-like 9
229130_PM_at	2.17	0.0188	-	147.85%	229130_PM_at	---
240646_PM_at	2.17	0.0034	-	120.68%	GIMAP8	GTPase, IMAP family member 8
201496_PM_x_at	2.18	0.022	+	100.05%	MYH11	myosin, heavy chain 11, smooth muscle
215322_PM_at	2.18	0.0262	+	96.83%	215322_PM_at	---
201893_PM_x_at	2.18	0.0339	-	141.53%	DCN	decorin
206088_PM_at	2.18	0.0095	-	124.43%	LRRC37A	leucine rich repeat containing 37A
210944_PM_s_at	2.18	0.0213	-	125.43%	CAPN3	calpain 3, (p94)
218665_PM_at	2.18	0.0086	-	135.38%	FZD4	frizzled homolog 4 (Drosophila)
226656_PM_at	2.18	0.0002	-	115.18%	CRTAP	cartilage associated protein
228770_PM_at	2.18	0.0096	-	148.00%	GPR146	G protein-coupled receptor 146
1553105_PM_s_at	2.19	0.0339	+	100.57%	DSG2	desmoglein 2
1555318_PM_at	2.19	0.0026	-	154.69%	HIF3A	hypoxia inducible factor 3, alpha subunit
1558906_PM_a_at	2.19	0.0101	-	110.37%	1558906_PM_a_at	---
200672_PM_x_at	2.19	0.0005	-	109.90%	SPTBN1	spectrin, beta, non-erythrocytic 1
203706_PM_s_at	2.19	0.015	-	140.49%	FZD7	frizzled homolog 7 (Drosophila)
204734_PM_at	2.19	0.0059	-	116.91%	KRT15	keratin 15

206373_PM_at	2.19	0.0176	-	171.54%	ZIC1	Zic family member 1 (odd-paired homolog, Drosophila)
225575_PM_at	2.19	0.006	-	126.89%	LIFR	leukemia inhibitory factor receptor alpha
226869_PM_at	2.19	0.0112	-	140.10%	MEGF6	multiple EGF-like-domains 6
227000_PM_at	2.19	0.0117	-	144.31%	C7orf41	chromosome 7 open reading frame 41
225895_PM_at	2.2	0.0281	+	107.90%	SYNPO2	synaptopodin 2
240595_PM_at	2.2	0.0135	+	102.20%	240595_PM_at	---
1552316_PM_a_at	2.2	0.031	-	140.15%	GIMAP1	GTPase, IMAP family member 1
209070_PM_s_at	2.2	0.007	-	181.55%	RGS5	regulator of G-protein signaling 5
213156_PM_at	2.2	0.0042	-	137.24%	213156_PM_at	---
215324_PM_at	2.2	0.0004	-	155.15%	SEMA3D	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D
231989_PM_s_at	2.2	0.0016	-	112.10%	LOC641298	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene
235570_PM_at	2.2	2.18E-05	-	219.63%	235570_PM_at	---
241417_PM_at	2.21	0.0082	+	103.52%	241417_PM_at	---
1567440_PM_at	2.21	0.0379	+	92.17%	PSEN1	presenilin 1
214093_PM_s_at	2.21	0.0211	-	152.15%	FUBP1	far upstream element (FUSE) binding protein 1
221834_PM_at	2.21	0.0064	-	125.45%	SIAH1	seven in absentia homolog 1 (Drosophila)
230231_PM_at	2.21	0.0084	-	203.59%	FGF14	fibroblast growth factor 14
243495_PM_s_at	2.21	0.0004	-	119.23%	ZNF652	zinc finger protein 652
244648_PM_at	2.21	0.0149	-	112.86%	CCDC93	coiled-coil domain containing 93
230891_PM_at	2.22	0.0253	+	109.58%	TUBE1	tubulin, epsilon 1
209183_PM_s_at	2.22	0.015	-	132.31%	C10orf10	chromosome 10 open reading frame 10
209574_PM_s_at	2.22	0.0105	-	123.87%	C18orf1	chromosome 18 open reading frame 1
231881_PM_at	2.22	0.0064	-	166.27%	CALD1	caldesmon 1
237061_PM_at	2.22	0.0076	-	123.61%	ZNF347	zinc finger protein 347
1559485_PM_at	2.23	0.0191	-	154.71%	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)
201958_PM_s_at	2.23	0.0175	-	133.70%	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B
209199_PM_s_at	2.23	0.0148	-	210.12%	MEF2C	myocyte enhancer factor 2C
219140_PM_s_at	2.23	0.0474	-	139.68%	RBP4	retinol binding protein 4, plasma
227529_PM_s_at	2.23	0.0082	-	160.02%	AKAP12	A kinase (PRKA) anchor protein 12
228934_PM_x_at	2.23	0.0059	-	122.66%	228934_PM_x_at	---
231411_PM_at	2.23	0.0011	-	156.12%	LHFP	lipoma HMGIC fusion

						partner
227917_PM_at	2.24	0.032	+	97.84%	FAM85A	family with sequence similarity 85, member A
202760_PM_s_at	2.24	1.49E-05	-	142.71%	PALM2	paralemmin 2
213158_PM_at	2.24	0.0023	-	152.43%	213158_PM_at	---
215483_PM_at	2.24	0.0173	-	122.19%	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9
220735_PM_s_at	2.24	0.0017	-	151.44%	SEN7	SUMO1/sentrin specific peptidase 7
226992_PM_at	2.24	0.0111	-	125.70%	NOSTRIN	nitric oxide synthase trafficker
227489_PM_at	2.24	0.0117	-	120.11%	SMURF2	SMAD specific E3 ubiquitin protein ligase 2
239262_PM_at	2.24	0.0271	-	138.27%	239262_PM_at	---
222102_PM_at	2.25	0.0212	+	109.77%	GSTA3	glutathione S-transferase alpha 3
203957_PM_at	2.25	0.0313	-	217.66%	E2F6	E2F transcription factor 6
220117_PM_at	2.25	0.0142	-	166.24%	ZNF385D	zinc finger protein 385D
230047_PM_at	2.25	0.0226	-	115.84%	FLJ32810	Rho-type GTPase-activating protein FLJ32810
234056_PM_at	2.25	0.0438	-	136.26%	234056_PM_at	---
204570_PM_at	2.26	0.0021	+	109.87%	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
1560119_PM_at	2.26	0.0475	+	108.49%	LOC157278	hypothetical protein LOC157278
206117_PM_at	2.26	0.0021	+	104.82%	TPM1	tropomyosin 1 (alpha)
205872_PM_x_at	2.26	0.0005	+	98.25%	PDE4DIP	phosphodiesterase 4D interacting protein
1559603_PM_at	2.26	0.016	+	79.35%	GPR12	G protein-coupled receptor 12
1566194_PM_at	2.26	0.0357	-	155.80%	1566194_PM_at	---
202973_PM_x_at	2.26	0.0278	-	135.34%	FAM13A	family with sequence similarity 13, member A
225721_PM_at	2.26	0.005	-	116.17%	SYNPO2	synaptopodin 2
227121_PM_at	2.26	0.0022	-	143.10%	227121_PM_at	---
201148_PM_s_at	2.27	0.0047	+	108.32%	TIMP3	TIMP metalloproteinase inhibitor 3
201539_PM_s_at	2.27	0.0135	+	106.52%	FHL1	four and a half LIM domains 1
205730_PM_s_at	2.27	0.0086	-	138.15%	ABLIM3	actin binding LIM protein family, member 3
216511_PM_s_at	2.27	0.0008	-	117.62%	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)
226047_PM_at	2.27	0.0414	-	148.77%	MRVI1	murine retrovirus integration site 1 homolog
225054_PM_x_at	2.28	0.0027	+	110.81%	LOC651250	hypothetical LOC651250
243030_PM_at	2.28	0.0331	+	104.57%	243030_PM_at	---
1566571_PM_at	2.28	0.0069	+	98.29%	MFSD4	major facilitator superfamily domain containing 4
207050_PM_at	2.28	0.0046	-	141.68%	CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1

215294_PM_s_at	2.28	0.012	-	185.97%	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
220298_PM_s_at	2.28	0.0082	-	121.06%	SPATA6	spermatogenesis associated 6
235110_PM_at	2.28	0.0087	-	124.62%	PLA2G16	phospholipase A2, group XVI
239049_PM_at	2.29	0.0275	-	136.07%	239049_PM_at	---
242134_PM_at	2.29	0.0015	-	149.06%	242134_PM_at	---
225835_PM_at	2.3	0.0277	+	111.40%	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
210280_PM_at	2.3	0.003	+	107.37%	MPZ	myelin protein zero
235412_PM_at	2.3	0.0037	+	107.07%	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7
203896_PM_s_at	2.3	0.0029	+	104.75%	PLCB4	phospholipase C, beta 4
1552774_PM_a_at	2.3	0.0137	-	120.93%	SLC25A27	solute carrier family 25, member 27
1562416_PM_at	2.3	0.0175	-	147.51%	FLNB	filamin B, beta
229820_PM_at	2.3	0.0095	-	128.70%	LOC440993	hypothetical LOC440993
235716_PM_at	2.3	0.023	-	145.71%	235716_PM_at	---
226697_PM_at	2.31	0.0004	-	153.27%	FAM114A1	family with sequence similarity 114, member A1
227646_PM_at	2.31	0.0096	-	146.47%	EBF1	early B-cell factor 1
239400_PM_at	2.31	0.0311	-	151.66%	FLJ45513	hypothetical LOC729220
233265_PM_at	2.32	0.0312	+	114.65%	PARD3	par-3 partitioning defective 3 homolog (C. elegans)
228959_PM_at	2.32	0.0078	+	102.89%	228959_PM_at	---
215023_PM_s_at	2.32	0.0052	-	124.68%	PEX1	peroxisomal biogenesis factor 1
227780_PM_s_at	2.32	0.0209	-	181.53%	ECSCR	endothelial cell-specific chemotaxis regulator
242590_PM_at	2.32	0.0166	-	144.49%	242590_PM_at	---
214234_PM_s_at	2.33	0.0147	+	96.53%	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5
217536_PM_x_at	2.33	0.0484	+	78.77%	217536_PM_x_at	---
201009_PM_s_at	2.33	7.13E-05	-	118.88%	TXNIP	thioredoxin interacting protein
212845_PM_at	2.33	0.0006	-	141.17%	SAMD4A	sterile alpha motif domain containing 4A
226975_PM_at	2.33	0.0005	-	120.98%	RNPC3	RNA-binding region (RNP1, RRM) containing 3
227082_PM_at	2.33	0.0227	-	179.87%	227082_PM_at	---
233286_PM_at	2.33	0.0157	-	120.71%	233286_PM_at	---
236168_PM_at	2.33	0.0237	-	132.44%	ACSL3	acyl-CoA synthetase long-chain family member 3
244416_PM_at	2.33	0.0259	-	126.18%	TTC17	tetratricopeptide repeat domain 17
228370_PM_at	2.34	0.0195	+	112.86%	SNRPN	small nuclear ribonucleoprotein polypeptide N
232435_PM_at	2.34	0.007	+	112.64%	ALG13	asparagine-linked

						glycosylation 13 homolog (S. cerevisiae)
214925_PM_s_at	2.34	0.0032	+	111.52%	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
227108_PM_at	2.34	0.0013	+	110.84%	STARD9	StAR-related lipid transfer (START) domain containing 9
1556306_PM_at	2.34	0.0446	-	129.81%	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)
213071_PM_at	2.34	0.0125	-	167.71%	DPT	dermatopontin
239745_PM_at	2.34	0.0253	-	142.69%	239745_PM_at	---
243864_PM_at	2.34	0.0382	-	204.76%	CCDC80	coiled-coil domain containing 80
205392_PM_s_at	2.35	0.0106	-	142.35%	CCL14	chemokine (C-C motif) ligand 14
227561_PM_at	2.35	0.0063	-	146.54%	DDR2	discoidin domain receptor tyrosine kinase 2
228907_PM_at	2.35	0.046	-	158.09%	228907_PM_at	---
242500_PM_at	2.35	0.0017	-	189.84%	242500_PM_at	---
205498_PM_at	2.36	0.0327	-	137.54%	GHR	growth hormone receptor
205518_PM_s_at	2.36	9.78E-05	-	124.43%	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene
212806_PM_at	2.36	0.0445	-	124.14%	PRUNE2	prune homolog 2 (Drosophila)
227390_PM_at	2.36	0.0418	-	137.58%	MEG3	maternally expressed 3 (non-protein coding)
243584_PM_at	2.36	0.044	-	133.36%	243584_PM_at	---
210298_PM_x_at	2.37	0.0045	+	98.70%	FHL1	four and a half LIM domains 1
228202_PM_at	2.37	0.0197	-	165.03%	PLN	phospholamban
208161_PM_s_at	2.38	0.0008	+	112.03%	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
209487_PM_at	2.38	0.0095	-	140.86%	LOC100134188	hypothetical protein LOC100134188
213764_PM_s_at	2.38	0.0127	-	137.73%	MFAP5	microfibrillar associated protein 5
219064_PM_at	2.38	0.0327	-	-232.13%	ITIH5	inter-alpha (globulin) inhibitor H5
227172_PM_at	2.38	0.0076	-	129.89%	TMEM116	transmembrane protein 116
43427_PM_at	2.38	0.0044	-	125.08%	ACACB	acetyl-Coenzyme A carboxylase beta
201718_PM_s_at	2.39	0.0109	-	128.17%	EPB41L2	erythrocyte membrane protein band 4.1-like 2
218656_PM_s_at	2.39	0.0025	-	181.31%	LHFP	lipoma HMGIC fusion partner
236079_PM_at	2.39	0.0117	-	201.25%	DKFZp667E0512	hypothetical protein DKFZp667E0512
213703_PM_at	2.4	0.0022	+	119.39%	LOC150759	hypothetical protein LOC150759

1563649_PM_at	2.4	0.0249	+	116.19%	1563649_PM_at	---
221625_PM_at	2.4	0.0073	+	115.66%	ZNF506	zinc finger protein 506
226038_PM_at	2.4	0.0011	+	109.85%	LONRF1	LON peptidase N-terminal domain and ring finger 1
243636_PM_s_at	2.4	0.0138	+	109.07%	243636_PM_s_at	---
203632_PM_s_at	2.4	0.0139	-	135.56%	GPRC5B	G protein-coupled receptor, family C, group 5, member B
239568_PM_at	2.4	0.008	-	122.52%	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2
240783_PM_at	2.4	0.0062	-	133.24%	240783_PM_at	---
243626_PM_at	2.41	0.0022	+	112.63%	Q6ZP57_HUMAN	CDNA FLJ26472 fis, clone KDN04506.
214598_PM_at	2.41	0.0028	+	89.22%	CLDN8	claudin 8
209842_PM_at	2.41	0.0112	-	134.87%	SOX10	SRY (sex determining region Y)-box 10
215133_PM_s_at	2.41	0.0178	-	130.19%	FAM153B	family with sequence similarity 153, member B
217626_PM_at	2.41	0.008	-	193.53%	AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)
229218_PM_at	2.41	0.0257	-	167.49%	COL1A2	collagen, type I, alpha 2
213397_PM_x_at	2.42	0.0056	+	120.76%	RNASE4	ribonuclease, RNase A family, 4
209292_PM_at	2.42	0.0081	+	118.56%	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
232098_PM_at	2.42	0.0019	+	118.44%	DST	dystonin
214701_PM_s_at	2.42	0.0056	-	154.35%	FN1	fibronectin 1
216850_PM_at	2.42	0.0492	-	131.09%	SNRPN	small nuclear ribonucleoprotein polypeptide N
221019_PM_s_at	2.42	0.0117	-	149.91%	COLEC12	collectin sub-family member 12
222880_PM_at	2.42	0.001	-	171.09%	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
232262_PM_at	2.42	0.0028	-	129.20%	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L
242080_PM_at	2.42	0.0082	-	122.38%	242080_PM_at	---
205549_PM_at	2.43	0.0382	+	101.22%	PCP4	Purkinje cell protein 4
238718_PM_at	2.43	0.0237	-	135.16%	238718_PM_at	---
203824_PM_at	2.44	0.0141	+	105.84%	TSPAN8	tetraspanin 8
1569608_PM_x_at	2.44	0.0129	-	131.81%	LOC100132733	similar to FLJ00310 protein
205752_PM_s_at	2.44	0.0106	-	185.28%	GSTM5	glutathione S-transferase mu 5
208963_PM_x_at	2.45	0.0492	+	121.93%	FADS1	fatty acid desaturase 1

228802_PM_at	2.45	0.0015	-	140.22%	RBPMS2	RNA binding protein with multiple splicing 2
209291_PM_at	2.46	2.80E-05	+	120.55%	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
1558828_PM_s_at	2.46	0.0407	+	119.15%	LOC728264	hypothetical LOC728264
1564424_PM_at	2.46	0.0032	+	114.51%	ESYT2	extended synaptotagmin-like protein 2
205979_PM_at	2.46	0.0137	+	108.49%	SCGB2A1	secretoglobin, family 2A, member 1
1559410_PM_at	2.46	0.0178	+	95.66%	1559410_PM_at	---
201008_PM_s_at	2.47	7.78E-06	+	114.47%	TXNIP	thioredoxin interacting protein
1558854_PM_a_at	2.47	0.0175	+	109.22%	1558854_PM_a_at	---
236542_PM_at	2.47	0.0403	+	96.63%	236542_PM_at	---
1556049_PM_at	2.47	0.0252	+	95.90%	RTN4	reticulon 4
1557700_PM_at	2.47	0.0316	-	145.31%	POLH	polymerase (DNA directed), eta
202291_PM_s_at	2.47	0.0044	-	138.94%	MGP	matrix Gla protein
204860_PM_s_at	2.47	0.0037	-	165.63%	NAIP	NLR family, apoptosis inhibitory protein
202555_PM_s_at	2.48	0.0008	+	104.04%	MYLK	myosin light chain kinase
1553191_PM_at	2.48	0.0008	-	157.91%	DST	dystonin
1563881_PM_at	2.48	0.0103	-	129.19%	1563881_PM_at	---
225714_PM_s_at	2.48	0.0116	-	129.36%	GLCCI1	glucocorticoid induced transcript 1
235733_PM_at	2.48	0.0235	-	162.90%	GLT8D4	glycosyltransferase 8 domain containing 4
243357_PM_at	2.48	0.0041	-	176.30%	NEGR1	neuronal growth regulator 1
209210_PM_s_at	2.49	0.0026	-	165.17%	FERMT2	fermitin family homolog 2 (Drosophila)
211813_PM_x_at	2.49	0.004	-	155.86%	DCN	decorin
221928_PM_at	2.49	0.0008	-	126.04%	ACACB	acetyl-Coenzyme A carboxylase beta
221795_PM_at	2.5	0.0095	-	135.59%	NTRK2	neurotrophic tyrosine kinase, receptor, type 2
227526_PM_at	2.5	6.11E-05	-	128.64%	LOC338667	hypothetical protein LOC338667
242532_PM_at	2.5	0.038	-	128.72%	242532_PM_at	---
244507_PM_at	2.5	0.0065	-	142.98%	244507_PM_at	---
218863_PM_s_at	2.51	0.0252	+	118.72%	TNS1	tensin 1
225817_PM_at	2.52	0.0112	+	125.62%	CGNL1	cingulin-like 1
243933_PM_at	2.52	0.018	+	118.24%	NFIB	nuclear factor I/B
1555778_PM_a_at	2.52	0.015	+	93.63%	POSTN	periostin, osteoblast specific factor
1562035_PM_at	2.52	0.0007	-	131.61%	1562035_PM_at	---
231067_PM_s_at	2.52	0.0242	-	161.66%	AKAP12	A kinase (PRKA) anchor protein 12

49452_PM_at	2.52	0.0053	-	128.27%	ACACB	acetyl-Coenzyme A carboxylase beta
219132_PM_at	2.53	0.0012	+	122.60%	PELI2	pellino homolog 2 (Drosophila)
226084_PM_at	2.53	0.0007	+	121.70%	MAP1B	microtubule-associated protein 1B
201116_PM_s_at	2.53	0.0025	-	160.70%	CPE	carboxypeptidase E
209119_PM_x_at	2.53	0.0003	-	158.41%	NR2F2	nuclear receptor subfamily 2, group F, member 2
226018_PM_at	2.53	0.0048	-	129.90%	C7orf41	chromosome 7 open reading frame 41
228827_PM_at	2.53	0.0197	-	163.05%	228827_PM_at	---
235291_PM_s_at	2.53	0.0409	-	-189.33%	FLJ32255	hypothetical protein LOC643977
201839_PM_s_at	2.54	0.0004	+	118.86%	EPCAM	epithelial cell adhesion molecule
241797_PM_at	2.54	0.0122	+	108.65%	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)
215516_PM_at	2.54	0.0035	+	92.33%	LAMB4	laminin, beta 4
213765_PM_at	2.54	0.0161	-	131.70%	MFAP5	microfibrillar associated protein 5
219295_PM_s_at	2.54	0.0416	-	168.08%	PCOLCE2	procollagen C-endopeptidase enhancer 2
201416_PM_at	2.55	6.21E-06	+	122.19%	SOX4	SRY (sex determining region Y)-box 4
239531_PM_at	2.55	0.0023	+	116.61%	239531_PM_at	---
1560316_PM_s_at	2.55	0.0311	+	108.40%	GLCCI1	glucocorticoid induced transcript 1
1563077_PM_at	2.55	0.0081	-	161.97%	LOC100289058	hypothetical protein LOC100289058
212226_PM_s_at	2.55	0.0267	-	185.25%	PPAP2B	phosphatidic acid phosphatase type 2B
214577_PM_at	2.55	0.0014	-	129.61%	MAP1B	microtubule-associated protein 1B
224337_PM_s_at	2.55	0.0389	-	133.95%	FZD4	frizzled homolog 4 (Drosophila)
225546_PM_at	2.56	0.0036	+	111.08%	EEF2K	eukaryotic elongation factor-2 kinase
227196_PM_at	2.56	0.0066	-	135.12%	RHPN2	rhophilin, Rho GTPase binding protein 2
203424_PM_s_at	2.57	0.0002	-	132.24%	IGFBP5	insulin-like growth factor binding protein 5
205876_PM_at	2.57	6.02E-05	-	137.54%	LIFR	leukemia inhibitory factor receptor alpha
216066_PM_at	2.57	0.002	-	166.88%	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
230360_PM_at	2.57	0.003	-	146.31%	GLDN	gliomedin
201150_PM_s_at	2.58	0.0003	+	122.76%	TIMP3	TIMP metalloproteinase inhibitor 3
1555997_PM_s_at	2.58	0.0008	+	113.40%	IGFBP5	insulin-like growth factor binding protein 5
221874_PM_at	2.58	0.0081	+	109.77%	KIAA1324	KIAA1324
230197_PM_s_at	2.58	0.0133	+	84.68%	TPPP	tubulin polymerization promoting protein

206170_PM_at	2.58	0.0131	+	83.18%	ADRB2	adrenergic, beta-2-, receptor, surface
213089_PM_at	2.59	0.0015	+	119.82%	LOC100272216	hypothetical LOC100272216
232481_PM_s_at	2.59	0.0164	+	117.14%	SLITRK6	SLIT and NTRK-like family, member 6
206873_PM_at	2.59	0.0049	+	92.29%	CA6	carbonic anhydrase VI
215311_PM_at	2.59	0.015	-	175.41%	NTRK3	neurotrophic tyrosine kinase, receptor, type 3
1556735_PM_at	2.6	0.0142	+	118.95%	1556735_PM_at	---
225241_PM_at	2.6	0.0044	-	178.56%	CCDC80	coiled-coil domain containing 80
218162_PM_at	2.61	0.0059	-	172.54%	OLFML3	olfactomedin-like 3
207284_PM_s_at	2.62	0.0144	+	121.72%	ASPH	aspartate beta-hydroxylase
227952_PM_at	2.62	0.0463	-	138.19%	ZNF595	zinc finger protein 595
239265_PM_at	2.62	0.0285	-	203.26%	TMEM20	transmembrane protein 20
217627_PM_at	2.63	0.0036	+	120.38%	ZNF573	zinc finger protein 573
215239_PM_x_at	2.63	0.0003	+	110.46%	ZNF273	zinc finger protein 273
1558640_PM_a_at	2.63	0.0047	+	103.13%	LOC728411	Glucuronidase, beta pseudogene
206548_PM_at	2.63	0.0169	-	138.07%	hCG_1776259	hypothetical protein FLJ23556
1560370_PM_x_at	2.64	0.0161	+	127.14%	ANKH	ankylosis, progressive homolog (mouse)
230071_PM_at	2.64	0.0003	-	150.20%	11-Sep	septin 11
209791_PM_at	2.65	0.0027	+	108.35%	PADI2	peptidyl arginine deiminase, type II
238595_PM_at	2.66	0.0002	+	128.38%	238595_PM_at	---
216512_PM_s_at	2.66	0.0028	+	127.68%	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)
213898_PM_at	2.66	0.0024	+	116.27%	RBM9	RNA binding motif protein 9
217504_PM_at	2.66	0.004	-	161.53%	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6
225242_PM_s_at	2.66	0.0269	-	178.64%	CCDC80	coiled-coil domain containing 80
231535_PM_x_at	2.66	0.0025	-	138.15%	ROPN1	ropporin, rhophilin associated protein 1
235631_PM_at	2.66	0.0012	-	159.07%	DDR2	discoidin domain receptor tyrosine kinase 2
201540_PM_at	2.67	0.0051	+	132.47%	FHL1	four and a half LIM domains 1
213901_PM_x_at	2.67	4.85E-05	-	134.94%	RBM9	RNA binding motif protein 9
233261_PM_at	2.67	0.028	-	180.53%	EBF1	early B-cell factor 1
241676_PM_x_at	2.68	0.0301	+	97.50%	241676_PM_x_at	---
1554250_PM_s_at	2.68	0.0301	-	121.88%	TRIM73	tripartite motif-containing 73
226304_PM_at	2.68	0.0062	-	147.71%	HSPB6	heat shock protein, alpha-crystallin-related, B6
212157_PM_at	2.69	0.0015	-	182.13%	SDC2	syndecan 2
228504_PM_at	2.71	0.0167	+	124.63%	SCN7A	sodium channel, voltage-

						gated, type VII, alpha
201149_PM_s_at	2.71	0.001	+	120.04%	TIMP3	TIMP metallopeptidase inhibitor 3
1560369_PM_at	2.71	0.0048	+	115.43%	ANKH	ankylosis, progressive homolog (mouse)
244456_PM_at	2.71	0.0139	+	114.34%	244456_PM_at	---
1557835_PM_at	2.71	0.0413	+	111.84%	LMF1	lipase maturation factor 1
238447_PM_at	2.72	0.0056	+	126.14%	RBMS3	RNA binding motif, single stranded interacting protein
242405_PM_at	2.72	0.0172	+	125.09%	MAML2	mastermind-like 2 (Drosophila)
244457_PM_at	2.72	0.013	+	101.45%	244457_PM_at	---
221796_PM_at	2.73	0.0108	+	135.10%	NTRK2	neurotrophic tyrosine kinase, receptor, type 2
228224_PM_at	2.73	0.0032	+	134.54%	PRELP	proline/arginine-rich end leucine-rich repeat protein
235897_PM_at	2.73	0.0112	+	134.26%	COPZ2	coatomer protein complex, subunit zeta 2
231074_PM_at	2.73	0.0465	+	133.68%	231074_PM_at	---
235539_PM_at	2.73	0.0424	+	116.92%	NUMA1	nuclear mitotic apparatus protein 1
244853_PM_at	2.73	0.0081	-	207.98%	244853_PM_at	---
204404_PM_at	2.74	0.0088	+	111.80%	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
218309_PM_at	2.74	0.0004	+	104.11%	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1
220184_PM_at	2.74	0.0486	+	102.19%	LOC100293888	similar to Touch ABnormal family member (tab-1)
1565666_PM_s_at	2.75	0.011	+	121.38%	MUC6	mucin 6, oligomeric mucus/gel-forming
224110_PM_at	2.75	0.0213	+	110.12%	LOC100133319	PRO1804
226933_PM_s_at	2.75	9.36E-05	+	105.83%	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
220141_PM_at	2.75	7.24E-05	-	182.34%	C11orf63	chromosome 11 open reading frame 63
222368_PM_at	2.76	0.0078	+	89.21%	222368_PM_at	---
215768_PM_at	2.77	0.0144	+	104.12%	215768_PM_at	---
229163_PM_at	2.77	0.0062	+	98.45%	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1
1570574_PM_at	2.78	0.0402	+	118.25%	1570574_PM_at	---
222049_PM_s_at	2.78	0.0389	-	166.68%	RBP4	retinol binding protein 4, plasma
209655_PM_s_at	2.8	0.001	+	126.17%	TMEM47	transmembrane protein 47
213369_PM_at	2.8	0.0006	+	100.98%	PCDH21	protocadherin 21
228051_PM_at	2.81	0.0093	+	103.94%	KIAA1244	KIAA1244
209763_PM_at	2.81	0.0222	-	176.63%	CHRD1	chordin-like 1
235008_PM_at	2.81	0.0032	-	158.81%	ANKRD10	ankyrin repeat domain 10

203426_PM_s_at	2.82	4.73E-05	+	132.12%	IGFBP5	insulin-like growth factor binding protein 5
239307_PM_at	2.83	0.0024	-	207.39%	MYH11	myosin, heavy chain 11, smooth muscle
227183_PM_at	2.84	0.0074	-	142.53%	LOC728264	hypothetical LOC728264
213800_PM_at	2.85	0.0241	+	118.94%	CFH	complement factor H
230104_PM_s_at	2.85	0.0048	+	100.64%	TPPP	tubulin polymerization promoting protein
239957_PM_at	2.88	0.0118	+	138.47%	SETD5	SET domain containing 5
230085_PM_at	2.88	0.0038	+	110.51%	230085_PM_at	---
204963_PM_at	2.88	7.24E-05	-	169.77%	SSPN	sarcospan (Kras oncogene-associated gene)
201525_PM_at	2.89	6.27E-05	+	123.11%	APOD	apolipoprotein D
233908_PM_x_at	2.89	0.0058	+	118.95%	233908_PM_x_at	---
220425_PM_x_at	2.9	0.0156	+	127.25%	ROPN1B	ropporin, rhophilin associated protein 1B
213122_PM_at	2.9	0.0014	-	166.66%	TSPYL5	TSPY-like 5
219398_PM_at	2.9	0.0274	-	162.66%	CIDEC	cell death-inducing DFFA-like effector c
227826_PM_s_at	2.91	0.0359	+	128.30%	SORBS2	sorbin and SH3 domain containing 2
227843_PM_at	2.93	0.0105	+	142.21%	MYH11	myosin, heavy chain 11, smooth muscle
1553613_PM_s_at	2.93	0.0267	+	84.08%	FOXC1	forkhead box C1
239864_PM_at	2.96	0.0069	+	100.79%	LOC100130175	hypothetical protein LOC100130175
229839_PM_at	2.97	0.0497	+	128.82%	SCARA5	scavenger receptor class A, member 5 (putative)
237857_PM_at	2.97	0.0041	-	156.90%	237857_PM_at	---
208964_PM_s_at	3.02	0.0226	+	140.26%	FADS1	fatty acid desaturase 1
240458_PM_at	3.03	0.0171	+	111.23%	240458_PM_at	---
235746_PM_s_at	3.03	0.0094	-	139.14%	PLA2R1	phospholipase A2 receptor 1, 180kDa
215695_PM_s_at	3.04	0.0145	+	150.67%	GYG2	glycogenin 2
1569607_PM_s_at	3.04	0.0282	+	135.27%	ANKRD20A1 /// ANKRD20A2 /// ANKRD20A3 /// ANKRD20A4 /// C21orf81 /// LOC100132733 /// LOC284232 /// LOC643187 /// LOC647595 /// LOC727770	ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family, member A2 /// ankyrin repeat domain 20 family, member A3 /// ankyrin repeat domain 20 family, member A4 /// chromosome 21 open reading frame 81 /// hypothetical protein LOC100132733 /// ankyrin repeat domain 20 family, member A2 pseudogene /// hypothetical LOC643187 /// similar to ankyrin repeat domain 20A /// similar to ankyrin repeat domain 20 family, member

						A1
1559455_PM_at	3.04	0.0155	-	170.67%	1559455_PM_at	---
1552283_PM_s_at	3.06	0.0006	+	133.98%	ZDHHC11	zinc finger, DHHC-type containing 11
1556229_PM_at	3.07	0.0481	+	120.89%	TRPV1	transient receptor potential cation channel, subfamily V, member 1
233882_PM_s_at	3.07	0.0197	-	190.25%	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D
207276_PM_at	3.09	6.02E-05	+	114.84%	CDR1	cerebellar degeneration-related protein 1, 34kDa
229461_PM_x_at	3.09	0.0062	-	222.93%	NEGR1	neuronal growth regulator 1
229694_PM_at	3.11	0.0136	+	131.82%	BRWD2	bromodomain and WD repeat domain containing 2
1558604_PM_a_at	3.11	0.0007	-	156.39%	1558604_PM_a_at	---
235368_PM_at	3.12	0.0039	-	257.87%	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5
226281_PM_at	3.13	0.0015	+	122.46%	DNER	delta/notch-like EGF repeat containing
208561_PM_at	3.13	0.0032	-	219.36%	ABCC9	ATP-binding cassette, subfamily C (CFTR/MRP), member 9
219195_PM_at	3.15	0.0039	+	95.53%	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
237483_PM_at	3.17	0.022	+	112.09%	PLEKHA5	pleckstrin homology domain containing, family A member 5
228693_PM_at	3.17	0.0011	-	172.20%	CCDC50	coiled-coil domain containing 50
229092_PM_at	3.17	0.0016	-	192.45%	NR2F2	nuclear receptor subfamily 2, group F, member 2
212079_PM_s_at	3.19	0.0047	-	163.52%	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)
214505_PM_s_at	3.2	0.0015	+	112.26%	FHL1	four and a half LIM domains 1
231998_PM_at	3.21	0.0017	+	129.77%	231998_PM_at	---
203549_PM_s_at	3.22	0.0472	+	158.30%	LPL	lipoprotein lipase
206378_PM_at	3.26	0.0019	+	119.73%	SCGB2A2	secretoglobulin, family 2A, member 2
210299_PM_s_at	3.27	0.0004	+	133.66%	FHL1	four and a half LIM domains 1
235849_PM_at	3.27	0.0119	-	172.70%	SCARA5	scavenger receptor class A, member 5 (putative)
223796_PM_at	3.28	0.0028	+	112.88%	RP11-138L21.1	similar to cell recognition molecule CASPR3
232125_PM_at	3.3	0.0003	-	169.01%	232125_PM_at	---
227643_PM_at	3.32	0.0021	+	110.61%	TPPP	tubulin polymerization

						promoting protein
210718_PM_s_at	3.33	0.0165	+	116.13%	LOC100294341	similar to ADP-ribosylation factor-like 17
229053_PM_at	3.39	0.0133	+	140.92%	SYT17	synaptotagmin XVII
209758_PM_s_at	3.4	0.0165	+	152.10%	MFAP5	microfibrillar associated protein 5
238361_PM_s_at	3.4	0.0428	+	104.38%	238361_PM_s_at	---
218087_PM_s_at	3.44	0.0039	+	138.57%	SORBS1	sorbin and SH3 domain containing 1
213524_PM_s_at	3.45	0.0214	+	163.76%	G0S2	G0/G1switch 2
225424_PM_at	3.45	0.0331	-	221.38%	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial
222513_PM_s_at	3.49	6.02E-05	+	120.08%	SORBS1	sorbin and SH3 domain containing 1
211819_PM_s_at	3.49	0.0047	+	113.68%	SORBS1	sorbin and SH3 domain containing 1
238880_PM_at	3.54	0.0018	-	178.86%	GTF3A	general transcription factor IIIA
201147_PM_s_at	3.55	6.90E-06	+	118.65%	TIMP3	TIMP metalloproteinase inhibitor 3
206799_PM_at	3.59	0.0077	+	99.91%	SCGB1D2	secretoglobin, family 1D, member 2
233202_PM_at	3.63	0.0039	+	124.57%	LOC100294401	similar to cell recognition molecule Caspr2
1553946_PM_at	3.67	0.0019	+	120.55%	DCD	dermcidin
237120_PM_at	3.7	0.0117	+	66.79%	KRT77	keratin 77
1564786_PM_at	3.71	0.0005	+	158.58%	LOC338667	hypothetical protein LOC338667
241316_PM_at	3.8	0.0008	+	108.89%	TNRC6A	trinucleotide repeat containing 6A
238009_PM_at	3.86	0.0016	-	212.03%	238009_PM_at	---
206179_PM_s_at	3.9	0.0015	+	116.17%	TPPP	tubulin polymerization promoting protein
224348_PM_s_at	3.91	0.0046	+	100.68%	224348_PM_s_at	---
206509_PM_at	4.12	0.0104	+	96.58%	PIP	prolactin-induced protein
209613_PM_s_at	4.29	0.0031	+	177.99%	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide
242379_PM_at	4.35	0.0007	+	101.32%	242379_PM_at	---
1560001_PM_at	4.38	1.79E-05	+	118.21%	LOC100131581	hypothetical LOC100131581
226210_PM_s_at	4.39	0.0004	-	308.03%	MEG3	maternally expressed 3 (non-protein coding)
207092_PM_at	4.46	0.025	-	218.75%	LEP	leptin
225420_PM_at	4.49	0.0083	-	280.12%	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial
237154_PM_at	4.5	0.0135	-	234.28%	237154_PM_at	---
227484_PM_at	4.74	0.0022	+	141.64%	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1
235978_PM_at	4.77	0.0047	-	218.23%	FABP4	fatty acid binding protein 4, adipocyte
203980_PM_at	4.83	0.002	+	226.13%	FABP4	fatty acid binding protein 4,

						adipocyte
207175_PM_at	4.88	0.0151	+	223.49%	ADIPOQ	adiponectin, C1Q and collagen domain containing
205913_PM_at	4.94	0.0188	+	203.69%	PLIN1	perilipin 1
229477_PM_at	5.15	0.0084	+	135.95%	THRSP	thyroid hormone responsive (SPOT14 homolog, rat)
229476_PM_s_at	5.59	0.0114	+	117.94%	THRSP	thyroid hormone responsive (SPOT14 homolog, rat)
203548_PM_s_at	5.72	0.005	+	213.84%	LPL	lipoprotein lipase
216359_PM_at	7.16	0.0003	+	223.18%	MUC7	mucin 7, secreted
221646_PM_s_at	7.25	7.73E-05	+	105.93%	ZDHHC11	zinc finger, DHHC-type containing 11