Molecular-timetable methods for detection of body time and rhythm disorders from single-time-point genome-wide expression profiles

Hiroki R. Ueda*^{†‡§}, Wenbin Chen*, Yoichi Minami*, Sato Honma¹, Kenichi Honma¹, Masamitsu lino[†], and Seiichi Hashimoto*

*Molecular Medicine Laboratories, Institute for Drug Discovery Research, Yamanouchi Pharmaceutical Company, Limited, 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan; [†]Department of Pharmacology, Graduate School of Medicine, University of Tokyo, 7-3-1 Bunkyo-ku, Tokyo 113-0033, Japan; [‡]Laboratory for Systems Biology, Center for Developmental Biology, RIKEN, 2-2-3 Minatojiima-minamimachi, Chuo-ku, Kobe, Hyogo 650-0047, Japan; and [§]Department of Physiology, Hokkaido University Graduate School of Medicine, Sapporo 060-8638, Japan

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Detection of individual body time (BT) via a single-time-point assay has been a longstanding unfulfilled dream in medicine, because BT information can be exploited to maximize potency and minimize toxicity during drug administration and thus will enable highly optimized medication. To achieve this dream, we created a "molecular timetable" composed of >100 "time-indicating genes," whose gene expression levels can represent internal BT. Here we describe a robust method called the "molecular-timetable method" for BT detection from a single-time-point expression profile. The power of this method is demonstrated by the sensitive and accurate detection of BT and the sensitive diagnosis of rhythm disorders. These results demonstrate the feasibility of BT detection based on single-time-point sampling, suggest the potential for expression-based diagnosis of rhythm disorders, and may translate functional genomics into chronotherapy and personalized medicine.

DNA microarray | gene expression | chronotherapy

D iverse physiological and metabolic processes exhibit circa-dian rhythms, which are endogenous self-sustained oscillations with a period of \approx 24 hours. In mammals, several clock genes, including Clock, Bmal1/Mop3, Per1, Per2, Cry1, Cry2, Cki ε , and RevErbA α , and clock-controlled transcription factors, including Dbp, E4bp4, Dec1/Stra13, Dec2, Per3, Npas2, *RevErbA* β , *Ror* α , *Ror* β , and *Ror* γ , regulate, at least in part, gene expression in central and/or peripheral clocks (1). Reflecting the temporal changes in gene expression in central and peripheral clocks (2-5), the potency and/or toxicity in drug administration depend on an individual's body time (BT) (6-10). It has been suggested that drug administration at the appropriate BT can improve the outcome of pharmacotherapy by maximizing potency and minimizing the toxicity of the drug (11), whereas drug administration at an inappropriate BT can induce severe side effects (12). Despite the effectiveness and importance of such BT-dependent therapy, termed "chronotherapy" (6-10), its clinical use has been obstructed by the lack of clinically applicable methods for BT detection. To address these difficulties, we attempted to create standard expression profiles, termed a "molecular timetable," composed of >100 "time-indicating genes" and their expression levels during the course of a day, and then to apply this timetable to BT detection.

Materials and Methods

Animals. To select time-indicating genes and construct their standard expression profiles, we analyzed the previously obtained genome-wide expression profiles (5) from pooled livers of four Balb/c mice (male) every 4 h over 2 d under 12-h light/12-h dark (LD) or constant-dark (DD) conditions. We independently sampled livers from eight individual Balb/c mice (male) at Zeitgeber time (ZT)12 (n = 4), ZT6 (n = 1), ZT18 (n = 1),

Circadian time (CT)6 (n = 1), and CT18 (n = 1) to verify the capability of the molecular-timetable method. ZT is used for a timescale under LD conditions, whereas CT is used for a timescale under DD conditions. ZT0 represents lights on, and ZT12 represents lights off, whereas CT0 represents subjective dawn, and CT12 represents subjective dusk. We use the term "subjective," because there are no external time cues in the DD condition. We sampled livers from seven individual Clock/Clock homozygous mutant mice (male) at ZT12 (n = 4) or ZT8 (n =3) and three individual Balb/c mice (male) at ZT8 (n = 3) to verify the feasibility of expression-based diagnosis of circadian rhythm disorders. We further sampled livers from three individual C3H mice (male) at ZT12 (n = 3) to verify the feasibility of the molecular-timetable method for individuals with heterogeneous genetic background. All these Balb/c, C3H, and *Clock*/ *Clock* homozygous mutant mice were adapted under LD conditions for 2 weeks from 5 weeks postpartum and then sampled.

Microarray Experiments. Total RNA was prepared by using Trizol reagent (GIBCO/BRL). cDNA synthesis and cRNA labeling reactions were performed as described (5). Affymetrix highdensity oligonucleotide arrays (Murine Genome Array U74A, Version 1.0, measuring 9,977 independent transcripts) were hybridized, stained, and washed according to the Technical Manual (Affymetrix). Affymetrix software was used to determine the average difference (AD) between perfectly matched probes and single-base-pair-mismatched probes. The AD of each probe was then scaled globally so that the total AD of each microarray was equal. The resulting AD values reflect the abundance of a given mRNA relative to the total RNA population and were used in all subsequent analyses.

Time-Indicating Genes. To select time-indicating genes whose expression exhibits circadian rhythmicity with high amplitude, the expression profile of each gene was analyzed through two filters, one for circadian rhythmicity and the other for high amplitude. To extract genes with circadian rhythmicity under both LD and DD conditions, we first calculated the correlation over time between 12-point time courses under LD (or DD) conditions and cosine curves of defined periods and phases. We prepared cosine curves of 24-h periodicity with peaks from 0 to 24 h in increments of 10 min, yielding a total of 144 test cosine curves, and calculated the correlation value of the best-fitted cosine curve for each probe set. We selected the probe sets

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Abbreviations: LD, light/dark; DD, constant dark; ZT, Zeitgeber time; CT, Circadian time; BT, body time(s).

[§]To whom correspondence should be addressed. E-mail: uedah-tky@umin.ac.jp.

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whose best correlation values in LD and DD conditions were both above the cutoff correlation value of 0.8. To further extract genes with high amplitude under both LD and DD conditions, we calculated the coefficient of variation of the expression levels under LD (or DD) conditions, which is defined as its SD divided by the average of expression levels. We selected the probe sets whose coefficients of variation in LD and DD conditions were both above the cutoff value of 0.15. Based on two successive filtrations, 168 genes (182 probes) in the liver were identified.

Estimation of Molecular Peak Time. To estimate the peak time of cycling genes, we tested for correlation over time between the 12-point time course of each gene and the 24-h period cosine curves with different peak times at 10-min intervals. We estimated the peak time of each cycling gene from the peak time of the best-fitted cosine curve and defined it as the molecular peak time.

Molecular-Timetable Method. We first normalized an expression level, X_i , of the time-indicating gene i ($i = 1 \dots N$) using its average μ_i and SD σ_i in the molecular timetable. The normalized expression level Y_i is described as follows: $Y_i = (X_i - \mu_i)/\sigma_i$. We created an expression profile $\{t_i, Y_i\}$ (i = 1 ... N) composed of the molecular peak time t_i of gene *i* and its normalized expression level Y_i . To estimate the BT of an expression profile, we calculated the correlation over genes $(i = 1 \dots N)$ between an expression profile $\{t_i, Y_i\}$ and a 24-h cosine curve $\{t_i, \sqrt{2}\}$ $Cos(2\pi(t_i - b)/24)$ with a certain phase b ($0 \le b < 24$). The amplitude of the cosine curve is set to $\sqrt{2}$, so that the SD of the normalized expression level Y_i matches the SD of a continuous cosine waveform $(\sqrt{1/24} \int_0^{24} Cos^2(2\pi(t-b)/24) dt = 1/\sqrt{2})$. We prepared 24-h cosine curves with a phase b from 0 to 24 h in increments of 10 min. We then selected the best-fitted cosine curve that gave the best correlation value c. We noted that the best correlation value c is always positive, because we calculated the maximum value of correlation between an expression profile and 144 test cosine curves. We also noted that the phase of the best-fitted cosine curve (b_c) indicates an estimated BT.

Statistical Significance in the Detection of BT. To evaluate the statistical significance of BT estimation, we generated a random expression profile $\{t_i, Y_r\}$ (i = 1 ... N), where Y_r represents a random variable following the distribution of Y_i and then calculated the correlation value c^r and the phase b_c^r of the best-fitted cosine curve as described above. We repeated this procedure 10,000 times to create the distribution of correlation value c^r and the phase b_c^r (e.g., Fig. 4A and B, which is published as supporting information on the PNAS web site). The probability (termed P_r value) that a random expression profile has a best-fitted cosine curve giving correlations equal to or greater than those of the real expression profiles was determined from the distribution of correlation value (c^r) from 10,000 random expression profiles.

Estimation of Measurement Noise. To estimate the measurement noise of eight Bablc/C expression profiles (see *Animals* above) at ZT12 (n = 4), ZT6 (n = 1), ZT18 (n = 1), CT6 (n = 1), and CT18 (n = 1), we first calculated the difference d_i between a real and an estimated expression level of gene i (i = 1 ... N). d_i is defined as $d_i \equiv Y_i - \sqrt{2} Cos(2\pi(t_i - b_c)/24)$, where b_c represents estimated BT. We then calculated the SD of d_i over all time-indicating genes and defined it as the measurement noise. Measurement noises of wild-type expression profiles range from 86% to 108% (95 ± 8% for mean ± SD).

Statistical Significance in the Detection of Circadian Rhythm Disorders. To evaluate the statistical significance of circadian rhythm disorders, we generated a control expression profile with 100% measurement noise $\{t_i, \sqrt{2} \cos(2\pi(t_i/24)) + d_r)\}$ (i = 1...N), where d_r represents a random variable following the distribution of d_i , and then calculated the correlation value c^c and the phase b_c^c of the best-fitted cosine curve, described above. We repeated this procedure 10,000 times to create the distribution of correlation value c^c and the phase b_c^c (e.g., Fig. 4 A and B). The probability (termed P_c value) that a control expression profile has a best-fitted cosine curve giving a correlation equal to or lower than those of the observed expression profiles was determined from the distribution of the correlation value c^c from 10,000 control expression profiles.

Sensitivity and Specificity of Molecular-Timetable Methods. We can calculate the sensitivity and specificity of the molecular timetable method in the presence of a certain level of measurement noise (100% or 200% measurement noise). First, we generated 10,000 control or random expression profiles in the presence of a certain measurement noise level and then calculated the distribution of c^c or c^r from 10,000 control or random expression profiles as described above. We determined the P_c or P_r value at the certain threshold value of correlation (c) from the distribution of c^c or c^r , respectively. Sensitivity (S_c) is defined as $S_c(c) \equiv$ $1 - P_c(c)$, indicating the probability of true positives or the probability of circadian rhythmicity (control expression profile), correctly identified by the test as meeting a certain threshold value of correlation. Specificity (S_r) is defined as $S_r(c) \equiv 1 - 1$ $P_r(c)$, indicating the probability of true negatives or of circadian rhythm disorder (random expression profile), correctly identified by the test as not meeting a certain threshold value of correlation. There are tradeoffs between sensitivity and specificity, because sensitivity monotonically decreases, whereas specificity monotonically increases, with the threshold correlation value. This tradeoff relationship is plotted as the receiver operating characteristic (ROC) curve (e.g., Fig. 4C). The ROC curve is defined as $\{S_r(c), S_c(c)\}\ (0 \le c \le 1)$.

Performance of Molecular-Timetable Methods with Different Numbers of Time-Indicating Genes with Simulated Expression Profiles. Performance of the molecular-timetable method with N timeindicating genes ($N \in \{3, 5, 10, 20, 30, 50, 100, 182\}$) was calculated with simulated expression profiles in the presence of 100% or 200% measurement noise. First, we randomly selected N from 168 time-indicating genes. Then, we generated control $\{t_i, \sqrt{2} Cos(2\pi(t_i/24)) + d_r\}$ and random expression profiles $\{t_i, Y_r\}$ in the presence of 100% measurement noise, where d_r and Y_r represent random variables following the distributions of d_i and Y_i , respectively. In the presence of 200% noise, we generated control $\{t_i, \sqrt{2} \cos(2\pi(t_i/24)) + 2d_r\}$ and random expression profiles $\{t_i, 2Y_r\}$. We repeated these procedures 10,000 times and then calculated the distribution of the correlation value (c^c and c^r) and the phase (b_c^c and b_c^r) from 10,000 control and random expression profiles and determined the P_c and P_r values, sensitivity S_c , and specificity (S_r) at a certain threshold value of correlation, as described above (Fig. 5, which is published as supporting information on the PNAS web site).

Performance of Molecular-Timetable Methods with Different Numbers of Time-Indicating Genes with Real Expression Data. Performance of the molecular-timetable method with N time-indicating genes ($N \in \{10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150\}$) was calculated with real expression profiles. To select N time-indicating genes from 168 time-indicating genes in the order of high-amplitude circadian rhythmicity, we first calculated the sum of correlation in LD, correlation in DD, coefficient of variation in LD, and coefficient of variation in DD for each gene. We then selected the top N time-indicating genes in the order of this sum.

To determine a cutoff correlation value in the detection of

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Fig. 1. Time-indicating genes in the mouse liver. (A) Temporal expression data of 168 time-indicating genes (182 probes) in the mouse liver. The colors, in ascending order from green to red to blue, represent the molecular peak time of time-indicating genes (the color code is represented above the diagrams). An expression level of each time-indicating gene is subtracted by its average and divided by its SD over 12-point time courses. The blocked horizontal bars below the diagrams correspond to the LD schedule. White blocks indicate periods of exposure to light, whereas black blocks correspond to periods of darkness, and gray blocks indicate the period of subjective light under constant darkness. (*B*) Distribution of the average of molecular peak time between LD and DD conditions. Average molecular peak times in LD and DD conditions are similar to each other. (*D*) Expression profiles of 168 time-indicating genes in the mouse liver at different ZT under LD conditions or CT under DD conditions. The best-fitted cosine curve is represented, and its peak indicates the estimated BT.

circadian rhythmicity and circadian rhythm disorders, we first calculated the receiver operating characteristic (ROC) curve of the molecular-timetable method with *N* time-indicating genes in the presence of 100% measurement noise, as described above. We then determined a cutoff correlation value c ($0 \le c \le 1$) as the value yielding equal sensitivity and specificity in the ROC curve [$S_r(c) = S_c(c)$]. We noted that c is a monotonically decreasing function of *N*.

To calculate sensitivity, specificity, and accuracy with real expression data, we examined 11 wild-type Balb/c expression profiles at ZT12 (n = 4), ZT6 (n = 1), ZT18 (n = 1), CT6 (n =1), CT18 (n = 1), and ZT8 (n = 3), and 7 Clock/Clock mutant expression profiles at ZT12 (n = 4) and ZT8 (n = 3). We calculated sensitivity, which is defined as the percent of wild-type Balb/c expression profiles (n = 11), with a correlation value higher than a cutoff. We also calculated specificity, which is defined as the percent of Clock/Clock mutant expression profiles (n = 7), with a correlation value lower than a cutoff. To evaluate the accuracy of molecular-timetable methods, we calculated mean estimation error in BT detection, which is defined as the average of absolute differences between sampling times and estimated BT of wild-type Balb/c expression profiles (n = 11). Calculated sensitivity, specificity, and mean errors are plotted along with N time-indicating genes (Fig. 6, which is published as supporting information on the PNAS web site).

Results and Discussion

Recently, we, along with others, performed genome-wide gene expression analyses using high-density DNA microarrays to identify clock-controlled genes in the mouse central [suprachiasmatic nucleus (SCN)] and peripheral (liver) clocks (2-5). We analyzed the previously obtained genome-wide expression profiles from four pooled livers every 4 h over 2 d under LD or DD conditions and found 168 time-indicating genes (Fig. 1 and Table 1, which is published as supporting information on the PNAS web site) whose expression exhibits high circadian rhythmicity and whose peak time, termed molecular peak time, can therefore indicate the time of day (see Materials and Methods). Importantly, the molecular peak times of time-indicating genes were distributed over 24 h (Fig. 1B). Moreover, each time-indicating gene exhibited similar expression patterns under LD and DD conditions (Fig. 1A), and the molecular peak times of each gene under LD and DD conditions were similar to each other (Fig. 1C), suggesting that expression profiles of time-indicating genes can indicate BT, the endogenous state of the circadian clock.

To verify this possibility, we attempted to extract the BT information from the expression profiles of 168 time-indicating genes (see *Materials and Methods*). As expected, BT information can be extracted from the expression profiles of 168 time-indicating genes with high accuracy and estimation errors from 0.0 to 1.3 h (0.4 ± 0.3 h for mean \pm SD, Fig. 1D). For instance, at ZTO (the beginning of day) or CTO (the beginning of a

subjective day), dawn-indicating genes (green), whose molecular peak times are approximately ZT0 or CT0, are highly expressed, whereas dusk-indicating genes (red), whose molecular peak times are approximately ZT12 or CT12, are expressed at a low level (Fig. 1D). At ZT12 or CT12, on the other hand, dawnindicating genes are expressed at a low level, whereas duskindicating genes are highly expressed (Fig. 1D). In both cases, the normalized expression levels of day-indicating genes (yellowgreen to orange) or night-indicating genes (purple to blue) gradually change from higher to lower expression levels or from lower to higher levels along their molecular peak times. Such gradual and cyclic changes in expression along the molecular peak time line allow us to extract the BT from the expression profiles via cosine curve fitting (Fig. 1D). The peak of the best-fitted cosine curve to an expression profile of 168 timeindicating genes indicates the estimated BT. For example, the BT extracted from expression profiles at ZT0 on the first day under LD or at CT0 on the first day under DD are BT0.2 and BT1.3, respectively. We termed this the molecular-timetable method (see Materials and Methods).

To demonstrate the capability of this molecular-timetable method, we attempted to infer BT from independent samples. We obtained fresh liver samples from four individual mice at ZT12, which was thought to be one of the noisiest time points, because lights out at that time resets the phase of circadian clocks in species, such as mice, with a free running period shorter than 24 h. We then measured the expression profiles of 168 timeindicating genes (Fig. 2A). Using the molecular-timetable method, we significantly detected the circadian rhythmicity in all expression profiles of these samples (P < 0.0001, Fig. 2A), and the estimated BT indicated BT12.8, BT10.2, BT11.2, and BT11.7, respectively (Fig. 2A). These results suggest that BT can be accurately inferred from individual expression profiles with estimation errors from 0.3 to 1.8 h (1.0 \pm 0.6 h for mean \pm SD, Fig. 2A). To further demonstrate the capability of the moleculartimetable method, we obtained new liver samples from individual mice at ZT6, ZT18, CT6, and CT18, all times that were different from the time points used to construct the molecular timetable, and measured the expression profiles of 168 timeindicating genes (Fig. 2B). We significantly detected the circadian rhythmicity in all expression profiles of ZT6, ZT18, CT6, and CT18 samples (P < 0.0001, Fig. 2B) and found that the estimated BT indicated BT6.7, BT19.3, BT5.7, and BT20.0, respectively (Fig. 2B). These results suggest that BT can be accurately inferred from expression profiles at time points that were not used to construct the molecular timetable, with estimation errors from 0.3 to 2.0 h (1.1 \pm 0.7 h for mean \pm SD, Fig. 2*B*).

The molecular-timetable method can be applied for the diagnosis of circadian rhythm disorders (see Materials and Methods). To demonstrate the feasibility of expression-based diagnosis of circadian rhythm disorders, we sampled livers at ZT12 from four individual Clock/Clock homozygous mutant mice, which were known to have altered circadian behavioral rhythms (13, 14), and then measured the expression profiles of 168 time-indicating genes (Fig. 3A). We significantly detected the rhythm disorders in all expression profiles of Clock/Clock homozygous mutant samples at ZT12 ($\hat{P} < 0.0001$, Fig. 3A). To further demonstrate the feasibility of the expression-based diagnosis of circadian rhythm disorders, we simultaneously sampled livers from three individuals of wild-type (+/+) mice and *Clock/Clock* mutant mice at ZT8 and measured the expression profiles for 168 time-indicating genes (Fig. 7, which is published as supporting information on the PNAS web site). We significantly detected the circadian rhythmicity in all expression profiles of wild-type (+/+) samples (P < 0.0001, Fig. 7) and found that the estimated BT indicated BT7.3, BT6.7, and BT9.5 (Fig. 7), which were around sampling time ZT8. On the other hand,



Fig. 2. Significant and quantitative detection of BT from individual expression profiles at ZT12 (*A*) or ZT6, ZT18, CT6, and CT18 (*B*). The colors, in ascending order from green to red to blue, represent the molecular peak time of time-indicating genes (the color code is represented below the diagrams). An expression level of each time-indicating gene is subtracted by its average and divided by its SD in the molecular timetable. The best-fitted cosine curve is represented, and its peak indicates the estimated BT, BT12.8 (*A Upper Left*), BT10.2 (*A Lower Left*), BT11.2 (*A Upper Right*), and BT11.7 (*A Lower Right*), and BT6.7 (*B Upper Left*), BT19.3 (*B Lower Left*), BT5.7 (*B Upper Right*), and BT20.0 (*B Lower Right*).

we significantly detected rhythm disorders in all expression profiles of Clock/Clock homozygous mutant samples at ZT8 (P < 0.0001, Fig. 7). These results suggest that the molecular-timetable method can be applied not only for BT detection but also for the detection of circadian rhythm disorders.

In clinical situations, methods for BT detection should be applicable for populations with heterogeneous genetic backgrounds. To demonstrate the capability of the moleculartimetable method for individuals with heterogeneous genetic backgrounds, we attempted to apply the molecular-timetable method for other inbred strains with different genetic backgrounds from the original strain used for the construction of the molecular timetable. We sampled livers at ZT12 from three individual C3H mice, which were different from the original Balb/c strains used to construct the molecular timetable, and measured expression profiles for 168 time-indicating genes (Fig. 3B). We significantly detected the circadian rhythmicity in all expression profiles of C3H samples (P < 0.0001, Fig. 3B) and found that the estimated BT indicated BT12.3, BT11.3, and BT11.3, respectively (Fig. 3B). These results suggest that BT can be accurately inferred from the expression profiles of individuals



Fig. 3. Significant detection of BT and rhythm disorders from expression profiles of *Clock/Clock* mutant mice at ZT12 (A) and C3H mouse at ZT12 (B). The colors, in ascending order from green to red to blue, represent the molecular peak time of time-indicating genes (the color code is represented below the diagrams). An expression level of each time-indicating gene is subtracted by its average and divided by its SD in the molecular timetable. The best-fitted cosine curve is represented, and its peak indicates the estimated BT, BT12.3 (*B Upper Left*), BT11.3 (*B Lower Left*), and BT11.3 (*B Lower Right*).

with heterogeneous genetic backgrounds, with estimation errors from 0.3 to 0.7 h (0.6 \pm 0.2 h for mean \pm SD, Fig. 3*B*).

In this study, we used mouse livers to construct the molecular timetable and demonstrated the feasibility of the moleculartimetable method based on single-time-point sampling for detection of BT and diagnosis of circadian rhythm disorders. Other tissues besides the liver can be used to construct molecular timetables, because there are circadian oscillators scattered throughout the body in various tissues and organs, including the mouse suprachiasmatic nucleus (SCN), liver, skeletal muscle, lung, cornea, kidney, heart, aorta, skin, oral mucosa, and white blood cells (2-5, 15-19). Genome-wide expression analyses in some of these tissues have been performed and have demonstrated that between 2% and 10% of the analyzed genes exhibit circadian oscillations in RNA expression levels (2-5). In fact, we analyzed the previous genome-wide expression data for the mouse SCN (5) and found that BT can be represented in the expression profiles of SCN time-indicating genes (Table 2, which is published as supporting information on the PNAS web site), with low estimation errors from 0.3 to 1.8 h (1.0 \pm 0.4 h for mean \pm SD, Fig. 8, which is published as supporting information on the PNAS web site).

The molecular-timetable method can be also applied to organisms other than the mouse because a wide range of organisms, including human, rat, Drosophila, Arabidopsis, Neurospora, and cyanobacteria, are known to have circadian clocks (20), and genome-wide expression analyses in some of these organisms have shown that a substantial portion of the analyzed genes exhibit circadian oscillations in RNA expression levels (21-27). Actually, we analyzed the previously obtained genome-wide expression data of Drosophila heads (24) and found that BT can be represented in the expression profiles of 113 time-indicating genes of Drosophila (Table 3, which is published as supporting information on the PNAS web site) with low estimation errors from 0 to 1.5 h (0.4 \pm 0.4 h for mean \pm SD, Fig. 9, which is published as supporting information on the PNAS web site). We applied this molecular timetable for the detection of BT and the diagnosis of circadian rhythm disorders in Drosophila. We simultaneously sampled heads from wild-type (+/+) and Drosophila Clock homozygous mutant (28) (dClock/dClock) flies at ZT13 and obtained expression profiles for 113 time-indicating genes (Fig. 10, which is published as supporting information on the PNAS web site). We significantly detected the circadian rhythmicity in all expression profiles of wild-type samples (+/+)at ZT13 (P < 0.0001, Fig. 10) and found that the estimated BT indicated BT13.7 and BT14.5, respectively (Fig. 10). On the other hand, rhythm disorders were significantly detected from dClock/dClock expression profiles (P < 0.0001, Fig. 10). These results suggest that the molecular-timetable method can be applied for the detection of BT and circadian rhythm disorders in organisms other than mouse.

Performance of the molecular-timetable method is characterized by three measures specificity, sensitivity, and estimation error (Fig. 4 and see *Materials and Methods*). The first measure, sensitivity, is defined as the percent of control expression profiles (blue) higher than threshold of correlation in cosine curve fitting (Fig. 4A). The second measure, specificity, is defined as the percent of random expression profiles (red) lower than threshold of correlation (Fig. 4A). There is a tradeoff between sensitivity and specificity, because changing the threshold of correlation influences these measures in opposite directions, and thus performance of molecular-timetable method depends on segregation between control and random expression profiles (Fig. 4C). The third measure, estimation error, is defined as the difference between estimated BT and true BT (blue, Fig. 4B). These results show that the molecular-timetable method with 168 time-indicating genes in mouse liver is a remarkably specific, sensitive, and accurate method.

In this study, we devised a method for BT detection utilizing single-time-point data for multiple molecules. To elucidate the importance of the use of many time-indicating genes, we assessed the specificity, sensitivity, and estimation error of the moleculartimetable method with different numbers of time-indicating genes in the presence of measurement noise, which is inevitable in clinical situations (see *Materials and Methods*). In the presence of 100% measurement noise, the application of the moleculartimetable method with 100 (or 150) time-indicating genes had the capability of detecting the BT with >99.99% (99.99%) sensitivity and 99.99% (99.99%) specificity and with low estimation errors 0.30 ± 0.24 h for mean \pm SD (0.25 \pm 0.21 h for mean \pm SD, Fig. 5). Even in the presence of 200% measurement noise, use of the molecular-timetable methods with 100 (or 150) time-indicating genes still had the capability of detecting BT with 98.58% (99.72%) sensitivity and 98.58% (99.72%) specificity and with low estimation errors 0.62 ± 0.48 h for mean \pm SD $(0.50 \pm 0.39 \text{ h} \text{ for mean} \pm \text{SD}, \text{Fig. 5})$. On the other hand, the molecular-timetable method with three (or five) time-indicating genes failed to specifically, sensitively, or accurately detect BT or rhythm disorders, suggesting the importance of the use of many time-indicating genes (Fig. 5). The use of >100 time-indicating genes can confer with high sensitivity, specificity, and accuracy, to the molecular timetable, even in the presence of high measurement noise. Interestingly, we noted that the moleculartimetable method, with as few as 60 time-indicating genes, if selected appropriately can sensitively and accurately detect BT and sensitively diagnose rhythm disorders in real expression profiles (Fig. 6).

Collectively, we constructed a molecular timetable and devised a specific, sensitive and accurate method for detection of BT and rhythm disorders from a single-time-point expression profile using this molecular timetable. The power of the molecular-timetable method can be demonstrated by the quantitative and accurate detection of BT from individual expression profiles and the accurate detection of circadian rhythm disorders in

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Clock/Clock homozygous mutant mice. These results demonstrate the feasibility of BT detection based on single-time-point sampling, suggest the capacity for the expression-based diagnosis of circadian rhythm disorders, and may lead to the development of chronotherapy and personalized medicine.

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			Molec	ular Peal	k Time	Corre	lation	Ampl	itude	Ave	rage	Standard	Deviation
Probe ID	Gene Symbol	Gene Name	Mean	LD	DD	LD	DD	LD	DD	LD	DD	LD	DD
93753_at	Litaf	LPS-induced TN factor	0.00	0.83	23.17	0.85	0.85	0.21	0.24	1386	1339	294	320
92539_at	S100a10	S100 calcium binding protein A10 (calpactin)	0.08	0.67	23.50	0.97	0.97	0.39	0.34	3041	3224	1180	1109
92833_at	Hal	histidine ammonia lyase	0.58	1.00	0.17	0.90	0.90	0.18	0.20	4905	4926	893	970
95660_at	0610025L15Rik	RIKEN cDNA 0610025L15 gene	0.75	0.50	1.00	0.97	0.93	0.27	0.24	6982	7473	1879	1776
103671_at	Htatip2	HIV-1 tat interactive protein 2, homolog (human)	0.83	0.33	1.33	0.89	0.88	0.21	0.26	732	802	151	210
102797_at	Rsdr1-pending	retinal short-chain dehydrogenase/reductase 1	1.17	1.83	0.50	0.93	0.91	0.29	0.31	2435	2068	700	646
101995_at	Sqstm1	sequestosome 1	1.17	1.17	1.17	0.97	0.94	0.19	0.21	6670	6848	1256	1449
93728_at	Tgfb1i4	transforming growth factor beta 1 induced transcript 4	1.25	2.00	0.50	0.86	0.90	0.34	0.44	3658	3694	1232	1631
95517_i_at	BC004004	cDNA sequence BC004004	1.50	1.50	1.50	0.96	0.86	0.26	0.23	3061	3190	805	720
96774_at	Plekhc1	pleckstrin homology domain containing, family C (with	1.75	2.33	1.17	0.96	0.88	0.22	0.21	6836	6618	1530	1367
93496_at	Helo1-pending	homolog of yeast long chain polyunsaturated fatty acid	1.75	2.33	1.17	0.87	0.89	0.16	0.17	11314	12173	1855	2126
99649_at	Gclc	glutamate-cysteine ligase, catalytic subunit	1.75	1.50	2.00	0.94	0.97	0.34	0.36	3107	3234	1047	1162
99512_at		Mus musculus 16 days embryo head cDNA, RIKEN fu	1.75	2.67	0.83	0.93	0.94	0.24	0.38	757	719	182	270
104148_at	AI785303	expressed sequence AI785303	1.83	1.33	2.33	0.88	0.90	0.19	0.24	5609	5845	1064	1427
96596_at	Ndrl	N-myc downstream regulated-like	2.00	2.33	1.67	0.92	0.94	0.93	0.54	401	262	373	141
103335_at	Lgals9	lectin, galactose binding, soluble 9	2.00	1.83	2.17	0.97	0.93	0.19	0.17	10001	10647	1924	1777
104616 <u>g</u> at	Galt	galactose-1-phosphate uridyl transferase	2.00	3.50	0.50	0.88	0.83	0.32	0.33	1648	1574	521	524
101093_at	Col4a1	procollagen, type IV, alpha 1	2.00	2.67	1.33	0.85	0.94	0.51	0.45	487	472	250	215
103983_at	Adh4	alcohol dehydrogenase 4 (class II), pi polypeptide	2.08	2.83	1.33	0.96	0.88	0.35	0.37	1427	1439	501	528
99638_at	Col18a1	procollagen, type XVIII, alpha 1	2.42	2.50	2.33	0.81	0.84	0.22	0.20	6686	6095	1461	1214
99120_f_at	Chd4	chromodomain helicase DNA binding protein 4	2.50	2.67	2.33	0.80	0.81	0.20	0.20	1851	1900	369	384
103982_s_at	Adh4	alcohol dehydrogenase 4 (class II), pi polypeptide	2.50	3.17	1.83	0.92	0.89	0.34	0.24	2614	2447	898	582
97241_at	MGC6696	hypothetical protein MGC6696	2.67	3.00	2.33	0.97	0.93	0.30	0.33	1546	1580	463	523
103200_at	E430013J17Rik	RIKEN cDNA E430013J17 gene	2.75	4.50	1.00	0.80	0.85	0.36	0.41	168	159	60	66
103888_at	Rbpms	RNA binding protein gene with multiple splicing	2.92	2.67	3.17	0.90	0.92	0.42	0.42	915	1076	384	454
103006_at	Atf5	activating transcription factor 5	3.08	3.67	2.50	0.89	0.88	0.31	0.37	2892	2781	902	1028
95661_at	Cd9	CD9 antigen	3.17	4.17	2.17	0.92	0.84	0.48	0.36	612	524	296	187
94795_at	Hsd3b5	hydroxysteroid dehydrogenase-5, delta<5>-3-beta	3.25	3.83	2.67	0.90	0.93	0.31	0.29	8667	10149	2689	2959
97240_g_at	MGC6696	hypothetical protein MGC6696	3.33	3.50	3.17	0.96	0.89	0.32	0.28	3153	3524	1005	1001
103634_at	lsgf3g	interferon dependent positive acting transcription factor	3.42	4.00	2.83	0.87	0.86	0.35	0.39	378	361	133	140
104717_at	D5Ertd689e	DNA segment, Chr 5, ERATO Doi 689, expressed	3.50	5.83	1.17	0.86	0.80	0.25	0.17	649	597	166	100
96771_at	Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homo	3.58	4.67	2.50	0.92	0.91	0.30	0.35	2824	2115	852	733
93268_at		Mus musculus 12 days embryo spinal cord cDNA, RIK	3.67	5.00	2.33	0.83	0.89	0.20	0.15	6433	6403	1295	971

93353_all Sca2 spinocerebellar alaxia 2 homolog (human) 3.8 4.50 3.13 0.95 0.82 0.27 0.28 1075 470 2.02 2.57 2.2 95474_at F2r coagulation factor III (hrombin) receptor 3.92 4.50 3.33 0.80 0.92 0.33 0.88 662 133 2 10058_at LOC219140 hypothetical protein LOC219140 3.92 4.00 4.17 3.83 0.96 0.95 0.81 0.45 0.43 639 645 1.03 0.96 0.95 0.81 0.45 0.43 639 645 1.03 0.96 0.96 0.25 0.22 6866 6821 1.095 1.15	94917_at	Fbxo8	F-box only protein 8	3.75	5.00	2.50	0.80	0.80	0.32	0.21	581	544	185	114
96474 att F2r coagulation factor if (mombin) receptor 3.92 4.50 3.33 0.82 0.92 0.33 0.83 6.84 6.93 0.33 5.88 6.62 1.73 2.25 94499_att LOC219140 hypothetical protein LOC219140 3.22 3.83 0.80 0.85 0.81 0.45 0.33 6.86 6.821 1.01 2706 1.01 93013_att Idb2 inhibitor of DNA binding 2 4.00 4.17 4.33 0.66 0.86 0.22 6.86 6.821 1.0152 1030002A08KR RIKEN ANA 1300002A08 gene 4.40 4.30 7.40 0.88 0.82 0.23 0.43 4.17 3.53 0.84 0.82 0.29 3.44 1.015 1.015 1.025 1.15 1.	93535_at	Sca2	spinocerebellar ataxia 2 homolog (human)	3.83	4.50	3.17	0.95	0.82	0.27	0.28	1075	870	292	246
9449 at Mega5 menipoma expressed ant/gen 5 (nyaluronidase) 3.92 5.80 6.90 0.92 0.83 0.81 0.43 0.43 4.33 949 1.01 100958_at LOC219140 inbibitor ODNA binding 2 4.00 4.17 3.83 0.66 0.85 0.45 0.39 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.037 6.043 6.037 6.04 0.04 9.04 6.037 6.037 6.04 0.04 9.04 6.03 0.24 6.04 6.03 6.04 0.24 6.04 7.03 0.04 9.07 1.03 0.04 9.01 1.041 0.33 0.44 6.07 4.33 0.94 0.34 0.04 0.31 0.31 0.31 9.04 0.33 0.44 0.33 0.44 0.33 0.44 0.33 0.34 0.31	95474_at	F2r	coagulation factor II (thrombin) receptor	3.92	4.50	3.33	0.82	0.92	0.37	0.39	694	728	257	280
100686_atl LOC219140 hypothetical protein LOC219140 3.92 3.83 4.00 0.45 0.43 4.43 3.43 3.66 1.9 1.9 93013_atl Ubb2 Inhibitor of DNA binding 2 4.00 4.17 4.33 0.66 0.89 0.45 0.39 6.037 5.107 2706 1.9 98059_atl 130002AORBM RIKEN ENAN 1300002AOB gene 4.00 4.71 4.33 5.17 3.00 0.84 0.82 0.35 0.24 2.47 7.975 6.010 1.655 1.9 95758_r_atl Enrine (or cysteine) proteinase inhibitor, clade F, mem 4.17 4.33 5.17 3.00 4.84 0.81 0.84 0.82 0.35 0.44 4.47 4.47 1.32 1.04 1.03 0.41 1.91 1.066 5.80 4.47 4.33 4.50 0.84 0.82 0.81 0.41 9.71 3.55 2.22 1.424 4.49 aquaponin 9 4.83 5.50 4.43 4.50 0.83 0.30 0.33 4.52 3.71 1.05	94499_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	3.92	5.50	2.33	0.89	0.92	0.33	0.33	588	662	193	222
9303.gt ldb2 Inbibor of DNA binding 2 4.00 4.01 3.83 0.96 0.89 0.45 0.39 6037 1507 2706 19 96680_att 1300002A08Rik RIKEN cDNA 1300002A08 gene 4.08 4.50 4.50 4.50 8.67 0.68 0.89 0.83 0.21 0.24 675 6.001 1655 19 96678_r_at 4.33 5.17 3.50 0.84 0.82 0.35 0.29 3.44 2.77 1.22 102425_att Te1 transducin-like enhancer of split 1, homolog of Droso, 4.42 6.67 4.33 0.40 0.84 0.83 0.60 0.41 171 106 5.69 4.43 94374_att Dazap2 DAZ associated protein 2 4.67 4.83 5.50 4.17 0.84 0.83 0.64 0.43 0.61 4.52 3.41 135 4.52 3.41 135 4.52 3.41 155 4.17 0.83 0.64 0.73 8.53 7.80 5.50 141 0.83 16.50 4	100958_at	LOC219140	hypothetical protein LOC219140	3.92	3.83	4.00	0.95	0.81	0.45	0.43	433	396	196	171
BBB0.att 1300002A08Rik RIKEN toNA 130002A08 gene 4.08 4.50 3.67 0.96 0.92 0.22 6856 6821 16155 171 101326_att Serpin/2	93013_at	ldb2	inhibitor of DNA binding 2	4.00	4.17	3.83	0.96	0.89	0.45	0.39	6037	5107	2706	1973
10122a_at Serpinf2 serine (or cysteine) proteinase inhibitor, clade F, mem 4.17 4.33 4.00 0.98 0.93 0.21 0.24 7975 8010 1665 19 9657a_r at 4.33 5.17 3.50 0.98 0.82 0.25 0.93 0.41 0.77 122 122 122 102425_at ESTs 4.50 4.50 4.67 4.33 0.94 0.84 0.60 0.41 971 1066 580 4.4 94454_at Dazep2 DAZ associated protein 2 4.67 4.83 5.83 0.80 0.93 0.64 0.41 971 1066 580 4.73 9207_at 2600014B10Rik RIKEN cDNA 2600014B10 gene 4.83 5.50 4.17 0.82 0.88 0.43 0.63 4.52 324 105 244 1053 128 128 128 128 128 128 128 128 128 128 128 128 149 128 128 128 128 128 148 128	96890_at	1300002A08Rik	RIKEN cDNA 1300002A08 gene	4.08	4.50	3.67	0.96	0.96	0.25	0.22	6856	6821	1695	1513
96578_rait 4.33 5.17 3.50 0.84 0.82 0.35 0.29 344 277 122 10242g at Tle1 transducin-like enhancer of split 1, homolog of Drosop 4.42 6.7 2.17 3.04 0.84 0.60 4.19 4.17 3.56 125 1 9378_at ESTs 4.67 4.83 4.50 0.93 0.84 0.60 0.14 971 1065 2.27 10432g at App9 aquaporin 9 4.83 5.50 4.17 0.82 0.88 0.43 0.63 4.52 3.24 16 1574 1791 3.55 17 122 10432g at App9 aquaporin 9 4.83 5.50 4.17 0.82 0.84 0.43 0.64 0.73 855 760 5.63 1033 114 124 124 133 432 33 33 128 148 48 5.17 5.17 0.87 0.89 0.81 0.28 0.27 1516 133 432 33 33 139	101928_at	Serpinf2	serine (or cysteine) proteinase inhibitor, clade F, mem	4.17	4.33	4.00	0.98	0.93	0.21	0.24	7975	8010	1655	1915
102425_at Tie1 transducin-like enhancer of split 1, homolog of Drosop 4.42 6.67 2.17 0.81 0.81 0.30 0.43 4.17 359 125 14 95378_at ESTs 4.50 4.57 4.33 0.94 0.84 0.60 0.41 971 1066 550 2 104328_at Aqp9 aguaporin 9 4.83 583 3.83 0.90 0.93 0.25 0.27 2728 2843 673 7 96207_at 2600014B10Rik RIKEN cDNA 2600014B10 gene 4.82 550 4.17 0.82 0.88 0.43 0.63 452 324 195 22 104109_at Fbxo21 Fbxo21 Fbxo20014B10FRik RIKEN cDNA 33015F09 gene 5.00 4.97 0.90 0.25 0.37 1184 1288 285 341 93011_att Gabarapi gama-aninobutyric acid (GABA(A)) receptor-ascid 5.76 7.67 0.91 0.94 0.34 0.42 783 270 264 39 94301_att Gabarapi gama-aninobutyric aci	96578_r_at			4.33	5.17	3.50	0.84	0.82	0.35	0.29	344	277	122	81
95378_at ESTs 4.50 4.67 4.33 0.94 0.84 0.60 0.41 971 1066 580 44 94454_at Dazap2 DAZ associated protein 2 4.67 4.83 4.80 0.90 0.93 0.25 0.27 2728 2243 673 7 96207_at 2600014B10Rik RIKEN cDNA 2600014B10 gene 4.83 5.50 4.17 0.02 0.88 0.43 0.63 452 324 195 22 104109_at Fbxo21 F-bxo only protein 21 4.92 5.33 4.50 0.44 0.63 0.42 0.23 0.64 0.73 883 780 648 53 103611_at Cd47 CD47 antigen (Rh-related antigen, integrin-associated 4.92 6.17 3.67 0.89 0.81 0.28 0.27 1184 129 295 4 930151F09Rik<	102425_at	Tle1	transducin-like enhancer of split 1, homolog of Drosop	4.42	6.67	2.17	0.81	0.81	0.30	0.43	417	359	125	155
94454_at Dazap2 DAZ associated protein 2 4.67 4.83 4.50 0.93 0.84 0.23 0.16 1574 1791 355 22 104328_at App9 aquaporin 9 4.83 5.83 3.83 0.90 0.93 0.25 0.27 228 2843 673 77 96207_at 2600014B1018 RIKEN CDNA 2600014B10 gene 4.82 5.33 4.50 0.94 0.93 0.64 0.73 853 700 513 432 533 4.50 0.94 0.93 0.64 0.73 853 700 433 514 0.74 0.81 0.25 0.37 1184 1299 295 44 93011_at Gabarap11 gama-aninobutynci acid (GABA(A)) receptor-associ 5.17 5.17 5.17 0.91 0.94 0.34 0.33 228 48 64 93011_at Gabarap1 gama-aninobutynci acid (GABAA)) receptor-associ 5.17 5.17 5.17 5.17 0.51 0.91	95378_at		ESTs	4.50	4.67	4.33	0.94	0.84	0.60	0.41	971	1066	580	437
104328_at Aqp9 aquaporin 9 4.83 5.83 3.83 0.90 0.93 0.25 0.27 2728 2843 673 77 96207_at 2600014B10Rik RIKEN cDNA 2600014B10 gene 4.83 5.50 4.17 0.62 0.88 0.43 0.63 452 324 195 22 104109_at Fbox 0nly protein 21 4.92 5.33 4.50 0.94 0.93 0.64 0.73 853 780 548 53 94261_at 9330151F09Rik RIKEN cDNA 9330151F09 gene 5.00 4.83 5.17 0.97 0.80 0.25 0.37 1184 1289 295 44 95031_at 1110059H15Rik RIKEN cDNA 1110059H15 gene 5.17 5.17 5.17 0.91 0.94 0.34 0.42 7893 9270 2644 39 9423_at 1500035H01Rik RIKEN cDNA A93001N09 gene 5.25 6.33 4.17 0.90 0.81 0.39 0.36 317 280 123 1 98038_at Hmgb3 hitgh mobility group box 3 5.33 <td>94454_at</td> <td>Dazap2</td> <td>DAZ associated protein 2</td> <td>4.67</td> <td>4.83</td> <td>4.50</td> <td>0.93</td> <td>0.84</td> <td>0.23</td> <td>0.16</td> <td>1574</td> <td>1791</td> <td>355</td> <td>292</td>	94454_at	Dazap2	DAZ associated protein 2	4.67	4.83	4.50	0.93	0.84	0.23	0.16	1574	1791	355	292
96207_at 2600014B10Rik RIKEN cDNA 2600014B10 gene 4.83 5.50 4.17 0.82 0.88 0.43 0.63 452 324 195 22 104109_at Fbxo21 F-box only protein 21 4.92 5.33 4.50 0.94 0.93 0.64 0.73 853 780 548 55 103611_at Cd47 CD47 antigen (Rh-related antigen, integrin-associated 4.92 6.17 3.67 0.89 0.81 0.28 0.27 1516 1333 4422 33 95031_at 1110059H15Rik RIKEN cDNA 330151F09 gene 5.08 7.50 2.67 0.87 0.85 0.30 0.33 228 184 68 93011_at Gabarapl1 gamma-aminobutyric acid (GABA(A)) receptor-associ 5.17 5.17 0.91 0.94 0.34 0.42 7893 9270 2644 39 98031_at 110059H15Rik RIKEN cDNA 150003H01 gene 5.25 6.17 0.30 0.81 0.39 0.36 317 280 120 141 9803a_at Hmgb3 high mobility group box 3 <t< td=""><td>104328_at</td><td>Aqp9</td><td>aquaporin 9</td><td>4.83</td><td>5.83</td><td>3.83</td><td>0.90</td><td>0.93</td><td>0.25</td><td>0.27</td><td>2728</td><td>2843</td><td>673</td><td>770</td></t<>	104328_at	Aqp9	aquaporin 9	4.83	5.83	3.83	0.90	0.93	0.25	0.27	2728	2843	673	770
104109_at Fbxo21 F-box only protein 21 4.92 5.33 4.50 0.94 0.93 0.64 0.73 853 780 548 55 103611_at Cd47 CD47 antigen (Rh-related antigen, integrin-associated 4.92 6.17 3.67 0.89 0.81 0.28 0.27 1516 1333 432 33 94261_at 9330151509Rik RIKEN cDNA 9330151F09 gene 5.00 4.83 5.17 0.87 0.87 0.85 0.30 0.33 128 144 68 93011_at Gabarapl1 gamma-aminobutyric acid (GABA(A)) receptor-associc 5.17 5.17 5.17 0.91 0.94 0.34 0.42 7803 9270 2644 39 9423_at 1500035H01Rik RIKEN cDNA 1500035H01 gene 5.25 6.17 5.17 5.17 0.91 0.81 0.39 0.36 317 2803 123 1103 1105 124 113 1103 156 24 0.15 1041 0.15 0.24 0.15 0.16 0.53 175 5.67 104 0.55	96207_at	2600014B10Rik	RIKEN cDNA 2600014B10 gene	4.83	5.50	4.17	0.82	0.88	0.43	0.63	452	324	195	203
103611_at Cd47 CD47 antigen (Rh-related antigen, integrin-associated 4.92 6.17 3.67 0.89 0.81 0.28 0.27 1516 1333 432 33 94261_at 9330151F09Rik RIKEN cDNA 9330151F09 gene 5.00 4.83 5.17 0.97 0.90 0.25 0.37 1184 1289 295 44 95031_at 1110059H15Rik RIKEN cDNA 1110059H15 gene 5.08 7.50 2.67 0.87 0.86 0.30 0.33 228 184 68 93011_at Gabarapl1 gamma-aminobutyric acid (GABA(A)) receptor-associ 5.17 5.17 6.33 0.92 0.86 0.16 0.25 969 1053 156 22 98255_r_at A930001N09Rik RIKEN cDNA 4930001N09 gene 5.25 6.33 4.17 0.90 0.81 0.39 0.36 317 280 123 1 98038_at Hmgb3 high mobility group box 3 5.53 5.50 6.17 0.93 0.88 0.34 0.34 175 175 597 68 104407_at	104109_at	Fbxo21	F-box only protein 21	4.92	5.33	4.50	0.94	0.93	0.64	0.73	853	780	548	570
94261_at 9330151F09Rik RIKEN cDNA 9330151F09 gene 5.00 4.83 5.17 0.97 0.90 0.25 0.37 1184 1289 295 4 95031_at 1110059H15Rik RIKEN cDNA 1110059H15 gene 5.08 7.50 2.67 0.87 0.85 0.30 0.33 228 184 68 97423_at 1500035H01Rik RIKEN cDNA 1500035H01 gene 5.25 4.17 6.33 0.92 0.86 0.16 0.25 969 1053 156 22 98855_r_at A930001N09Rik RIKEN cDNA 4930001N09 gene 5.25 6.33 4.17 0.90 0.81 0.39 0.36 317 280 123 1 98038_at Hmgb3 high mobility group box 3 5.33 4.67 6.00 0.81 0.34 0.34 1750 1757 597 68 104407_at Alcam activated leukocyte cell adhesion molecule 5.83 5.67 6.00 0.82 0.83 0.34 0.34 1750 1757 597 68 93528_s_at Kif9 Kruppel-like factor 9	103611_at	Cd47	CD47 antigen (Rh-related antigen, integrin-associated	4.92	6.17	3.67	0.89	0.81	0.28	0.27	1516	1333	432	360
95031_at 1110059H15Rik RIKEN cDNA 1110059H15 gene 5.08 7.50 2.67 0.87 0.85 0.30 0.33 228 184 68 93011_at Gabarapl1 gamma-aminobutyric acid (GABA(A)) receptor-associe 5.17 5.17 5.17 0.91 0.94 0.34 0.42 7893 9270 2644 39 97423_at 1500035H01Rik RIKEN cDNA 1500035H01 gene 5.25 6.33 4.17 0.90 0.81 0.39 0.36 317 280 123 11 98038_at Hmgb3 high mobility group box 3 5.33 4.67 6.00 0.91 0.85 0.24 0.15 1070 1037 254 11 98023_at Rnac-pending RNA cyclase homolog 5.83 5.50 6.17 0.93 0.83 0.34 0.34 1750 1757 597 66 104407_at Alcam activated leukocyte cell adhesion molecule 5.83 5.67 6.00 0.82 0.83 0.38 0.53 615 541 237 22 98528_s_at Klf9	94261_at	9330151F09Rik	RIKEN cDNA 9330151F09 gene	5.00	4.83	5.17	0.97	0.90	0.25	0.37	1184	1289	295	472
93011_at Gabarapl1 gamma-aminobutyric acid (GABA(A)) receptor-associ 5.17 5.17 5.17 5.17 0.91 0.94 0.34 0.42 7893 9270 2644 39 97423_at 1500035H01Rik RIKEN cDNA 1500035H01 gene 5.25 4.17 6.33 0.92 0.86 0.16 0.25 969 1053 116 22 98855_r_at A930001N09Rik RKEN cDNA A930001N09 gene 5.25 6.33 4.17 0.90 0.81 0.39 0.36 317 280 123 1 98038_at Hmgb3 high mobility group box 3 5.33 4.67 6.00 0.91 0.85 0.24 0.15 1070 1037 254 11 98038_at Rnac-pending RNA cyclase homolog 5.83 5.50 6.17 0.93 0.83 0.34 0.34 1757 597 66 104407_at Alcam activated leukocyte cell adhesion molecule 5.83 5.67 6.00 0.82 0.82 0.38 0.53 615 541 237 94528_s_sat Trip6	95031_at	1110059H15Rik	RIKEN cDNA 1110059H15 gene	5.08	7.50	2.67	0.87	0.85	0.30	0.33	228	184	68	61
97423_at 1500035H01Rik RIKEN cDNA 1500035H01 gene 5.25 4.17 6.33 0.92 0.86 0.16 0.25 969 1053 156 22 98855_r_at A930001N09Rik RIKEN cDNA A930001N09 gene 5.25 6.33 4.17 0.90 0.81 0.39 0.36 317 280 123 1 98038_at Hmgb3 high mobility group box 3 5.33 4.67 6.00 0.91 0.85 0.24 0.15 1070 1037 254 1 98038_at Rnac-pending RNA cyclase homolog 5.83 5.50 6.17 0.93 0.83 0.34 0.34 1750 1757 597 66 104407_at Alcam activated leukocyte cell adhesion molecule 5.83 5.67 6.00 0.82 0.82 0.83 0.28 0.49 302 168 7 93528_s_at Kil9 Kruppel-like factor 9 6.03 6.17 5.33 7.00 0.91 0.83 0.38 0.53 615 541 237 227 2273 2274 723	93011_at	Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associa	5.17	5.17	5.17	0.91	0.94	0.34	0.42	7893	9270	2644	3910
98855_r_at A930001N09Rik RIKEN cDNA A930001N09 gene 5.25 6.33 4.17 0.90 0.81 0.39 0.36 317 280 123 11 98038_at Hmgb3 high mobility group box 3 5.33 4.67 6.00 0.91 0.85 0.24 0.15 1070 1037 254 11 98923_at Rnac-pending RNA cyclase homolog 5.83 5.50 6.17 0.93 0.83 0.34 0.34 1750 1757 597 66 104407_at Alcam activated leukocyte cell adhesion molecule 5.83 5.67 6.00 0.82 0.82 0.38 0.28 449 302 168 93528_s_at Kif9 Kruppel-like factor 9 6.08 6.33 5.83 0.90 0.85 0.27 0.29 3287 3330 902 99 94948_at Trip6 thyroid hormone receptor interactor 6 6.17 5.33 7.00 0.91 0.83 0.32 0.25 2273 2274 723 95 94073_at Nt1d1 nuclear receptor subf	97423_at	1500035H01Rik	RIKEN cDNA 1500035H01 gene	5.25	4.17	6.33	0.92	0.86	0.16	0.25	969	1053	156	268
98038_at Hmgb3 high mobility group box 3 5.33 4.67 6.00 0.91 0.85 0.24 0.15 1070 1037 254 1 98923_at Rnac-pending RNA cyclase homolog 5.83 5.50 6.17 0.93 0.83 0.34 0.34 1750 1757 597 66 104407_at Alcam activated leukocyte cell adhesion molecule 5.83 5.67 6.00 0.82 0.82 0.38 0.28 449 302 168 93528_s_at Klf9 Kruppel-like factor 9 6.08 6.33 5.83 0.90 0.85 0.27 0.29 3287 3330 902 92 94948_at Trip6 thyroid hormone receptor interactor 6 6.17 5.33 7.00 0.91 0.83 0.38 0.55 1291 1143 887 77 98507_at Nrtd1 nuclear receptor subfamily 1, group D, member 1 6.17 6.17 0.87 0.85 0.69 0.65 1291 1143 887 77 104070_at Pcaf p300/CBP-associated factor <td>98855_r_at</td> <td>A930001N09Rik</td> <td>RIKEN cDNA A930001N09 gene</td> <td>5.25</td> <td>6.33</td> <td>4.17</td> <td>0.90</td> <td>0.81</td> <td>0.39</td> <td>0.36</td> <td>317</td> <td>280</td> <td>123</td> <td>101</td>	98855_r_at	A930001N09Rik	RIKEN cDNA A930001N09 gene	5.25	6.33	4.17	0.90	0.81	0.39	0.36	317	280	123	101
98923_at Rnac-pending RNA cyclase homolog 5.83 5.50 6.17 0.93 0.83 0.34 0.34 1750 1757 597 66 104407_at Alcam activated leukocyte cell adhesion molecule 5.83 5.67 6.00 0.82 0.82 0.38 0.28 449 302 168 93528_s_at Klf9 Kruppel-like factor 9 6.08 6.33 5.83 0.90 0.85 0.27 0.29 3287 3330 902 99 94948_at Trip6 thyroid hormone receptor interactor 6 6.17 5.33 7.00 0.91 0.83 0.38 0.53 615 541 237 22 98507_at Nr1d1 nuclear receptor subfamily 1, group D, member 1 6.17 6.17 6.87 0.88 0.69 0.65 1291 1143 887 77 104070_at Pcaf p300/CBP-associated factor 6.58 6.50 6.67 0.91 0.83 0.31 0.30 877 900 223 2274 723 55 94733_at Abcb4	98038_at	Hmgb3	high mobility group box 3	5.33	4.67	6.00	0.91	0.85	0.24	0.15	1070	1037	254	159
104407_atAlcamactivated leukocyte cell adhesion molecule5.835.676.000.820.820.820.4844930216893528_s_atKlf9Kruppel-like factor 96.086.035.830.900.850.270.29328733309029994948_atTrip6thyroid hormone receptor interactor 66.175.337.000.910.830.380.536155412372298507_atNr1d1nuclear receptor subfamily 1, group D, member 16.176.176.170.870.850.690.651291114388777104070_atPcafp300/CBP-associated factor6.586.506.670.910.830.320.25227322747235594733_atAbcb4ATP-binding cassette, sub-family B (MDR/TAP), mem6.587.006.170.850.890.160.165763535289488104034_atMus musculus, clone IMAGE:4973354, mRNA7.177.506.830.860.410.4626652265109110094440_atAl876593expressed sequence Al8765937.257.507.000.890.900.430.49702765552987322102668_atPparaperoxisome proliferator activated receptor alpha7.587.837.330.940.840.310.2943722799135588104343 f at	98923_at	Rnac-pending	RNA cyclase homolog	5.83	5.50	6.17	0.93	0.83	0.34	0.34	1750	1757	597	600
93528_s_atKIf9Kruppel-like factor 96.086.335.830.900.850.270.29328733309029994948_atTrip6thyroid hormone receptor interactor 66.175.337.000.910.830.380.536155412372298507_atNr1d1nuclear receptor subfamily 1, group D, member 16.176.176.170.870.850.690.65129111438877104070_atPcafp300/CBP-associated factor6.586.506.670.910.830.320.25227322747235594733_atAbcb4ATP-binding cassette, sub-family B (MDR/TAP), mem6.587.006.170.860.800.310.308779002732298114_atNpc1Niemann Pick type C17.257.177.330.900.860.410.4626652265109110094440_atAl876593expressed sequence Al8765937.257.507.000.890.900.430.49702765552987322102668_atPparaperoxisome proliferator activated receptor alpha7.587.837.330.940.840.310.294372279913558899076_atNr1d2nuclear receptor subfamily 1, group D, member 28.258.837.670.860.800.370.25151919555624 <td>104407_at</td> <td>Alcam</td> <td>activated leukocyte cell adhesion molecule</td> <td>5.83</td> <td>5.67</td> <td>6.00</td> <td>0.82</td> <td>0.82</td> <td>0.38</td> <td>0.28</td> <td>449</td> <td>302</td> <td>168</td> <td>84</td>	104407_at	Alcam	activated leukocyte cell adhesion molecule	5.83	5.67	6.00	0.82	0.82	0.38	0.28	449	302	168	84
94948_atTrip6thyroid hormone receptor interactor 66.175.337.000.910.830.380.536155412372298507_atNr1d1nuclear receptor subfamily 1, group D, member 16.176.176.170.870.850.690.65129111438877104070_atPcafp300/CBP-associated factor6.586.506.670.910.830.320.2522732274723594733_atAbcb4ATP-binding cassette, sub-family B (MDR/TAP), mem6.587.006.170.850.890.160.165763535289488104034_atMus musculus, clone IMAGE:4973354, mRNA7.177.506.830.860.810.310.308779002732298114_atNpc1Niemann Pick type C17.257.177.330.900.860.410.4626652265109110094440_atAl876593expressed sequence Al8765937.257.507.000.890.900.430.4970276555298732102668_atPparaperoxisome proliferator activated receptor alpha7.587.837.330.940.840.310.294372279913558899076_atNr1d2nuclear receptor subfamily 1, group D, member 28.258.837.670.860.800.370.25151919555624 <td>93528_s_at</td> <td>Klf9</td> <td>Kruppel-like factor 9</td> <td>6.08</td> <td>6.33</td> <td>5.83</td> <td>0.90</td> <td>0.85</td> <td>0.27</td> <td>0.29</td> <td>3287</td> <td>3330</td> <td>902</td> <td>978</td>	93528_s_at	Klf9	Kruppel-like factor 9	6.08	6.33	5.83	0.90	0.85	0.27	0.29	3287	3330	902	978
98507_at Nr1d1 nuclear receptor subfamily 1, group D, member 1 6.17 6.17 0.87 0.85 0.69 0.65 1291 1143 887 7 104070_at Pcaf p300/CBP-associated factor 6.58 6.50 6.67 0.91 0.83 0.32 0.25 2273 2274 723 5 94733_at Abcb4 ATP-binding cassette, sub-family B (MDR/TAP), mem 6.58 7.00 6.17 0.85 0.89 0.16 0.16 5763 5352 894 8 104034_at Mus musculus, clone IMAGE:4973354, mRNA 7.17 7.50 6.83 0.86 0.81 0.31 0.30 877 900 273 22 98114_at Npc1 Niemann Pick type C1 7.25 7.17 7.33 0.90 0.86 0.41 0.46 2665 2265 1091 100 94440_at Al876593 expressed sequence Al876593 7.25 7.50 7.00 0.89 0.90 0.43 0.49	94948_at	Trip6	thyroid hormone receptor interactor 6	6.17	5.33	7.00	0.91	0.83	0.38	0.53	615	541	237	287
104070_atPcafp300/CBP-associated factor6.586.506.670.910.830.320.25227322747235594733_atAbcb4ATP-binding cassette, sub-family B (MDR/TAP), mem6.587.006.170.850.890.160.165763535289488104034_atMus musculus, clone IMAGE:4973354, mRNA7.177.506.830.860.810.310.308779002732298114_atNpc1Niemann Pick type C17.257.177.330.900.860.410.4626652265109110094440_atAl876593expressed sequence Al8765937.257.507.000.890.900.430.4970276555298732102668_atPparaperoxisome proliferator activated receptor alpha7.587.837.330.940.840.310.294372279913558899076_atNr1d2nuclear receptor subfamily 1, group D, member 28.258.837.670.860.800.370.25151919555624	98507_at	Nr1d1	nuclear receptor subfamily 1, group D, member 1	6.17	6.17	6.17	0.87	0.85	0.69	0.65	1291	1143	887	738
94733_at Abcb4 ATP-binding cassette, sub-family B (MDR/TAP), mem 6.58 7.00 6.17 0.85 0.89 0.16 0.16 5763 5352 894 88 104034_at Mus musculus, clone IMAGE:4973354, mRNA 7.17 7.50 6.83 0.86 0.81 0.31 0.30 877 900 273 22 98114_at Npc1 Niemann Pick type C1 7.25 7.17 7.33 0.90 0.86 0.41 0.46 2665 2265 1091 100 94440_at Al876593 expressed sequence Al876593 7.25 7.50 7.00 0.89 0.90 0.43 0.49 7027 6555 2987 32 102668_at Ppara peroxisome proliferator activated receptor alpha 7.58 7.83 7.33 0.94 0.84 0.31 0.29 4372 2799 1355 88 99076_at Nr1d2 nuclear receptor subfamily 1, group D, member 2 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 1955 562 4	104070_at	Pcaf	p300/CBP-associated factor	6.58	6.50	6.67	0.91	0.83	0.32	0.25	2273	2274	723	559
104034_at Mus musculus, clone IMAGE:4973354, mRNA 7.17 7.50 6.83 0.86 0.81 0.31 0.30 877 900 273 22 98114_at Npc1 Niemann Pick type C1 7.25 7.17 7.33 0.90 0.86 0.41 0.46 2665 2265 1091 100 94440_at Al876593 expressed sequence Al876593 7.25 7.50 7.00 0.89 0.90 0.43 0.49 7027 6555 2987 32 102668_at Ppara peroxisome proliferator activated receptor alpha 7.58 7.83 7.33 0.94 0.84 0.31 0.29 4372 2799 1355 8 99076_at Nr1d2 nuclear receptor subfamily 1, group D, member 2 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 1955 562 4	94733_at	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), mem	6.58	7.00	6.17	0.85	0.89	0.16	0.16	5763	5352	894	831
98114_at Npc1 Niemann Pick type C1 7.25 7.17 7.33 0.90 0.86 0.41 0.46 2665 2265 1091 100 94440_at Al876593 expressed sequence Al876593 7.25 7.50 7.00 0.89 0.90 0.43 0.49 7027 6555 2987 32 102668_at Ppara peroxisome proliferator activated receptor alpha 7.58 7.83 7.33 0.94 0.84 0.31 0.29 4372 2799 1355 88 99076_at Nr1d2 nuclear receptor subfamily 1, group D, member 2 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 1955 562 4	104034_at		Mus musculus, clone IMAGE:4973354, mRNA	7.17	7.50	6.83	0.86	0.81	0.31	0.30	877	900	273	270
9440_at Al876593 expressed sequence Al876593 7.25 7.50 7.00 0.89 0.90 0.43 0.49 7027 6555 2987 32 102668_at Ppara peroxisome proliferator activated receptor alpha 7.58 7.83 7.33 0.94 0.84 0.31 0.29 4372 2799 1355 88 99076_at Nr1d2 nuclear receptor subfamily 1, group D, member 2 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 356 2987 32 104343 f at Pla2g12 phospholipase A2, group XII 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 1955 562 44	98114_at	Npc1	Niemann Pick type C1	7.25	7.17	7.33	0.90	0.86	0.41	0.46	2665	2265	1091	1042
102668_at Ppara peroxisome proliferator activated receptor alpha 7.58 7.83 7.33 0.94 0.84 0.31 0.29 4372 2799 1355 88 99076_at Nr1d2 nuclear receptor subfamily 1, group D, member 2 8.25 8.33 8.17 0.95 0.95 0.82 0.77 431 367 354 22 104343 f at Pla2g12 phospholipase A2, group XII 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 1955 562 44	94440_at	AI876593	expressed sequence AI876593	7.25	7.50	7.00	0.89	0.90	0.43	0.49	7027	6555	2987	3231
99076_at Nr1d2 nuclear receptor subfamily 1, group D, member 2 8.25 8.33 8.17 0.95 0.82 0.77 431 367 354 2 104343 f at Pla2g12 phospholipase A2, group XII 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 1955 562 4	102668_at	Ppara	peroxisome proliferator activated receptor alpha	7.58	7.83	7.33	0.94	0.84	0.31	0.29	4372	2799	1355	801
104343 f at Pla2g12 phospholipase A2, group XII 8.25 8.83 7.67 0.86 0.80 0.37 0.25 1519 1955 562 4	99076_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	8.25	8.33	8.17	0.95	0.95	0.82	0.77	431	367	354	284
	104343_f_at	Pla2g12	phospholipase A2, group XII	8.25	8.83	7.67	0.86	0.80	0.37	0.25	1519	1955	562	483

98447_at	Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	8.42	8.17	8.67	0.85	0.87	0.17	0.18	14077	14853	2342	2621
93320_at	Cpt1a	carnitine palmitoyltransferase 1, liver	8.75	9.00	8.50	0.96	0.89	0.41	0.34	6865	6064	2801	2045
95727_at	Apoa5	apolipoprotein A-V	8.92	9.00	8.83	0.89	0.88	0.21	0.21	15008	16066	3097	3374
103357_at	Slc2a2	solute carrier family 2 (facilitated glucose transporter),	9.25	9.00	9.50	0.94	0.84	0.33	0.24	4882	4356	1622	1048
96037_at	Bri3	brain protein I3	9.33	9.33	9.33	0.95	0.87	0.27	0.23	3959	3951	1068	919
96348_at	0610039C21Rik	RIKEN cDNA 0610039C21 gene	9.42	8.50	10.33	0.81	0.87	0.64	0.43	1153	1049	744	454
103553_at	2410041F14Rik	RIKEN cDNA 2410041F14 gene	9.42	8.83	10.00	0.90	0.90	0.42	0.31	1392	1673	587	520
96041_at	Rbm3	RNA binding motif protein 3	9.50	9.17	9.83	0.94	0.84	0.43	0.32	613	678	263	219
98942_r_at	2310032D16Rik	RIKEN cDNA 2310032D16 gene	9.50	9.17	9.83	0.90	0.80	0.96	0.64	425	201	410	129
95729_at	Apoa5	apolipoprotein A-V	9.83	10.67	9.00	0.92	0.81	0.26	0.24	5169	5534	1364	1324
97924_at	Uae1	UDP-N-acetylglucosamine-2-epimerase/N-acetylmanr	9.92	9.83	10.00	0.96	0.93	0.31	0.29	2920	2738	909	781
94896_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	9.92	10.50	9.33	0.83	0.83	0.23	0.28	788	651	185	180
104116_at	D5Ertd593e	DNA segment, Chr 5, ERATO Doi 593, expressed	10.17	9.83	10.50	0.87	0.91	0.49	0.42	2293	2119	1122	883
100877_at	1810058l24Rik	RIKEN cDNA 1810058I24 gene	10.42	11.00	9.83	0.91	0.93	0.37	0.31	3740	3964	1385	1213
103473_at	Pak4	p21 (CDKN1A)-activated kinase 4	10.67	11.00	10.33	0.81	0.83	0.16	0.39	708	519	114	204
94928_at	Tnfrsf1b	tumor necrosis factor receptor superfamily, member 11	10.83	10.17	11.50	0.86	0.84	0.27	0.20	397	419	106	84
104213_at	1700124F02Rik	RIKEN cDNA 1700124F02 gene	11.00	10.67	11.33	0.97	0.96	0.60	0.56	9588	9057	5717	5037
92821_at	Usp2	ubiquitin specific protease 2	11.17	10.67	11.67	0.89	0.81	0.71	0.74	516	426	364	316
95148_at	Ak2	adenylate kinase 2	11.25	10.67	11.83	0.91	0.87	0.27	0.23	3025	3635	813	829
93836_at	Bnip3	BCL2/adenovirus E1B 19kDa-interacting protein 1, NII	11.25	10.67	11.83	0.84	0.88	0.52	0.38	990	974	513	366
92925_at	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	11.33	11.00	11.67	0.85	0.85	0.50	0.27	3625	3538	1819	952
95057_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress	11.42	11.50	11.33	0.93	0.92	0.55	0.48	5123	4922	2807	2375
104674_s_at	Pcsk4	proprotein convertase subtilisin/kexin type 4	11.67	11.33	12.00	0.91	0.93	0.73	0.64	675	577	492	370
104701_at	Bhlhb2	basic helix-loop-helix domain containing, class B2	11.83	10.50	13.17	0.93	0.82	0.35	0.37	1039	1038	368	380
93315_at	Map2k3	mitogen activated protein kinase kinase 3	11.83	10.67	13.00	0.88	0.84	0.20	0.18	2245	2303	442	413
96806_at	Lpin2	lipin 2	11.92	12.00	11.83	0.95	0.94	0.38	0.29	1325	1123	502	320
101007_at	Mknk2	MAP kinase-interacting serine/threonine kinase 2	12.08	11.67	12.50	0.96	0.91	0.52	0.43	1560	1357	808	580
92587_at	Fdx1	ferredoxin 1	12.17	11.00	13.33	0.92	0.93	0.16	0.16	10043	9612	1564	1551
98324_at	Foxa3	forkhead box A3	12.17	12.00	12.33	0.89	0.84	0.40	0.43	1279	1345	514	582
104745_at	Arl6ip2	ADP-ribosylation-like factor 6 interacting protein 2	12.50	11.83	13.17	0.84	0.93	0.33	0.24	1908	1903	628	454
98596_s_at	Siat9	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpl	12.67	12.83	12.50	0.85	0.87	1.03	0.86	839	1037	867	888
99404_at	Cyp7a1	cytochrome P450, family 7, subfamily a, polypeptide 1	12.67	11.50	13.83	0.86	0.92	0.87	0.68	1064	561	926	379
93451_at	C130003G01	hypothetical protein C130003G01	12.67	10.00	15.33	0.87	0.89	0.20	0.24	726	639	146	155
97430_at	G6pt1	glucose-6-phosphatase, transport protein 1	12.83	12.33	13.33	0.96	0.91	0.39	0.41	4687	4415	1820	1825
99535_at	Ccrn4I	CCR4 carbon catabolite repression 4-like (S. cerevisia	13.00	13.00	13.00	0.89	0.82	0.85	0.98	1143	1169	967	1142

99521_at	Ak4	adenylate kinase 4	13.00	13.50	12.50	0.85	0.89	0.23	0.22	1100	968	251	208
94489_at	Ptp4a1	protein tyrosine phosphatase 4a1	13.17	12.00	14.33	0.87	0.85	0.36	0.31	6240	6095	2228	1909
99019_at	Por	P450 (cytochrome) oxidoreductase	13.50	13.17	13.83	0.93	0.93	0.53	0.61	4002	3233	2125	1979
100737_at	Onecut1	one cut domain, family member 1	13.50	11.33	15.67	0.80	0.93	0.34	0.34	1041	869	351	291
93500_at	Alas1	aminolevulinic acid synthase 1	13.58	13.33	13.83	0.91	0.92	0.71	0.72	8813	9221	6217	6652
102847_s_at	Cyp2a4	cytochrome P450, family 2, subfamily a, polypeptide 4	13.58	14.50	12.67	0.82	0.90	0.25	0.24	17852	19897	4449	4801
93694_at	Per2	period homolog 2 (Drosophila)	13.75	13.33	14.17	0.93	0.90	0.94	0.79	252	203	238	161
104285_at	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	13.75	13.33	14.17	0.91	0.91	0.71	0.67	287	235	203	158
99978_s_at	Mapk14	mitogen activated protein kinase 14	14.08	12.33	15.83	0.90	0.86	0.17	0.16	2363	2281	413	372
96564_at	Hspa8	heat shock protein 8	14.08	14.00	14.17	0.85	0.84	0.69	0.57	4847	4674	3334	2644
97261_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	14.17	13.33	15.00	0.85	0.89	0.34	0.37	3511	3955	1186	1455
102233_at	AI256744	EST AI256744	14.42	13.50	15.33	0.91	0.92	0.70	0.55	1018	919	716	507
97334_at	Hes6	hairy and enhancer of split 6 (Drosophila)	14.58	13.83	15.33	0.87	0.94	0.35	0.38	2004	2135	699	818
97473_at	Tm4sf7	transmembrane 4 superfamily member 7	14.75	14.33	15.17	0.90	0.95	0.48	0.47	1860	1978	900	934
97243_at	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), i	15.17	15.33	15.00	0.90	0.88	0.17	0.21	4714	4190	797	861
98111_at	Hsp105	heat shock protein	15.25	15.17	15.33	0.84	0.88	0.59	0.56	1757	1809	1040	1022
96607_at	Chp-pending	calcium binding protein P22	15.33	15.83	14.83	0.87	0.86	0.20	0.18	2048	2309	403	414
95050_at	Chordc1	cysteine and histidine-rich domain (CHORD)-containir	15.42	16.17	14.67	0.85	0.93	0.24	0.27	1096	1047	263	287
103665_at	Lce-pending	long chain fatty acyl elongase	15.58	15.33	15.83	0.86	0.93	0.46	0.63	679	708	313	443
94418_at	Lce-pending	long chain fatty acyl elongase	15.58	15.17	16.00	0.83	0.90	0.47	0.52	409	452	193	233
99849_at		EST	16.67	17.33	16.00	0.90	0.87	0.34	0.28	10624	10446	3597	2958
101538_i_at	Ces3	carboxylesterase 3	16.67	17.00	16.33	0.96	0.86	0.30	0.16	15103	15724	4475	2511
101539_f_at	Ces3	carboxylesterase 3	16.75	16.33	17.17	0.89	0.96	0.21	0.17	13479	14616	2890	2468
95405_at	Mesdc2	mesoderm development candiate 2	16.83	16.83	16.83	0.89	0.86	0.23	0.27	922	996	209	268
98575_at	Fasn	fatty acid synthase	17.00	16.83	17.17	0.89	0.93	0.57	0.72	3237	3207	1842	2306
95282_at	Hspca	heat shock protein 1, alpha	17.17	17.00	17.33	0.91	0.96	0.55	0.53	5128	5356	2845	2820
100494_at	Fgf1	fibroblast growth factor 1	17.25	16.67	17.83	0.87	0.91	0.36	0.48	874	760	318	365
92809_r_at	Fkbp4	FK506 binding protein 4	17.42	17.00	17.83	0.86	0.93	0.27	0.34	3526	3440	953	1161
98572_at	Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	17.92	17.67	18.17	0.88	0.82	0.17	0.33	949	861	161	282
95733_at	Slc29a1	solute carrier family 29 (nucleoside transporters), men	18.08	18.33	17.83	0.82	0.91	0.25	0.17	4660	4828	1187	811
96298_f_at	Dnclc1	dynein, cytoplasmic, light chain 1	18.25	18.00	18.50	0.85	0.93	0.22	0.30	2426	2458	544	733
103565_at		Mus musculus adult retina cDNA, RIKEN full-length er	18.33	18.33	18.33	0.88	0.81	0.26	0.26	1865	1912	493	500
103581_at	Cte1	cytosolic acyl-CoA thioesterase 1	18.33	19.00	17.67	0.84	0.81	0.26	0.20	920	792	235	157
99951_at	Rorc	RAR-related orphan receptor gamma	18.42	17.67	19.17	0.91	0.82	0.49	0.44	1025	957	506	417
94420_f_at	Cry1	cryptochrome 1 (photolyase-like)	18.58	18.50	18.67	0.96	0.93	0.60	0.66	863	848	520	560

104566_at	Asl	argininosuccinate lyase	18.58	19.17	18.00	0.91	0.95	0.24	0.27	5953	5398	1400	1463
92808_f_at	Fkbp4	FK506 binding protein 4	18.67	19.00	18.33	0.90	0.92	0.33	0.35	3742	3802	1237	1322
93290_at	Pnp	purine-nucleoside phosphorylase	18.83	18.83	18.83	0.93	0.98	0.22	0.28	5839	6004	1273	1687
94288_at	Hist1h1c	histone 1, H1c	19.25	20.17	18.33	0.81	0.90	0.69	0.67	689	1053	477	706
103078_at	MGC25977	fasting-inducible integral membrane protein TM6P1	19.33	19.00	19.67	0.84	0.92	0.16	0.19	3642	3511	571	674
99098_at	Fdps	farnesyl diphosphate synthetase	19.58	19.83	19.33	0.96	0.93	0.48	0.54	3298	3417	1598	1845
99452_at	Lisch7-pending	liver-specific bHLH-Zip transcription factor	19.67	19.50	19.83	0.95	0.94	0.25	0.24	3797	3570	951	858
100343_f_at	Tuba1	tubulin, alpha 1	19.92	20.50	19.33	0.81	0.85	0.29	0.20	3448	3819	986	777
95423_at	Cai	calcium binding protein, intestinal	20.08	21.00	19.17	0.84	0.85	0.25	0.24	3001	2571	765	620
95303_at		Mus musculus adult male spinal cord cDNA, RIKEN fu	20.33	1.83	14.83	0.83	0.89	0.22	0.23	248	235	55	53
98759_f_at	Tuba2	tubulin, alpha 2	20.42	21.00	19.83	0.91	0.89	0.22	0.18	5421	6012	1198	1065
99847_at	Siat4a	sialyltransferase 4A (beta-galactosidase alpha-2,3-sia	20.83	21.50	20.17	0.86	0.89	0.62	0.41	552	516	342	213
96594_at	Hspa4	heat shock protein 4	20.92	23.00	18.83	0.81	0.87	0.15	0.28	2003	1879	301	526
98989_at	Dhcr7	7-dehydrocholesterol reductase	21.00	21.50	20.50	0.84	0.83	0.38	0.44	253	328	96	145
102382_at	Arntl	aryl hydrocarbon receptor nuclear translocator-like	21.33	21.50	21.17	0.83	0.89	0.43	0.43	537	521	232	227
96269_at	ldi1	isopentenyl-diphosphate delta isomerase	21.42	22.33	20.50	0.85	0.86	0.36	0.43	1030	911	376	395
102955_at	Nfil3	nuclear factor, interleukin 3, regulated	21.42	20.83	22.00	0.91	0.89	0.49	0.52	611	546	299	282
100516_at	Chk	choline kinase	21.50	21.50	21.50	0.88	0.91	0.51	0.56	554	510	285	285
104451_at	Slc11a2	solute carrier family 11 (proton-coupled divalent metal	21.58	21.33	21.83	0.85	0.92	0.26	0.23	859	796	222	183
93924_f_at	Tuba3	tubulin, alpha 3	21.58	21.67	21.50	0.90	0.86	0.31	0.31	778	577	241	182
103619_at	Cyb5m-pending	cytochrome b5 outer mitochondrial membrane precurs	21.67	21.67	21.67	0.90	0.86	0.16	0.16	4880	5283	804	841
103636_at	Brp17	brain protein 17	21.67	21.67	21.67	0.86	0.94	0.34	0.29	2953	2854	1001	823
94835_f_at	Tubb2	tubulin, beta 2	21.83	21.83	21.83	0.99	0.99	0.62	0.60	4882	4969	3043	2980
92440_at	Irf6	interferon regulatory factor 6	21.92	21.83	22.00	0.81	0.91	0.27	0.34	840	806	227	272
93933_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 30	22.00	22.33	21.67	0.87	0.82	0.33	0.32	754	789	249	253
94788_f_at	Tubb5	tubulin, beta 5	22.17	22.33	22.00	0.97	0.96	0.33	0.37	2757	2519	918	938
93104_at	Btg1	B-cell translocation gene 1, anti-proliferative	22.50	22.50	22.50	0.89	0.89	0.39	0.49	685	736	264	358
92532_at	Avpr1a	arginine vasopressin receptor 1A	22.50	22.67	22.33	0.96	0.90	0.30	0.26	899	814	266	210
97224_at	Prol2	proline rich 2	22.50	22.50	22.50	0.94	0.98	0.36	0.55	2055	1694	743	930
104390_at	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family,	22.75	0.17	21.33	0.84	0.84	0.27	0.28	871	775	234	213
101593_at	Crip2	cysteine rich protein 2	22.75	23.17	22.33	0.88	0.92	0.37	0.33	653	689	244	227
99930_s_at	Psen2	presenilin 2	22.75	23.00	22.50	0.86	0.91	0.34	0.33	3639	3439	1224	1133
95054_at	D15Wsu59e	DNA segment, Chr 15, Wayne State University 59, ex	22.92	23.00	22.83	0.94	0.87	0.37	0.46	1441	1577	532	730
102200_at	Aqp8	aquaporin 8	22.92	23.17	22.67	0.95	0.92	0.33	0.38	1609	1855	529	699
95603_at	Gldc	glycine decarboxylase	22.92	23.17	22.67	0.93	0.93	0.36	0.36	2067	1874	751	668

94325_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	23.08	23.50	22.67	0.84	0.88	0.32	0.40	1921	1554	610	629
93838_at	2700038C09Rik	RIKEN cDNA 2700038C09 gene	23.17	0.00	22.33	0.96	0.83	0.17	0.19	3617	3596	604	669
97546_at	Cldn1	claudin 1	23.17	23.00	23.33	0.91	0.87	0.50	0.95	205	151	103	144
93889_f_at			23.17	23.83	22.50	0.89	0.91	0.27	0.25	837	841	228	209
102021_at	ll4ra	interleukin 4 receptor, alpha	23.25	23.17	23.33	0.80	0.95	0.55	0.49	287	354	159	173
103284_at	Cyp8b1	cytochrome P450, family 8, subfamily b, polypeptide 1	23.25	22.50	0.00	0.96	0.93	0.29	0.35	6594	5845	1904	2052
97527_at	Cks2	CDC28 protein kinase regulatory subunit 2	23.42	1.33	21.50	0.83	0.96	0.26	0.32	875	750	224	238
94383_at	Tfpi2	tissue factor pathway inhibitor 2	23.83	0.50	23.17	0.94	0.96	0.27	0.29	2219	2282	594	667
104388_at	Ccl9	chemokine (C-C motif) ligand 9	23.92	1.17	22.67	0.90	0.88	0.19	0.19	2921	2943	564	548



			Molec	ular Pea	k Time	Corre	lation	Ampl	itude	Ave	age	Standard	Deviation
Probe ID	Gene Symbol	Gene Name	Mean	LD	DD	LD	DD	LD	DD	LD	DD	LD	DD
92913_at	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	0.5833	0.6667	0.5	0.6032	0.5021	0.393	0.3651	112.762	94.6144	44.3185	34.5457
99363_at		ESTs	1.0833	21.5	4.6667	0.5738	0.8416	0.6248	0.2259	200.929	221.869	125.539	50.1153
100708_at	H3f3b	H3 histone, family 3B	1.9167	2.3333	1.5	0.5756	0.7638	0.1566	0.1225	8459.73	8693.83	1325.02	1065.02
97224_at	Prol2	proline rich 2	2.9167	5.1667	0.6667	0.3883	0.5338	0.1951	0.0889	2158.02	2266.34	420.93	201.381
98967_at	Fabp7	fatty acid binding protein 7, brain	3	2.5	3.5	0.9516	0.9106	0.357	0.4583	4944.9	3899.16	1765.22	1786.82
95418_at	1190017B18Rik	RIKEN cDNA 1190017B18 gene	3.3333	3.8333	2.8333	0.9278	0.9555	0.666	0.6427	1823.35	1667.51	1214.44	1071.76
103683_at	Dhodh	dihydroorotate dehydrogenase	3.75	9	22.5	0.5441	0.783	0.4937	0.2976	304.041	416.194	150.107	123.875
93503_at	Sfrp2	secreted frizzled-related sequence protein 2	3.8333	4.3333	3.3333	0.6817	0.8393	0.1324	0.141	1211.87	960.83	160.497	135.507
161609_at	Rgs16	regulator of G-protein signaling 16	4.0833	4.3333	3.8333	0.9639	0.9041	0.5406	0.6173	2286.7	2028.93	1236.21	1252.54
93325_at	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	4.1667	6.1667	2.1667	0.6379	0.7462	0.2211	0.1609	453.251	635.924	100.209	102.329
94378_at	Rgs16	regulator of G-protein signaling 16	4.25	4	4.5	0.9573	0.9742	0.4329	0.4559	8379.57	6984.98	3627.81	3184.19
101541_at		ESTs, Weakly similar to S50828 hypothetical protein -	4.9167	8.8333	1	0.6031	0.7324	0.2701	0.2756	152.587	140.946	41.2091	38.8454
96653_at	0610007007Rik	RIKEN cDNA 0610007007 gene	4.9167	5.6667	4.1667	0.7554	0.8162	0.1647	0.1496	3247.33	3778.93	534.88	565.409
160317_at	Rab34	RAB34, member of RAS oncogene family	5	4.6667	5.3333	0.7283	0.7981	0.1962	0.1154	862.546	1079.23	169.209	124.566
95737_at	1200015A19Rik	RIKEN cDNA 1200015A19 gene	5.0833	5.1667	5	0.3569	0.7294	0.1039	0.0714	2800.09	2609.76	290.789	186.401
96122_at	2310016A09Rik	RIKEN cDNA 2310016A09 gene	5.3333	6.5	4.1667	0.6827	0.7445	0.1152	0.1105	1276.76	1375.16	147.064	151.91
103029_at	Pdcd4	programmed cell death 4	5.5	5.6667	5.3333	0.7682	0.913	0.2227	0.2096	2889.83	2119.11	643.556	444.182
104598_at	Dusp1	dual specificity phosphatase 1	5.5833	6.5	4.6667	0.9427	0.9544	0.347	0.2807	1601.25	1374.54	555.606	385.875
98149_s_at	1110033J19Rik	RIKEN cDNA 1110033J19 gene	5.5833	7.1667	4	0.636	0.8744	0.1806	0.0762	776.917	949.202	140.33	72.3075
101135_at	Calcr	calcitonin receptor	5.5833	6	5.1667	0.6751	0.8661	0.3033	0.2366	904.699	762.58	274.421	180.448
99076_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	5.6667	6	5.3333	0.9785	0.8967	0.2693	0.2323	1800.3	1958.78	484.821	454.954
160841_at	Dbp	D site albumin promoter binding protein	5.6667	5.8333	5.5	0.9562	0.9627	0.5694	0.5393	888.805	1108.16	506.057	597.663
94761_at	Ccl7	chemokine (C-C motif) ligand 7	5.8333	6.5	5.1667	0.434	0.7166	0.6635	0.9163	38.363	15.058	25.455	13.7982
98038_at	Hmgb3	high mobility group box 3	5.9167	6	5.8333	0.9508	0.9419	0.2383	0.2391	3842.36	3944.97	915.527	943.413
92310_at	Snk	serum-inducible kinase	6	6.6667	5.3333	0.8852	0.8473	0.2252	0.2016	1819.66	1973.58	409.817	397.829
103443_at	Aim1	absent in melanoma 1	6.4167	6.6667	6.1667	0.7159	0.7603	0.4362	0.4416	193.001	161.529	84.1874	71.3298
102140_at		ESTs	6.5	8.6667	4.3333	0.7122	0.6819	0.9379	0.6621	93.9683	91.3778	88.1342	60.5015
93619_at	Per1	period homolog 1 (Drosophila)	6.6667	6.5	6.8333	0.8663	0.8771	0.7072	0.6109	636.72	588.961	450.287	359.809
98055_at	Blcap	bladder cancer associated protein homolog (human)	6.75	6.6667	6.8333	0.7617	0.829	0.1602	0.1865	3050.72	2700.02	488.809	503.458
101889_s_at	Rora	RAR-related orphan receptor alpha	7.0833	7.8333	6.3333	0.9628	0.9145	0.3569	0.3215	3166.64	2481.59	1130.13	797.902
94076_i_at	Rpn2	ribophorin II	7.25	10.167	4.3333	0.5741	0.3982	0.1237	0.1194	1439.4	1319.13	178.049	157.446
93381_at	Avp	arginine vasopressin	7.5	7.8333	7.1667	0.9126	0.8702	0.5784	0.4585	4708.37	7059.9	2723.22	3237.24
99100_at	Stat3	signal transducer and activator of transcription 3	7.9167	7.5	8.3333	0.8226	0.8066	0.1839	0.1559	858.97	916.642	158.002	142.908

95057_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress	8	8.8333	7.1667	0.9557	0.8519	0.1762	0.1109	1772.58	1824.04	312.392	202.3
96041_at	Rbm3	RNA binding motif protein 3	8.3333	9.8333	6.8333	0.7736	0.8952	0.2006	0.2759	1879.64	1774.41	377.081	489.643
95679_at	D19Ertd144e	DNA segment, Chr 19, ERATO Doi 144, expressed	8.5833	6.8333	10.333	0.6094	0.8158	0.2207	0.0907	1080.42	1566	238.475	142.042
93694_at	Per2	period homolog 2 (Drosophila)	8.8333	9.1667	8.5	0.9185	0.9739	0.8009	0.5813	1126.29	984.335	902.038	572.191
94034_at	Smfn	small fragment nuclease	8.9167	10.167	7.6667	0.635	0.8519	0.3118	0.1666	537.134	663.38	167.492	110.502
96076_at	Stx5a	syntaxin 5A	9	7.8333	10.167	0.7969	0.6815	0.1287	0.1323	1225.21	1340.9	157.74	177.394
100566_at	lgfbp5	insulin-like growth factor binding protein 5	9.1667	8.8333	9.5	0.854	0.8498	0.1662	0.2144	9942.6	8277.22	1652.21	1774.89
104628_at	Man2a1	mannosidase 2, alpha 1	9.4167	9.1667	9.6667	0.8816	0.7669	0.3465	0.2308	424.826	432.973	147.181	99.9165
94420_f_at	Cry1	cryptochrome 1 (photolyase-like)	10.333	10	10.667	0.9078	0.7798	0.2039	0.1807	1818.16	1684.93	370.761	304.544
99815_at	Hrh2	histamine receptor H 2	10.5	10	11	0.802	0.8225	0.4479	0.0996	405.789	316.044	181.765	31.4905
101979_at	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	10.5	10.333	10.667	0.8784	0.8716	0.2761	0.3957	1029.1	1285.11	284.157	508.512
96114_at	Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1,	10.667	10.167	11.167	0.7052	0.8274	0.7533	0.7277	258.545	296.297	194.761	215.611
101975_at	Dlk1	delta-like 1 homolog (Drosophila)	11.083	11	11.167	0.7763	0.6354	0.1608	0.1629	8526.7	5333.06	1371.01	868.554
97890_at	Sgk	serum/glucocorticoid regulated kinase	11.333	11.5	11.167	0.8618	0.8521	0.4006	0.4551	1287.88	1329.8	515.978	605.17
102081_at	Rbig1	retinoblastoma inhibiting gene 1	11.833	11	12.667	0.7486	0.7901	0.3325	0.1873	246.37	273.123	81.9169	51.1645
96954_at	1810013H02Rik	RIKEN cDNA 1810013H02 gene	12.667	10.333	15	0.7041	0.7663	0.1871	0.1061	1887.93	1707.09	353.306	181.124
94821_at	Xbp1	X-box binding protein 1	12.75	12.167	13.333	0.8232	0.7174	0.2682	0.1794	3024.66	2442.68	811.364	438.232
94274_at	6720465F12Rik	RIKEN cDNA 6720465F12 gene	13.083	11.5	14.667	0.7601	0.8768	0.2862	0.1975	1173.44	1209.34	335.795	238.814
102110_at		EST, Weakly similar to RIKEN cDNA 5730493B19 [M	13.25	14.333	12.167	0.7873	0.7293	0.2739	0.1925	157.981	182.939	43.2701	35.2156
95704_at	Ap1b1	adaptor protein complex AP-1, beta 1 subunit	13.917	16.333	11.5	0.4013	0.8311	0.2764	0.2347	2441.24	2200.25	674.724	516.451
96254_at	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	14.25	14.5	14	0.8964	0.8464	0.2765	0.279	1328.21	1255.6	367.184	350.344
93875_at	Hspa1a	heat shock protein 1A	14.333	14.667	14	0.8221	0.8113	0.2447	0.2691	545.914	521.679	133.558	140.381
95749_at	Armet	arginine-rich, mutated in early stage tumors	14.417	12.167	16.667	0.5693	0.8367	0.1142	0.1881	1650.53	1530.02	188.445	287.786
103861_s_at	D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, ex	14.5	11.667	17.333	0.7039	0.7547	0.1787	0.2362	1000.39	891.822	178.769	210.666
104139_at	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pre	14.667	14.5	14.833	0.8126	0.795	0.1854	0.1604	578.053	601.539	107.157	96.4729
92487_at	Sox7	SRY-box containing gene 7	14.667	16.167	13.167	0.5767	0.8797	0.2593	0.2225	1028.01	971.588	266.558	216.21
100946_at	Hspa1b	heat shock protein 1B	14.75	15.167	14.333	0.8227	0.8044	0.5984	0.5965	360.977	334.982	216.01	199.821
94261_at	9330151F09Rik	RIKEN cDNA 9330151F09 gene	14.75	15.5	14	0.7584	0.7871	0.1437	0.1531	4430.54	3986.55	636.538	610.298
99032_at	Rasd1	RAS, dexamethasone-induced 1	15.167	15.333	15	0.9752	0.9295	0.5137	0.5525	3512.48	3509.02	1804.34	1938.71
92519_at	Phka1	phosphorylase kinase alpha 1	15.417	15.833	15	0.7045	0.8589	0.2422	0.1475	693.619	457.575	168.01	67.4925
102955_at	Nfil3	nuclear factor, interleukin 3, regulated	15.5	15.833	15.167	0.7739	0.824	0.4193	0.4158	218.927	212.104	91.7873	88.2008
101955_at	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)	15.833	16.333	15.333	0.7962	0.7646	0.1801	0.1131	7827.89	7432.99	1410.04	840.673
160330_at	Chordc1	cysteine and histidine-rich domain (CHORD)-containir	16	16.5	15.5	0.8252	0.9279	0.1883	0.1476	3132.48	3255.21	589.828	480.622
103012_at	Ccl21b	chemokine (C-C motif) ligand 21 (leucine)	16.167	11.333	21	0.7972	0.5563	0.2391	0.1793	165.797	161.663	39.6363	28.9911
102382_at	Arntl	aryl hydrocarbon receptor nuclear translocator-like	16.25	15.667	16.833	0.8469	0.8655	0.217	0.2219	1148.69	1217.16	249.279	270.049

104682_at	Tuba8	tubulin, alpha 8	16.25	15.667	16.833	0.8452	0.8879	0.2391	0.2715	1755.96	1419.33	419.775	385.287
96266_at	2610023M21Rik	RIKEN cDNA 2610023M21 gene	16.917	17.167	16.667	0.8528	0.7494	0.2185	0.1105	1991.37	2260.21	435.114	249.695
93277_at	Hspd1	heat shock protein 1 (chaperonin)	17.167	19	15.333	0.8439	0.9427	0.1245	0.0635	7224.71	6425.25	899.652	408.056
94359_at	AA960558	expressed sequence AA960558	17.25	17.667	16.833	0.7364	0.8132	0.0825	0.084	5164.34	4419.43	425.92	371.202
92532_at	Avpr1a	arginine vasopressin receptor 1A	17.333	18	16.667	0.9141	0.9212	0.2139	0.2748	1213.99	1268.54	259.668	348.649
161235_f_at	Bat4	HLA-B associated transcript 4	17.583	20.333	14.833	0.4713	0.6972	0.0853	0.0897	536.722	531.639	45.7566	47.6646
160182_at	Sfrs6	splicing factor, arginine/serine-rich 6	17.583	18.167	17	0.6689	0.8415	0.1891	0.1642	2025.58	2093.55	383.063	343.705
102292_at	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	17.667	16.833	18.5	0.8963	0.8992	0.2953	0.3518	1158.3	879.123	342.082	309.26
92611_at	Gpiap1	GPI-anchored membrane protein 1	17.667	17.667	17.667	0.7854	0.686	0.1779	0.1431	2462.17	2607.28	438.141	373.057
96474_at	Zfp161	zinc finger protein 161	17.75	15.167	20.333	0.8591	0.7826	0.3691	0.2732	189.174	151.299	69.815	41.3398
161189_r_at	Avpr1a	arginine vasopressin receptor 1A	17.75	17.5	18	0.9269	0.9052	0.3817	0.2831	171.064	155.529	65.2915	44.0322
96698_at	Psmd5	proteasome (prosome, macropain) 26S subunit, non-A	17.833	18.833	16.833	0.7978	0.692	0.156	0.1019	1747.84	2028.86	272.719	206.78
161666_f_at	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	17.917	19	16.833	0.7506	0.8522	0.8211	0.3724	103.32	207.131	84.8322	77.1443
102144_f_at			18	17.167	18.833	0.7369	0.7926	0.3197	0.1699	410.925	308.41	131.379	52.3896
98111_at	Hsp105	heat shock protein	18	18.667	17.333	0.8823	0.9169	0.1661	0.1335	8527.22	8070.83	1416.4	1077.64
93370_at		ESTs, Moderately similar to 2205282A B/K protein [Ra	18.333	18.833	17.833	0.9358	0.8065	0.3477	0.3261	1192.1	991.37	414.523	323.318
94207_at	P5-pending	protein disulfide isomerase-related protein	18.417	19	17.833	0.8174	0.8474	0.2244	0.1956	915.268	937.234	205.413	183.319
96216_at	C730042F17Rik	RIKEN cDNA C730042F17 gene	18.5	19.667	17.333	0.667	0.8378	0.2609	0.2871	530.525	450.812	138.428	129.423
94322_at	Sqle	squalene epoxidase	18.5	19.167	17.833	0.8955	0.7577	0.1021	0.1525	3272.15	3095.48	334.18	471.982
94285_at	H2-Eb1	histocompatibility 2, class II antigen E beta	18.667	14.5	22.833	0.7646	0.6302	0.6565	0.2303	381.082	326.386	250.178	75.1732
95913_at	C230056F04Rik	RIKEN cDNA C230056F04 gene	18.75	19	18.5	0.7623	0.8366	0.2425	0.2479	1979.15	1835.43	479.965	454.989
101381_at	Rab5ep-pending	rabaptin 5	19	17.833	20.167	0.8919	0.7934	0.1941	0.2098	461.985	395.422	89.658	82.9776
92767_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	19.083	16.667	21.5	0.7918	0.7966	0.2037	0.2441	119.706	117.734	24.3875	28.7346
102858_at	Pkib	protein kinase inhibitor beta, cAMP dependent, testis	19.167	19	19.333	0.9592	0.9311	0.2302	0.2193	1891.14	1579.15	435.261	346.344
104183_at	Trp53bp1	transformation related protein 53 binding protein 1	19.167	19.5	18.833	0.5959	0.8447	0.1882	0.0666	646.787	601.247	121.716	40.0627
93868_at	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	20	18.333	21.667	0.7755	0.8383	0.1693	0.1634	757.658	856.27	128.247	139.931
102302_at	Bckdhb	branched chain ketoacid dehydrogenase E1, beta poly	20	17	23	0.7796	0.7657	0.1294	0.1054	892.096	916.017	115.464	96.583
162095_f_at	Gas7	growth arrest specific 7	20.667	18.667	22.667	0.7831	0.7966	0.2832	0.1844	385.395	302.31	109.133	55.7485
160511_at	Cxcl12	chemokine (C-X-C motif) ligand 12	20.75	20.333	21.167	0.8719	0.8619	0.2952	0.1948	213.749	240.659	63.0907	46.8827
99185_at	2810443J12Rik	RIKEN cDNA 2810443J12 gene	21.333	21.167	21.5	0.8541	0.904	0.1841	0.1783	2312.39	2642.31	425.602	471.041
94872_at	Asml3a-pending	acid sphingomyelinase-like phosphodiesterase 3a	21.583	20.5	22.667	0.6809	0.7936	0.1467	0.1282	499.693	535.212	73.3264	68.5882
99575_at	Ubqln1	ubiquilin 1	22.083	3.5	16.667	0.3599	0.6672	0.1081	0.0749	6891.01	6761.4	744.965	506.396
93013_at	ldb2	inhibitor of DNA binding 2	22.417	22.167	22.667	0.7706	0.9057	0.2872	0.1932	3885.31	3128.73	1116.03	604.322
160179_at	2010200l23Rik	RIKEN cDNA 2010200I23 gene	22.583	1	20.167	0.8707	0.7383	0.1547	0.1245	2073.32	2004.26	320.828	249.512
162198_f_at	Ccl6	chemokine (C-C motif) ligand 6	23.583	19.667	3.5	0.6916	0.7031	0.5695	0.5761	97.81	59.1284	55.7048	34.0642

Α



Normalized expression level





			Molec	ular Peal	k Time	Corre	lation	Ampl	itude	Aver	age	Standard I	Deviation
Probe ID	Gene Symbol	Gene Name	Mean	LD	DD	LD	DD	LD	DD	LD	DD	LD	DD
144351_at	CG5273		2E-05	0.8333	23.167	0.6615	0.8616	0.138	0.096	9534.34	7055.32	1315.49	677.053
152457_at	CG3672		0.0834	23.667	0.5	0.8518	0.8139	0.3259	0.2381	6724.39	3908.26	2191.61	930.734
143162_at	flw	flap wing	0.1667	0.8333	23.5	0.8811	0.7782	0.1123	0.1434	12049.9	11650.7	1353.36	1670.46
152313_at	Cyp6a17		0.1667	23.5	0.8333	0.7323	0.7857	0.2658	0.2287	1936.07	1085.71	514.697	248.27
141685_at	CG3066		0.25	0.6667	23.833	0.8123	0.7868	0.2775	0.4042	1934.31	1821.83	536.756	736.336
155081_at	CG3767		0.25	23	1.5	0.7693	0.8178	0.3162	0.333	547.155	503.562	173.035	167.675
152688_at	CG11915		0.4167	1	23.833	0.7062	0.8757	0.2491	0.4932	1139.9	513.025	283.9	253.027
144146_at	Eaat1	Excitatory amino acid transporter 1	0.4167	18.667	6.1667	0.8637	0.397	0.2299	0.1974	5981.72	2682.64	1374.98	529.455
148109_at	CG12014		0.5	18.5	6.5	0.6725	0.7599	0.1585	0.2133	333.142	360.207	52.8067	76.8373
152966_at	CG7724		0.5834	1.5	23.667	0.6199	0.8741	0.1706	0.1982	1441.97	943.993	245.967	187.065
154936_at	CG9285		0.9167	1.6667	0.1667	0.9813	0.8613	0.2419	0.3104	2560.1	2134.15	619.228	662.545
142664_at	CG8889		1.1667	2.6667	23.667	0.9391	0.6513	0.179	0.1303	6401.44	6077.26	1145.65	792.13
142271_at	Ugt35b	UDP-glycosyltransferase 35b	1.3333	1.8333	0.8333	0.9252	0.9122	0.6698	0.4843	2852.21	3232.86	1910.41	1565.62
150085_at	CG14329		1.5	2	1	0.7725	0.7866	0.3932	0.3196	581.258	794.886	228.551	254.013
151795_at	CG7176		1.8333	1.5	2.1667	0.8692	0.6208	0.1463	0.1506	10824	8988.24	1583.8	1353.66
142367_at	CG9649		2	2.1667	1.8333	0.7906	0.9165	0.6145	0.558	680.85	381.894	418.361	213.115
143970_at	Clk	Clock	2	2.1667	1.8333	0.9659	0.8705	0.6185	0.4932	738.782	413.26	456.922	203.821
153433_at	Pdh	Photoreceptor dehydrogenase	2.0833	2.6667	1.5	0.8424	0.62	0.1452	0.1031	17272.5	33171.8	2507.54	3419.18
145570_at	CG5156		2.5833	2.6667	2.5	0.9023	0.8196	0.6159	0.4212	647.628	390.826	398.904	164.624
151899_at	CG11796		2.6667	4	1.3333	0.9584	0.8647	0.4829	0.4064	2596.49	3457.69	1253.87	1405.21
151927_at	CG4784		3.25	2.6667	3.8333	0.8	0.6213	0.4956	0.4071	7781.16	5008.74	3856.11	2038.84
153186_at	CG18578		3.3333	4.5	2.1667	0.8294	0.8217	0.3504	0.443	862.75	362.822	302.328	160.734
149882_at	CG9645		3.6667	4.5	2.8333	0.8441	0.8186	0.2773	0.1662	2278.89	2116.54	631.913	351.741
146526_at	CG10680		4	6.3333	1.6667	0.7222	0.7598	0.1483	0.1906	5287.87	3224.45	783.939	614.471
149053_at	CG9451		4.25	3.5	5	0.8198	0.7192	0.2817	0.4571	865.433	494.62	243.822	226.111
152083_at	CG15093		4.4167	3.3333	5.5	0.9001	0.8385	0.4437	0.2997	2593.64	1572.58	1150.81	471.364
150377_at	CG6926		4.4167	8.8333	0	0.5979	0.7474	0.4317	0.3593	363.261	205.905	156.808	73.9839
151003_at	Buffy	Buffy	4.75	9.6667	23.833	0.8136	0.4932	0.5929	0.5509	296.223	185.131	175.619	101.989
152673_at	cry	cryptochrome	5.1667	5.3333	5	0.9759	0.8148	0.5005	0.2922	2424.38	2639.58	1213.51	771.399
153364_at	CG9232		5.4167	3.8333	7	0.7678	0.6634	0.1509	0.379	4249.53	2303.53	641.167	873.138
151800_at	CG4847		5.5833	6	5.1667	0.9318	0.7497	0.2334	0.1562	7989.93	5351.08	1865.22	836.031
150106_at	Rim		6	7.6667	4.3333	0.7883	0.6468	0.2595	0.26	916.053	1258	237.758	327.047
154916 at	CG7417		6.75	8.5	5	0.7817	0.7702	0.175	0.1798	1822.14	1301.99	318.952	234.146

143854_at	Drip	Drip	6.9167	9.3333	4.5	0.8937	0.6644	0.4382	0.3786	353.248	295.142	154.805	111.743
152569_at	CG18003		7.5	6.5	8.5	0.7606	0.6266	0.4657	0.2537	1693.14	1539.02	788.451	390.399
148825_at	CG6151		7.5833	8.3333	6.8333	0.8339	0.4719	0.3556	0.3286	552.12	358.684	196.33	117.86
149305_at	CG1124		7.5833	7.6667	7.5	0.8358	0.7801	0.1702	0.1634	8670.95	6157.4	1475.61	1005.83
152334_at	Трі	Triose phosphate isomerase	8.8333	9.8333	7.8333	0.7461	0.7697	0.1196	0.1488	6613.94	4307.42	791.11	640.828
144241_at	CG11902		9.3334	10.667	8	0.7843	0.5165	0.1455	0.2184	570.544	552.082	83.0391	120.583
147785_at	CG13559		9.4167	9.8333	9	0.7102	0.4961	0.226	0.2388	481.599	386.305	108.846	92.2585
154763_at	CG5165		9.8333	9.3333	10.333	0.6358	0.4982	0.1492	0.167	4474.41	4559.12	667.469	761.363
154176_at	CG2827		10.083	9.5	10.667	0.8253	0.7142	0.2919	0.2361	7751.63	3743.58	2262.87	883.974
153373_at	CG8036		10.25	8.6667	11.833	0.7975	0.7861	0.1462	0.2027	14020.7	15283.7	2049.62	3097.57
152482_at	CG11594		10.333	9.3333	11.333	0.785	0.7639	0.268	0.2456	2209.28	1525.14	592.028	374.639
154852_at	CG10639		10.5	11.333	9.6667	0.6442	0.6386	0.0886	0.1236	1444.07	933.853	127.951	115.449
153236_at	Fdh	Formaldehyde dehydrogenase	10.583	9.6667	11.5	0.8908	0.807	0.195	0.1325	2659.27	2622.75	518.482	347.579
145956_at	CG5958		10.833	10.333	11.333	0.8324	0.7573	0.2186	0.3268	2031.23	1660.83	444.122	542.783
148009_at	CG13936		11	9.6667	12.333	0.856	0.7422	0.5795	0.3312	261.364	430.392	151.463	142.535
152608_at	CG7054		11	11.167	10.833	0.7572	0.6431	0.2913	0.2604	274.593	245.435	80.0012	63.9027
143015_at	XNP		11.167	9.6667	12.667	0.8137	0.7201	0.1556	0.1487	1027.54	909.133	159.876	135.19
141732_at	puc	puckered	11.333	12.333	10.333	0.884	0.722	0.4598	0.3146	1269.06	887.033	583.476	279.041
141450_at	Sodh-1	Sorbitol dehydrogenase 1	11.833	10.333	13.333	0.89	0.8523	0.405	0.328	2358.77	2640.38	955.338	866.122
151760_at			11.833	13.333	10.333	0.8317	0.6705	0.4351	0.2742	825.454	550.202	359.164	150.843
152256_at	CG2121		11.917	12	11.833	0.8273	0.8082	0.6935	0.5659	676.33	271.14	469.002	153.429
149914_at	smp-30	Senescence marker protein-30	11.917	10.167	13.667	0.8442	0.702	0.3673	0.2029	1338.55	1178.48	491.613	239.167
151897_at	CG4919		12.167	11.333	13	0.8948	0.5813	0.3609	0.2716	3313.2	1429.23	1195.79	388.168
141593_at	CG5798		12.25	12.333	12.167	0.9297	0.7982	0.7396	0.7592	3033.57	1668.75	2243.58	1266.98
147488_at	CG18607		12.667	8.1667	17.167	0.6731	0.7314	0.382	0.3345	290.987	227.446	111.159	76.0788
143869_at	vri	vrille	13	13.5	12.5	0.959	0.8818	0.7934	0.6207	4154.15	2400.61	3295.74	1489.95
153278_at	Cct5	T-complex Chaperonin 5	13	9.5	16.5	0.7063	0.6609	0.1545	0.2022	3976.01	2585.76	614.459	522.915
146468_at	CG15171		13.25	14.5	12	0.8719	0.7877	0.3182	0.5104	536.995	430.337	170.878	219.645
151642_at			13.25	13	13.5	0.9564	0.7344	0.3634	0.2483	1721.81	1083.6	625.701	269.046
152682_at	Slob	Slowpoke binding protein	13.417	14.5	12.333	0.9156	0.9069	0.3598	0.4104	5157.67	5275.92	1855.88	2165.46
146022_at	CG14275		13.5	13.833	13.167	0.8987	0.8658	0.3382	0.3716	2118.71	1768.88	716.62	657.349
143300_at	per	period	13.5	13.5	13.5	0.9199	0.8633	0.648	0.561	576.997	399.574	373.884	224.179
151933_at	BcDNA:GH03693		13.917	17.833	10	0.8596	0.4968	0.3965	0.3042	1245.47	848.856	493.822	258.254
153055_at	Pdp1	PAR-domain protein 1	14	14	14	0.9371	0.7274	0.2883	0.2203	1288.32	721.945	371.409	159.062
153809_at	prod	proliferation disrupter	14.25	15.833	12.667	0.7995	0.7286	0.3463	0.7317	137.676	85.7142	47.674	62.715

144167_at	EG:22E5.12		14.25	12.667	15.833	0.5491	0.7095	0.3728	0.6272	221.45	128.72	82.5562	80.739
142154_at	tim	timeless	15	14.833	15.167	0.9931	0.9305	0.8009	0.6969	3577.89	1470.18	2865.42	1024.51
150831_at	Obp99a	Odorant-binding protein 99a	15.25	14.833	15.667	0.7907	0.7807	0.6256	0.6165	10213	6705.57	6388.83	4133.91
142169_at	CG4468		16.25	17.667	14.833	0.5996	0.7826	0.2108	0.2107	7854.86	5705.07	1655.58	1202.24
143606_at	Cyp18a1	Cytochrome P450-18a1	16.583	17.667	15.5	0.9441	0.7897	0.4848	0.4123	1083.49	312.637	525.273	128.902
152192_at	Cnx99A	Calnexin 99A	16.833	17.667	16	0.7714	0.7759	0.1766	0.2808	6740.86	5154.52	1190.59	1447.24
141658_at	CG5853		17.5	16.167	18.833	0.9174	0.9371	0.5054	0.3916	1249.66	797.864	631.604	312.45
154495_at	CG6459		17.5	17.167	17.833	0.8512	0.5666	0.2491	0.09	3589.15	2038.09	894.085	183.417
152596_at	CG9507		17.75	18.333	17.167	0.9295	0.684	0.382	0.2808	808.847	852.622	308.94	239.452
141342_at	CG6145		17.75	16.833	18.667	0.7617	0.8226	0.3334	0.179	3784.93	1522.58	1261.88	272.591
152727_at	CG7224		17.917	18.833	17	0.906	0.6975	0.5187	0.15	4700.7	2774.25	2438.16	416.207
150450_at	CG10175		18.25	17.5	19	0.7968	0.9059	0.3696	0.5983	557.649	287.108	206.13	171.769
141762_at	Cp1	Cysteine proteinase-1	18.333	17.5	19.167	0.562	0.8849	0.1824	0.2106	13662.6	11542.1	2492.45	2430.9
152455_at	CG7470		18.5	16.667	20.333	0.7848	0.7604	0.1702	0.1444	8289.5	7134.84	1410.96	1030.3
151736_at			18.583	18.167	19	0.8485	0.7546	0.276	0.1367	15844.6	9786.24	4372.71	1338.23
146138_at	CG5390		19.083	18.5	19.667	0.7112	0.7791	0.2085	0.1567	4826.76	3470.05	1006.39	543.682
141360_at	CG9701		19.167	21.5	16.833	0.7796	0.7781	0.3131	0.3287	739.352	554.406	231.455	182.26
152086_at	CG6409		19.333	19.5	19.167	0.6212	0.5718	0.4429	0.3604	6873.28	3341.67	3044.3	1204.18
154554_at	CG6815		19.417	18.333	20.5	0.7644	0.5555	0.3485	0.2061	797.271	363.958	277.877	75.0002
153002_at	Timp	Tissue inhibitor of metalloproteases	19.417	19.167	19.667	0.6924	0.7409	0.1681	0.2037	4211.17	2268.21	707.836	462.101
151849_at	Uch	Ubiquitin carboxy-terminal hydrolase	19.583	14.833	0.3333	0.7531	0.4357	0.2162	0.2845	1152.18	382.281	249.108	108.77
150586_at	CG10553		19.583	19.667	19.5	0.9413	0.8997	0.5033	0.4494	1101.24	502.306	554.25	225.749
146532_at	CG10746		19.833	19.167	20.5	0.7732	0.7589	0.2407	0.1416	5203.39	2891.82	1252.62	409.571
141260_at	CG4572		19.917	17.333	22.5	0.7967	0.8059	0.3567	0.0991	1996.7	1243.2	712.201	123.255
141414_at	CG9886		20	19.833	20.167	0.7479	0.6864	0.3067	0.2343	1457.99	900.537	447.126	210.971
151859_at	CG15668		20	18.5	21.5	0.6211	0.7515	0.117	0.1702	2630.92	812.598	307.813	138.293
151475_at	CG12397		20.083	18.833	21.333	0.8941	0.5943	0.2242	0.2289	1777.27	1501.34	398.499	343.665
151885_at	BcDNA:GH02901		20.167	20.833	19.5	0.7888	0.8064	0.3178	0.2357	2313.99	1087.19	735.454	256.269
148295_at	CG9953		20.167	19.167	21.167	0.7788	0.6794	0.1464	0.2121	4561.38	3979.81	667.68	844.048
147139_at	CG10799		21	19.833	22.167	0.7389	0.7426	0.2951	0.2301	1480.49	675.958	436.871	155.555
143164_at	Fps85D	Fps oncogene analog	21.083	17.167	1	0.8797	0.5512	0.1672	0.0998	1392.8	972.556	232.861	97.086
144963_at	CG15723		21.25	21.5	21	0.9426	0.8297	0.3129	0.3001	5943.21	7129.64	1859.78	2139.32
151371_at	CG17777		21.333	21.167	21.5	0.9696	0.9472	0.8319	0.4618	1920.36	2046.08	1597.57	944.975
141455_at	CG9328		21.417	22	20.833	0.8963	0.8745	0.3228	0.3042	766.097	786.094	247.296	239.164
142987_at	msta		21.583	22.333	20.833	0.8952	0.8179	0.207	0.0814	8372.18	12070.4	1732.74	983.071

150574_at	CG11891		21.667	22.167	21.167	0.8199	0.898	0.8066	0.5512	1226.93	783.717	989.592	431.976
151681_at	CG12790		22	21.833	22.167	0.7699	0.8768	0.2124	0.1867	4519.76	3931.82	960.125	734.178
152521_at	CG1441		22	22.167	21.833	0.8041	0.9382	0.3367	0.3501	2061.79	1474.93	694.299	516.342
147662_at	CG11275		22.417	21.667	23.167	0.8771	0.8039	0.46	0.2567	1320.1	1328.9	607.262	341.098
151458_at	CG14403		22.583	22.833	22.333	0.909	0.7698	0.2915	0.2282	1479.23	1544.36	431.207	352.468
142736_s_at	CG16796		22.583	20.667	0.5	0.9611	0.7275	0.2434	0.2671	3031.85	1699.54	737.86	453.944
144170_at	CSN3	COP9 complex homolog subunit 3	22.75	18	3.5	0.7951	0.7857	0.1218	0.1796	881.079	472.019	107.286	84.776
141437_at	CG5618		22.917	22	23.833	0.7822	0.8793	0.3251	0.2988	2640.72	1676.78	858.551	501.068
152019_at	to	takeout	23.417	23.5	23.333	0.8522	0.9202	0.4575	0.5373	1445.96	1016.3	661.587	546.039
146323_at	CG5945		23.917	1	22.833	0.7801	0.7541	0.2234	0.3289	9249.4	4129.76	2065.91	1358.28
144842_at	CG1552		24	23.333	0.6667	0.86	0.7837	0.5634	0.1992	880.38	1746.6	495.98	347.859
152310_at	CG13848		24	0.1667	23.833	0.8954	0.8308	0.2951	0.2413	908.608	894.139	268.145	215.741



Normalized expression level

Α

Β



Β

С



Α



Normalized expression level