

Separating the Contribution of Glucocorticoids and Wakefulness to the Molecular and Electrophysiological Correlates of Sleep Homeostasis

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Study Objectives: The sleep-deprivation–induced changes in delta power, an electroencephalographical correlate of sleep need, and brain transcriptome profiles have importantly contributed to current hypotheses on sleep function. Because sleep deprivation also induces stress, we here determined the contribution of the corticosterone component of the stress response to the electrophysiological and molecular markers of sleep need in mice.

Design: N/A

Settings: Mouse sleep facility.

Participants: C57BL/6J, AKR/J, DBA/2J mice.

Interventions: Sleep deprivation, adrenalectomy (ADX).

Measurements and Results: Sleep deprivation elevated corticosterone levels in 3 inbred strains, but this increase was larger in DBA/2J mice; i.e., the strain for which the rebound in delta power after sleep deprivation failed to reach significance. Elimination of the sleep-deprivation–associated corticosterone surge through ADX in DBA/2J mice did not, however, rescue the delta power rebound but did greatly reduce the number of transcripts affected by sleep deprivation. Genes no longer affected by sleep deprivation cover pathways previously implicated in sleep homeostasis, such as lipid, cholesterol (e.g., *Ldlr*, *Hmgcs1*, *Dhcr7*, *-24*, *Fkbp5*), energy and carbohydrate metabolism (e.g., *Eno3*, *G6pc3*, *Mpdu1*, *Ugdh*, *Man1b1*), protein biosynthesis (e.g., *Sgk1*, *Alad*, *Fads3*, *Eif2c2*, *-3*, *Mat2a*), and some circadian genes (*Per1*, *-3*), whereas others, such as *Homer1a*, remained unchanged. Moreover, several microRNAs were affected both by sleep deprivation and ADX.

Conclusions: Our findings indicate that corticosterone contributes to the sleep-deprivation–induced changes in brain transcriptome that have been attributed to wakefulness *per se*. The study identified 78 transcripts that respond to sleep loss independent of corticosterone and time of day, among which genes involved in neuroprotection prominently feature, pointing to a molecular pathway directly relevant for sleep function.

Keywords: Sleep regulation, corticosterone, neuroprotection, microarray, microRNA

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A NEED OR PRESSURE FOR SLEEP ACCUMULATES WHILE AWAKE BUT, BECAUSE THE NEUROPHYSIOLOGICAL FUNCTION OF SLEEP REMAINS ELUSIVE, sleep need is not easily defined or objectively measured. Sleep research has profited much from the use of the electroencephalogram (EEG)-derived variable delta power, as illustrated by its central role in theories concerning sleep function (e.g.¹). Delta power, a measure that quantifies the delta oscillations (1-4 Hz) that are characteristic of the non rapid-eye-movement (NREM) sleep EEG, is widely used to index sleep need in mammals.^{2,3} Using this sleep homeostatic index in a panel of 6 inbred strains of mice, we observed that the rate at which sleep need accumulates during wakefulness varies greatly according to genetic background. Specifically, within this panel of 6, the sleep deprivation-induced increase in delta power is smallest in DBA/2J (D2) and largest in AKR/J (AK) mice.³ Subsequent studies in humans confirmed the importance of genetic factors in sleep homeostasis.⁴ To gain insight into the genetic pathways under-

lying the homeostatic regulation of sleep, we and others have searched for molecular correlates of sleep need using microarrays and extensive changes in brain gene expression after sleep deprivation have been reported in both mice and rats.⁵ Also, these gene-profiling studies have contributed to current hypotheses on sleep function.⁵

Sleep deprivation-induced brain gene-expression profiles have been found to differ with genetic background as well, and one transcript, *Homer1a*, is considered to be of particular relevance because the sleep-deprivation–induced expression was smaller in D2 mice, compared with AK mice,⁴ thus matching the strain differences observed in delta power after sleep deprivation, as discussed above. Moreover, mapping of the delta-power phenotype in recombinant offspring derived from D2 and C57BL/6J (B6) mice yielded a quantitative trait locus centered around *Homer1*,^{3,6} suggesting a causal implication of *Homer1* in the homeostatic regulation of delta power. Other transcripts implicated in sleep homeostasis, such as clock genes,⁷ also vary according to genetic background (i.e., we observed large strain differences in the rate at which the expression of the *Period1* (*Per1*) and *-2* genes increased in the forebrain over the course of sleep deprivation).⁸

An unavoidable confound in sleep-deprivation studies is that, besides activating sleep homeostatic processes, sleep deprivation also activates the hypothalamic-pituitary-adrenal (HPA) axis, as evidenced by the surge in circulating levels of glucocorticoids; i.e., corticosterone in rodents^{9,10} and cortisol

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in humans.¹¹ Accordingly, stress and differences in stress susceptibility could contribute to the reported strain differences on the effects of sleep deprivation on both delta power and brain gene expression. For some types of stress, a relationship with delta power has been demonstrated, although the directions of change are not consistent. For example, mice selected for high stress susceptibility have been found to show lower delta power,¹² whereas social-defeat stress increases delta power in the rat.¹³ Similarly, in humans, a negative correlation has been reported between rates of endogenous cortisol secretion and delta power,¹⁴ whereas the administration of the stress hormone cortisol has been found to increase delta power.¹⁵ The stress-related surge in plasma corticosterone, which affects the expression of many genes in the brain,¹⁶ including the expression and protein levels of some clock genes,^{17,18} has never been directly controlled for in studies that have investigated the molecular correlates of sleep homeostasis.

The present study aimed at determining the contribution of the corticosterone component of the stress response to the sleep-wake associated changes in the electrophysiological and molecular correlates of sleep need. We first compared the changes in corticosterone plasma levels after sleep deprivation in the two mouse strains that differed for the increase in delta power after sleep deprivation (i.e., D2 and AK), and in B6 mice, a strain with an intermediate response to sleep deprivation.³ We observed that genotype greatly affected the increase in corticosterone, with D2 mice showing the highest response, suggesting that the reduced increase in EEG delta power after sleep deprivation observed in this strain might be a consequence of a higher stress susceptibility. However, in a second experiment, we found that removing the sleep deprivation-dependent corticosterone increase through adrenalectomy (ADX) did not 'rescue' the blunted delta-power response to sleep deprivation in D2 mice. Conversely, in a last experiment of similar design, inactivating the corticosterone component of the HPA axis profoundly diminished the brain transcriptome response to enforced wakefulness.

METHODS

Animals and Surgery

Adult male mice from 3 inbred strains were used in this study: C57BL/6J (B6), AKR/J (AK), and DBA/2J (D2). Mice were purchased from Jackson Laboratory and maintained under standard animal housing conditions, with free access to food and water, and a 12-hour light/12-hour dark cycle. Age was 12 weeks at the time of the experiment. For the first experiment, 10 B6, 8 AK, and 9 D2 mice were used to assess the corticosterone increase after sleep deprivation ending at ZT6 (Zeitgeber time 6; i.e., 6 h after light onset), and 11 B6, 9 AK, and 9 D2 were used as non-sleep-deprived control animals. Also, 6 B6, 8 AK, and 6 D2 mice were sacrificed at ZT18 to measure basal corticosterone levels after the main active period. For the sleep recording experiment, 16 D2 animals were used (control: $n = 16$; sham-lesioned: $n = 9$; ADX: $n = 7$). For the gene-expression experiment, D2 mice ($n = 26$: control, $n = 7$ and 6; sleep deprivation, $n = 7$ and 6 in sham-lesioned and ADX, respectively) were raised on site, and animals between 8 and 12 weeks were used. Bilateral ADX or sham lesions were performed under

deep anesthesia (pentobarbital sodium 65–75 mg/kg or ketamine/xylazine 75 and 10 mg/kg, respectively, intraperitoneal injection). Animals were allowed to recover for a week while supplemented with either saline (gene expression experiment) or corticosterone (sleep and EEG experiment; Sigma, St. Louis, MO; 25 $\mu\text{g/mL}$ in 0.2% ethanol–0.5% NaCl) in drinking water. Mice supplemented with saline were adapted to this before surgery.

Electrode implantation for EEG and electromyography (EMG) recordings was performed as detailed previously.¹⁹ Briefly, surgery was carried out under deep pentobarbital sodium anesthesia (65–75 mg/kg, intraperitoneal injection). Two gold-plated screws (diameter 1.1 mm) served as EEG electrodes and were screwed through the skull over the right cerebral hemisphere (frontal: 1.7 mm lateral to midline, 1.5 mm anterior to bregma; parietal: 1.7 mm lateral to midline, 1.0 mm anterior to lambda). Two other screws were implanted at the same coordinates over the left hemisphere as anchor screws. Two gold wires served as electromyography electrodes and were inserted between 2 neck muscles. The EEG and EMG electrodes were soldered to a connector and, together with the anchor screws, were cemented to the skull. Recording leads were connected to a swivel contact, and animals were allowed 10 to 14 days of recovery from surgery and habituation before the experiment.

Corticosterone Measurements

For corticosterone and gene-expression measurements, mice were rapidly killed by cervical dislocation immediately at the end of the sleep deprivation (ZT6) together with their non-sleep-deprived controls. The brain and blood plasma were rapidly collected, frozen on dry ice, and stored at -80°C . The measurements of corticosterone levels of animals undergoing sleep recordings were achieved by radioimmunoassay.⁹ Briefly, triplicate samples of plasma (10 μL) were heat denatured at 80°C . [^3H] corticosterone (Sigma) and corticosterone antiserum (Endocrine Sciences, Agoura Hills, CA) were added to the samples that were incubated overnight. [^3H] corticosterone was separated from nonradiolabeled corticosterone using Dextran T70 (Amersham Pharmacia Biotech AB, Uppsala, Sweden) coated charcoal, and quantified in a liquid scintillation counter (Beckman model LS 3801, Brea, CA). Competition binding was assessed against a standard curve of corticosterone (Sigma) ranging from 0.001 to 5 ng/mL and analyzed using a nonlinear least-squares formula and best-fit analysis based on the F distribution. The quantification of corticosterone levels of animals involved in gene-expression assays was performed according to manufacturer instructions using an enzyme immunoassay commercial kit (Assay Designs, Ann Arbor, MI).

EEG Recordings and Analysis

All mice were recorded continuously for 48 hours, of which the first 24 hours served as baseline, followed by 6 hours of sleep deprivation, initiated at ZT0, and 18 hours of recovery sleep. Sleep deprivation was achieved by gentle handling.¹⁹ All mice were submitted to the same sleep recording protocol twice; i.e., before and after undergoing ADX or sham lesion. The EEG and EMG signals were amplified, filtered and analog-to-digital converted. Behavioral states (wakefulness, NREM sleep and rapid eye movement (REM) sleep) were visually as-

signed to 4-second epochs, as previously described.¹⁹ The EEG signal of artifact-free epochs was subjected to spectral analysis using discrete Fourier transform to calculate the EEG power density in the delta frequency range (1–4 Hz; i.e., delta power) during NREM sleep. Interindividual differences in the absolute level of delta power were accounted for by expressing delta power as a percentage of the mean delta power in NREM sleep during the last 4 hours of the baseline light period. Delta power was averaged for 8 intervals, to which an equal number NREM sleep epochs contribute (i.e., percentiles) both during the baseline light period and during the 6 hours immediately following sleep deprivation (recovery).

Quantitative PCR

RNA was isolated from forebrain (hindbrain excised) using the RNeasy Lipid Tissue Midi kit and was Dnase-treated (QIAGEN, Hombrechtikon, Switzerland). All RNA sample amounts were measured with a NanoDrop ND-1000 spectrophotometer (Thermo Scientific, Wilmington, DE), and the quality of RNA samples was verified on Agilent 2100 bioanalyzer chips (Agilent Technologies, Basel, Switzerland). For each sample, reverse transcription was performed on 0.5 µg of RNA. First, RNA, 0.25 µg random hexamers, and 10µM dNTP mix was incubated for 5 minutes at 65°C for the denaturation step. Then, first-strand buffer, 0.1 M DTT, RNazin Plus Rnase inhibitor, and SuperScript II reverse transcriptase (Invitrogen, Basel, Switzerland) were added to the denaturation mix and incubated for 10 minutes at 25°C followed by 60 minutes at 42°C.

Quantitative polymerase chain reaction (qPCR) was performed according to Applied Biosystems protocol using a real-time cycler ABI Prism 7700 (Applied Biosystems, Foster City, CA). Briefly, approximately 14 ng of cDNA was used in 10 µL for qPCR with Master Mix reagent (Applied Biosystems) under the following cycling conditions: 95°C for 10 minutes, followed by 40 cycles of 95°C for 15 seconds, and 60°C for 1 minute. The assays, designed at exon-exon junctions, were performed with oligos (sequences provided in Supplementary Table 6 [Supplementary tables and figures are available online only at www.journalsleep.org]). Primers were purchased from Invitrogen or Microsynth (Balgach, Switzerland) and probes from Eurogentec SA (Seraing, Belgium). Each PCR reaction was done in triplicate. *Tbp*, *GusB*, and *Rps9* were used as endogenous controls after selection of the most stable control genes using geNorm v3.5 program and relative quantification of mRNA levels was evaluated using the modified $\Delta\Delta C_t$ method from qBase v1.3.5 program, as performed previously.⁶

Statistical Analysis

To assess the differential effects of sleep deprivation on corticosterone secretion in inbred mouse strains, a 2-way analysis of variance (ANOVA) with factors Strain (B6, AK, D2) and Condition (sleep deprivation vs control) was performed. To evaluate the effects of time on corticosterone secretion, a 2-way ANOVA was used with Strain and Time (ZT6 vs ZT18) as factors. The effect of ADX on accumulated difference in NREM sleep time after sleep deprivation was assessed at each time point using 1-way ANOVA with factor Group (control, sham, ADX). The effect of ADX on delta power was tested using a repeated-measures ANOVA with factors Group (sham vs ADX),

Condition (control vs sleep deprivation), and Interval (1 to 8). Lastly, the effect of ADX on sleep-deprivation-induced forebrain gene expression was assessed using 2-way ANOVA with factors Group (sham vs ADX) and Condition (control vs sleep deprivation). Significant interactions were decomposed using posthoc *t* tests, Tukey HSD test, or simple effect analysis (contrasts). Statistical analyses were done using SAS (SAS Institute Inc, Cary, NC) or Statistica (Statsoft Inc, Tulsa, OK). Statistical significance was set to $P = 0.05$, and results are reported as mean \pm SEM.

Microarray

RNA samples isolated from forebrain were diluted to 300 ng/3µL and independently used to perform the target preparation using the whole transcript sense target labeling protocol procedure (Affymetrix, High Wycombe, UK). Then, 5.5 µg of each fragmented cDNA was end labeled with biotin and hybridized to a GeneChip Mouse Gene 1.0 ST array (Affymetrix), processed, and scanned according to standard procedures. Normalized expression signals were calculated from Affymetrix CEL files using RMA normalization method implemented in the Affymetrix Expression Console software, as in our previous publication.⁶ RMA processing was performed separately for each animal. All subsequent statistical analyses were performed using R (R Core, 2004, <http://www.R-project.org>) and Bioconductor packages (<http://www.Bioconductor.org>). Control and unannotated probe sets were removed, leaving 28,198 probe sets for statistical analysis. Differential hybridized features were identified using Bioconductor package “limma”, as before.⁶ *P* values were adjusted for multiple testing with the Benjamini and Hochberg method to control the false discovery rate (FDR).²⁰ We fitted a model with a coefficient for each of the 4 factor combinations (Sham-control, Sham-sleep deprivation, ADX-control, ADX-sleep deprivation) and then extracted the comparisons of interest as contrasts. Functional enrichment analysis was performed using Ingenuity Pathway Analysis Tool (Ingenuity Systems, Inc., Redwood City, CA). MicroRNA (miRNA) targets enrichment analysis was performed using Miranda Mus musculus putative targets (microrna.sanger.ac.uk/cgi-bin/targets/v5/download.pl). Enrichment of putative targets of *mmu-miR-29c*, *-410*, *-212*, *-151-3p* and *-151-5p* were tested separately among genes upregulated or downregulated by sleep deprivation (FDR < 0.05) using Fisher exact test.

RESULTS

Genotype Influences the Sleep Deprivation-Induced Corticosterone Surge

To evaluate the effect of genetic background on the corticosterone surge associated with sleep deprivation, corticosterone levels were measured in 3 inbred mouse strains (i.e., B6, D2, and AK). Consistent with previous work,^{9,10} a 6-hour sleep deprivation increased corticosterone levels in all 3 strains compared with baseline levels (Figure 1A). Across genotypes, significant differences in the corticosterone response to sleep deprivation were noted, and the relative increase was 2- to 3-fold larger for D2 mice compared with B6 and AK mice (Figure 1B). The strain differences in plasma corticosterone levels were specific to the enforced wakefulness because concentra-

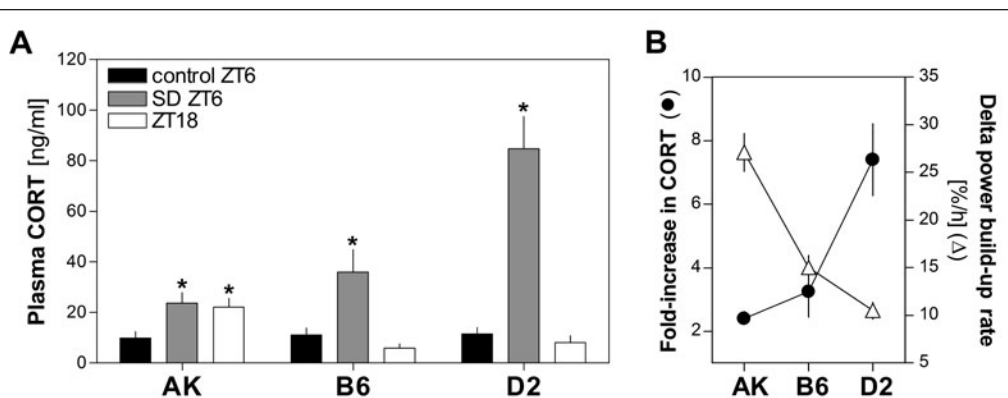


Figure 1—Corticosterone (CORT) secretion induced by sleep deprivation (SD) in inbred mice. (A) CORT was measured at ZT6 in control condition, at ZT6 after 6 h of SD, and at ZT18 after an extended period of spontaneous wakefulness in AK, B6, and D2 mice. SD induced an increase in CORT secretion in all 3 strains (sleep deprivation effect: $F_{1,50} = 45.2$, $P < 0.0001$), but this increase depended on strain (Interaction: $F_{2,50} = 10.5$, $P < 0.001$), with a larger increase in CORT in D2 mice ($P < 0.01$). At ZT18, CORT in AK was higher than in other strains (Interaction: $F_{2,43} = 5.6$, $P < 0.01$; t test $P < 0.02$). Asterisks indicate significant difference ($P < 0.05$) from the control ZT6 condition. (B) Fold increases in CORT secretion after sleep deprivation (black circles, left y axis) and the rate of increase of delta power as a function of time spent awake (triangles, right y axis; taken from Franken et al.³) in the 3 strains. D2 mice show the largest increase in CORT after sleep deprivation but the lowest increase in delta power.

tions in the non-sleep-deprivation control groups sampled at the same time of day (ZT6; i.e., 6 hours after light onset) did not differ. Also, sustained periods of spontaneous wakefulness, in the mouse strains used here occurring between ZT12 and ZT18,¹⁹ did not increase corticosterone levels in D2 and B6 mice (Figure 1A). Interestingly, in AK mice, which responded the least to sleep deprivation in terms of increased corticosterone levels, similar concentrations were reached after a spontaneous sustained period of wakefulness (i.e., at ZT18 in baseline) compared with after sleep deprivation (Figure 1A).

HPA activity is known to vary with genetic background,¹² and, consistent with our findings, D2 mice were reported to be more susceptible to various other stressors, compared with B6 mice.^{21,22} Our data thus confirm that, in mice, sleep deprivation activates the HPA axis and that genetic factors importantly modulate this effect. The strain differences in the fold increase in corticosterone secretion after sleep deprivation appeared inversely proportional to the rate of increase of the homeostatic sleep pressure reflected by the dynamics of delta power (Figure 1B).³ Indeed, D2 mice showed the lowest delta power rebound and the highest corticosterone surge with sleep deprivation, whereas AK mice showed the reverse and B6 mice had intermediate phenotypes. This raises the possibility that the strain differences in the corticosterone response might have contributed to the strain differences in the expression of delta power during recovery sleep.

Adrenalectomy Does Not Influence the Delta-Power Response to Sleep Deprivation

To determine whether the higher corticosterone increase following sleep deprivation in D2 mice contributed to their blunted delta power rebound, we performed ADX with corticosterone replacement. We contrasted the effects of sleep deprivation on delta power in this group with the sleep-deprivation effects before the surgery in the same mice and to the sleep-deprivation effects in a group of sham-lesioned mice recorded in parallel.

Also in this cohort of D2 mice, the sleep-deprivation-induced rebound in delta power was low compared with previously published data for other strains,¹⁹ and the levels reached in both intact controls and the sham-lesioned mice ($171\% \pm 6\%$ and $183\% \pm 10\%$, respectively; Figure 2A) were well within the range of values previously reported for this strain ($179\% \pm 14\%$).¹⁹ Although ADX successfully abolished the sleep-deprivation-induced increase in corticosterone secretion (Figure 2B), ADX affected neither the baseline dynamics of delta power nor the increase in delta power after sleep deprivation ($178\% \pm 10\%$; Figure 2A). Not only delta power during NREM sleep, but also baseline amount and distribution of total sleep time

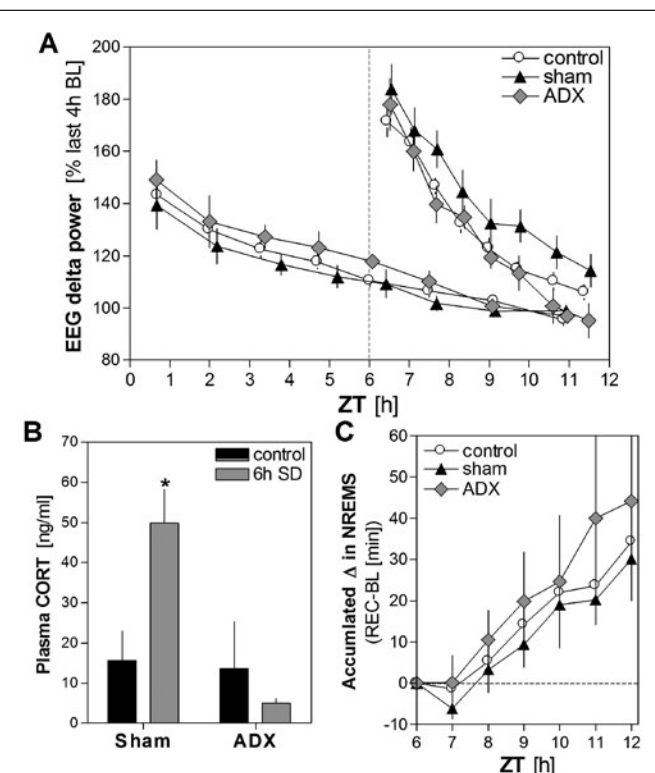


Figure 2—Effects of adrenalectomy (ADX) on recovery from sleep deprivation (SD). (A) Delta power time course during the light period of baseline (ZT0-ZT12) or after 6 hours of SD (ZT6-ZT12) in control, sham-lesioned, and ADX mice. Delta power changes during baseline and recovery did not differ among experimental groups (Interaction: $F_{14,464} = 0.2$, $P > 0.99$). (B) Corticosterone (CORT) secretion was assessed at ZT6 in control condition or after 6 hours of SD in D2 mice having received sham-lesion or ADX. ADX abolished the SD-dependent increase in CORT secretion (Interaction: $F_{1,20} = 5.7$, $P < 0.05$). (C) Accumulated differences in non-rapid eye movement sleep (NREMS) time between baseline (BL) and recovery (REC) for the first 6 hours after SD. NREMS rebound after SD did not differ among control, sham-lesioned, and ADX mice ($F_{2,29} \leq 1.0$, $P > 0.3$).

(Supplementary Figure 1) and recovery time spent in NREM sleep following the sleep deprivation (Figure 2C) did not vary across the 3 experimental groups.

Adrenalectomy Attenuates the Effect of Sleep Deprivation on *Period (Per)* Gene Expression

The contribution of the increase in corticosterone to the sleep-deprivation-dependent increase in the expression of the clock genes *Per1-3* was investigated in a separate set of D2 mice by comparing forebrain expression using qPCR among ADX and sham-operated mice that were either sleep deprived or were allowed to sleep *ad lib* prior to sacrifice at ZT6. Also in this experiment, sleep deprivation elevated corticosterone in sham-operated mice only (Figure 3, bottom left panel). Similar to previous studies,^{6,8,23,24} sleep deprivation induced an increase in the expression of the *Per* genes in the forebrain of sham-operated mice. This increase was strongly attenuated in ADX mice and no longer reached significance levels for *Per1* and *Per3*, whereas the increase in *Per2*, although still significant, was reduced by approximately 40% (Figure 3, left panels). ANOVA revealed a significant interaction between factors Sleep Deprivation and ADX for *Per2* and *Per3* expression (Figure 3).

Other clock genes that we evaluated in this qPCR experiment were *Npas2* (*Neuronal PAS domain protein 2*), *Rev-Erba* (or *Nr1d1*; *nuclear receptor subfamily 1, group D, member 1*), and the “clock-controlled” gene *Dbp* (*D site albumin promoter binding protein*). The typical sleep-deprivation-dependent decrease in forebrain *Dbp* levels^{8,23} was equally observed in ADX mice (Figure 3). Also *Rev-Erba* mRNA levels were decreased with sleep deprivation, but this decrease was significant in sham-operated mice only. Similarly, a significant increase in *Npas2* expression after sleep deprivation was found only in sham mice. Although ANOVA analyses identified a significant interaction between factors Sleep Deprivation and ADX for the transcripts *Per2* and *-3* only, ADX seemed, in general, to attenuate the sleep-deprivation-induced changes in clock-gene expression.

Finally, we examined the expression of the activity-induced transcript *Homer1a*, which we previously identified as a core molecular marker of sleep pressure.⁶ In contrast with the clock genes, *Homer1a* was not affected by ADX and showed a robust increase in both experimental groups (Figure 3, bottom right panel). Thus, like delta power (see above), *Homer1a* also proved to be a reliable marker of time spent awake not affected by the corticosterone component of the HPA axis.

Adrenalectomy Reduces the Sleep-Deprivation-Dependent Changes in Brain Transcriptome

In addition to evaluating the aforementioned candidate genes that we and others had previously found to be implicated in the homeostatic regulation of sleep, we performed a transcriptome analysis to quantify for which forebrain transcripts the sleep-deprivation-induced changes in expression were modulated by ADX. Using an FDR of 5%, we identified 1,476 probe sets significantly affected by sleep deprivation in the brain of sham-operated mice, with 634 being increased and 842 being decreased (Figure 4A; Supplementary Table 1). Transcripts increased by sleep deprivation included synaptic plasticity genes (e.g., *Homer1*, *Arc*, *Bdnf*), genes encoding heat-shock proteins (*Hsp1*, *-90*,

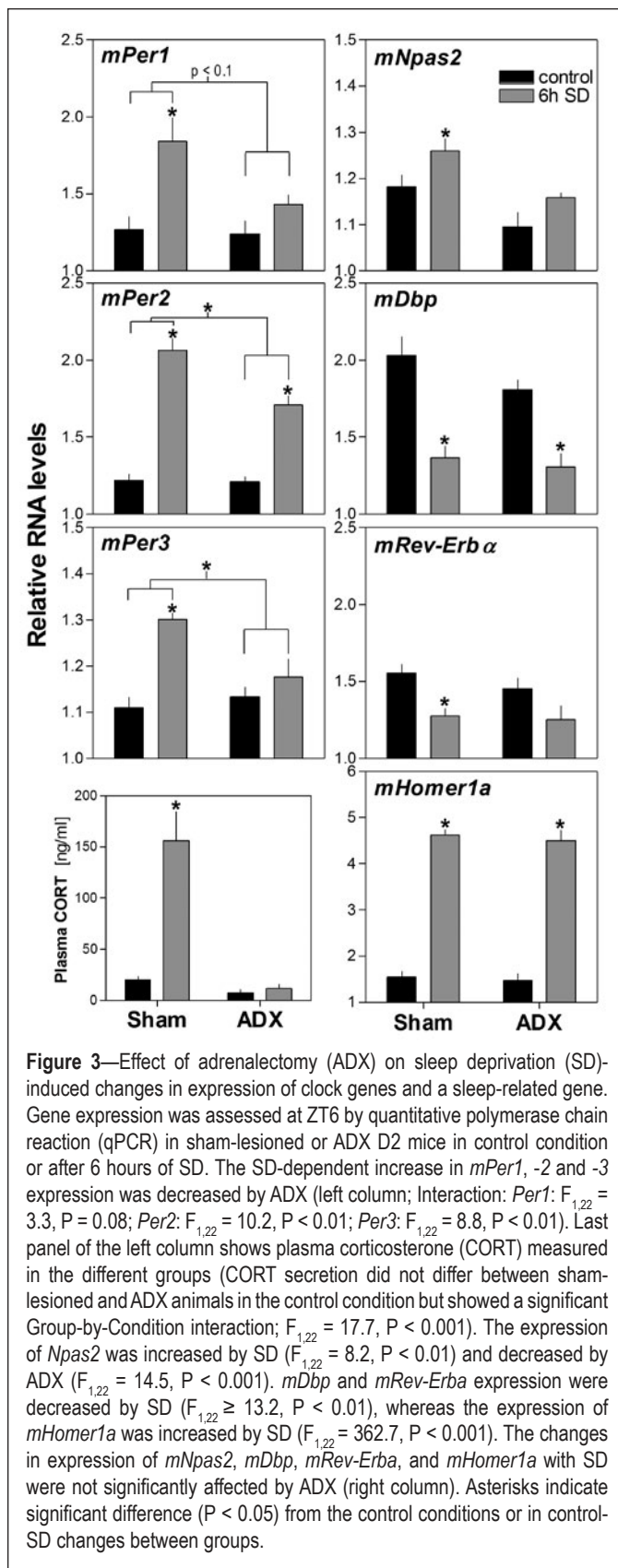


Figure 3—Effect of adrenalectomy (ADX) on sleep deprivation (SD)-induced changes in expression of clock genes and a sleep-related gene. Gene expression was assessed at ZT6 by quantitative polymerase chain reaction (qPCR) in sham-lesioned or ADX D2 mice in control condition or after 6 hours of SD. The SD-dependent increase in *mPer1*, *-2* and *-3* expression was decreased by ADX (left column; Interaction: *Per1*: $F_{1,22} = 3.3$, $P = 0.08$; *Per2*: $F_{1,22} = 10.2$, $P < 0.01$; *Per3*: $F_{1,22} = 8.8$, $P < 0.01$). Last panel of the left column shows plasma corticosterone (CORT) measured in the different groups (CORT secretion did not differ between sham-lesioned and ADX animals in the control condition but showed a significant Group-by-Condition interaction; $F_{1,22} = 17.7$, $P < 0.001$). The expression of *Npas2* was increased by SD ($F_{1,22} = 8.2$, $P < 0.01$) and decreased by ADX ($F_{1,22} = 14.5$, $P < 0.001$). *mDbp* and *mRev-Erba* expression were decreased by SD ($F_{1,22} \geq 13.2$, $P < 0.01$), whereas the expression of *mHomer1a* was increased by SD ($F_{1,22} = 362.7$, $P < 0.001$). The changes in expression of *mNpas2*, *mDbp*, *mRev-Erba*, and *mHomer1a* with SD were not significantly affected by ADX (right column). Asterisks indicate significant difference ($P < 0.05$) from the control conditions or in control-SD changes between groups.

and *-40*), early response genes (*Fos*, *Egr*, *Hif*), potassium channel subunits (*Kcnf1*, *Kcnq2*, *Kcnk1*), and clock genes (*Per1*, *Per2*). Functional clustering of these probes highlights their involvement in transcriptional and in posttranslational processes, in cell cycle regulation, and in cell development (Supplemen-

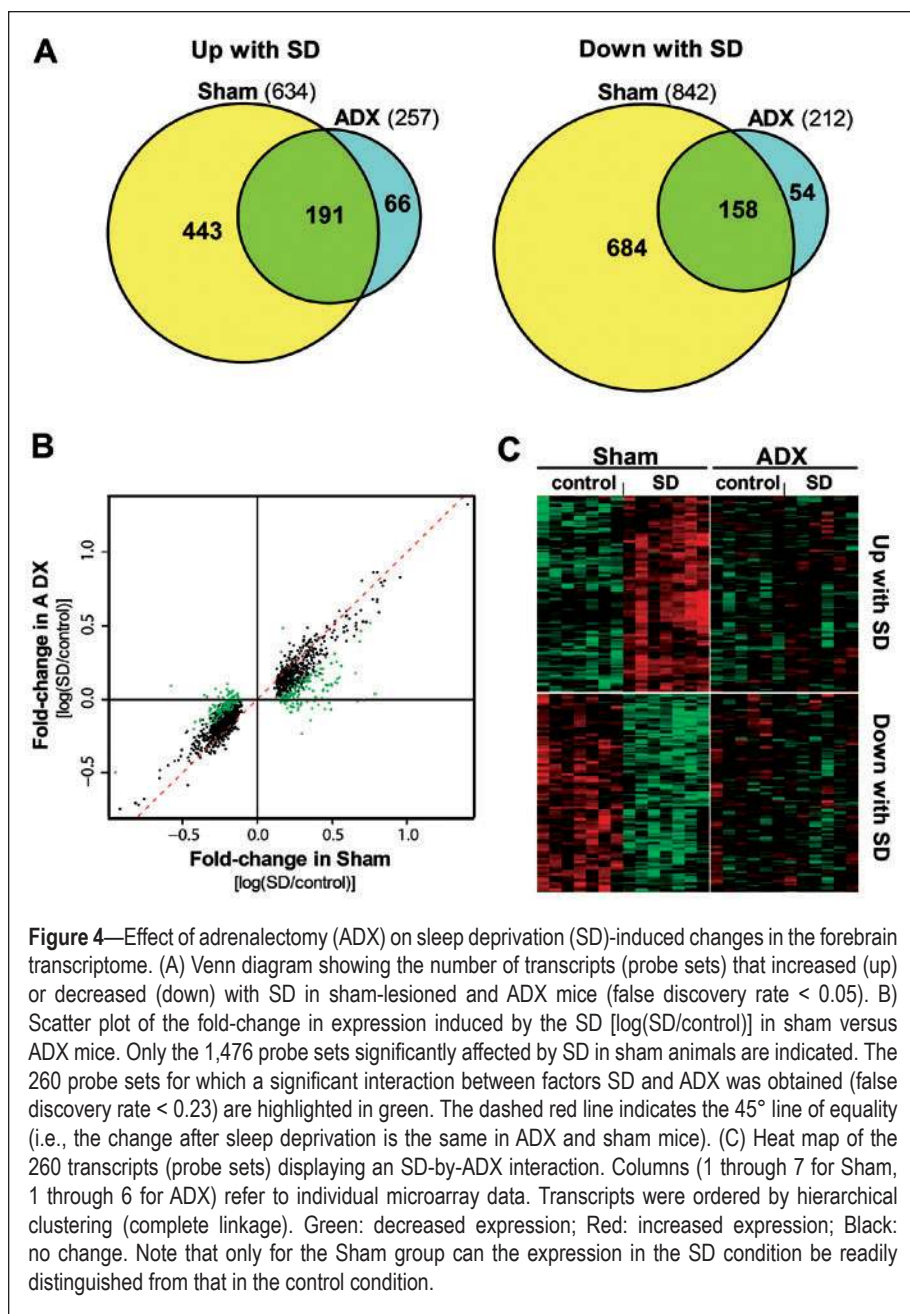


Figure 4—Effect of adrenalectomy (ADX) on sleep deprivation (SD)-induced changes in the forebrain transcriptome. (A) Venn diagram showing the number of transcripts (probe sets) that increased (up) or decreased (down) with SD in sham-lesioned and ADX mice (false discovery rate < 0.05). (B) Scatter plot of the fold-change in expression induced by the SD [$\log(\text{SD}/\text{control})$] in sham versus ADX mice. Only the 1,476 probe sets significantly affected by SD in sham animals are indicated. The 260 probe sets for which a significant interaction between factors SD and ADX was obtained (false discovery rate < 0.23) are highlighted in green. The dashed red line indicates the 45° line of equality (i.e., the change after sleep deprivation is the same in ADX and sham mice). (C) Heat map of the 260 transcripts (probe sets) displaying an SD-by-ADX interaction. Columns (1 through 7 for Sham, 1 through 6 for ADX) refer to individual microarray data. Transcripts were ordered by hierarchical clustering (complete linkage). Green: decreased expression; Red: increased expression; Black: no change. Note that only for the Sham group can the expression in the SD condition be readily distinguished from that in the control condition.

tary Table 2). Among the transcripts decreased by sleep deprivation were RNA-binding proteins (*Rbm* and *Cirbp*), adhesion proteins (synaptotagmin [*Syt12*, *Syt3*], *Mcam*, *Cadm4*), and regulatory enzymes of neurotransmitters (*Maoa*, *Ache*). These transcripts belong to a variety of functional categories, such as lipid, steroid, and cholesterol metabolism; protein synthesis and degradation, and cell-to-cell signaling and interaction (Supplementary Table 2). Many of the brain transcripts that changed their expression after sleep deprivation in the current study have been reported previously, (Supplementary Table 1) demonstrating the reproducibility of these finding in general and the validity of our present findings specifically.

Comparison of the ADX and sham-operated mice that were not sleep deprived demonstrated that ADX, *per se*, did not affect forebrain gene-expression levels; none of the 28,198 probe sets reached the 5% FDR (best adjusted P value 0.33; second best > 0.99). ADX did, however, alter the brain transcriptome

response to sleep deprivation; the expression of only 469 transcripts (i.e., 68% fewer compared with shams) was significantly affected by sleep deprivation (FDR < 5%) in ADX mice, 349 of which overlapped with those changed by sleep deprivation in sham-operated mice (Figure 4A, Supplementary Table 1). The 1,127 probes changed by sleep deprivation in sham animals but not in ADX are part of a variety of functional groups among which are genes coding for heat-shock proteins (*Hspa4*, *Hspd1*, *Hspe1*, *Hsp90aa1*, *Dnaj1*, *Dnajb4*), metabolic enzymes (*Pdk4*, *Gpt2*, *Dgat2*, *Hmgcs1*, *Dhcr7-24*, *G6pc3*, *Ugdh*), histone and histone-regulatory proteins (*Hdac4*, *Hdac6*, *Jhdm1d*, *H1f0*, *H2afj*, *Hist1h4i*), and adhesion proteins (*Pcdh10*, *Pcdhb11*, *Pcdhb13*, *Pcdhb15*, *Pcdhb20*). To compare, in a quantitative way, the sleep-deprivation-responses between ADX and sham-operated mice, we contrasted the fold-change in the ADX group with that for the sham group for each of the 1,476 probe sets affected by sleep deprivation in sham-operated mice (Figure 4B). We observed that, for the vast majority of probe sets, the *absolute* sleep-deprivation response was reduced in ADX animals.

To further identify specific probe sets within the 1,476 that respond differently to sleep deprivation in ADX and sham-operated mice, we calculated an FDR for the interaction between the factors Sleep Deprivation and ADX. Since for only 18 probe sets an FDR < 5% was reached, we designed a data-mining approach to select the top affected genes. We used a range of FDR cutoffs to define growing lists of affected probe sets. Then, hierarchical clustering was applied to the gene-expression

data for each of these probe-set lists to select a FDR cutoff at which non-sleep-deprived animals would segregate together while separating sleep-deprived ADX and sleep-deprived sham-operated mice (Supplementary Figure 2). The lowest FDR at which such segregation was achieved for the Sleep Deprivation-ADX interaction was 0.23, corresponding here with a nominal P value of 0.04. At this FDR, 260 probes were identified showing an interaction due to attenuation of both the increases and decreases in gene expression after sleep deprivation in ADX mice (Figure 4B and C, Supplementary Table 3). Functional clustering of these probes indicated that they take part in most of the molecular, cellular, and system-development functions modulated by sleep deprivation, including metabolic processes (protein, lipid, and carbohydrate metabolism), cell cycle, cell death, and cellular functioning (see Supplementary Table 2).

For 5 of those 260 transcripts, we verified whether the interaction could be confirmed using qPCR analysis (i.e., *Sgk1*,

Pdk4, *Xdh*, *Mertk*, and *Ppp1r1a*). These genes were chosen to represent the diversity of pathways regulated by corticosterone, with an emphasis on metabolism. For instance, *Sgk1*, the expression of which is directly affected by corticosterone, is involved in cellular functions such as glucose transport,²⁵ regulation of voltage-gated channels,²⁶ and apoptotic processes.²⁷ Also, *Mertk* is implicated in apoptosis.²⁸ *Pdk4* is an essential component of energy metabolism via its role in carbohydrate and lipid metabolic pathways,²⁹ whereas *Xdh* is relevant to redox mechanism and response to hypoxia,³⁰ and *Ppp1r1a* to glycogen metabolism.³¹ Except for *Ppp1r1a*, which was the only transcript among these 5 that was decreased by sleep deprivation, qPCR confirmed the interactions found for the microarray results (Figure 5).

Interestingly, among the 260 transcripts with an interaction, the effect of sleep deprivation was enhanced by ADX for 2 transcripts, contrasting all other transcripts in this list for which ADX reduced the effect of sleep deprivation (Figure 5B, Supplementary Table 3). These 2 transcripts, *Ier5* and *Midn*, are involved in neurogenesis.^{32,33} Although qPCR analysis could not confirm the interaction for *Ier5* (Figure 5B), the sleep-deprivation-induced increase in expression was significant in ADX mice only. This observation is consistent with the fact that corticosterone, besides playing a role as a transcriptional coactivator, can also act as a transcriptional corepressor.¹⁶ Similarly, among the probe sets for which a decrease after sleep deprivation was observed in sham-lesioned animals only, as well as the probe sets among which an increase was observed in ADX but not in sham mice ($n = 684$ and 66 , respectively; Figure 4A, Supplementary Table 1), many are likely to be repressed by corticosterone. Conversely, transcripts increased by sleep deprivation in sham-mice only and decreased by sleep deprivation in ADX mice only ($n = 443$ and 54 , respectively; Figure 4A, Supplementary Table 1) are likely to be under the control of corticosterone-mediated transcriptional activation. This indicates that the corticosterone surge not only amplifies the sleep-deprivation-induced decreases and increases in transcription, but may also mask transcripts relevant to sleep homeostasis.

Molecular Correlates of Sleep Homeostasis

The expression of 349 probe sets was significantly affected by sleep deprivation in both sham-lesioned and ADX mice (Figure 4A). As pointed out for *Homer1a* (see above), molecules modulated by sleep deprivation, independent of the activation of the HPA axis, might be part of the circuitry underlying sleep homeostasis or, at least, be used as molecular markers of sleep pressure, as reflected by the dynamics of delta power. Among these 349 probe sets are immediate/early response genes (*Fos12*, *Fos*, *Egr1,3*), specific heat shock protein genes (*Hspa1a*, *Hspa5*, *Hspa8*, *Hspb1*, *Dnajb5*, *Dnajc3*), RNA-binding protein genes (*Rbm3*, *Rbm11*, *Rbm14*), and plasticity and growth-factor genes (*Homer1*, *Arc*, *Bdnf*, *Vgf*, *Vegfa*). We verified whether the expression of this set of genes was similarly affected by a spontaneous period of wakefulness under undisturbed baseline conditions (ZT18) because, also under these conditions, delta power is high,³ whereas corticosterone levels are low (Figure 1A). Contrasting ZT18 versus ZT12 baseline data (i.e., just after and before the main period of sustained wakefulness) in D2 mice from our previous microarray study,⁶ we found that,

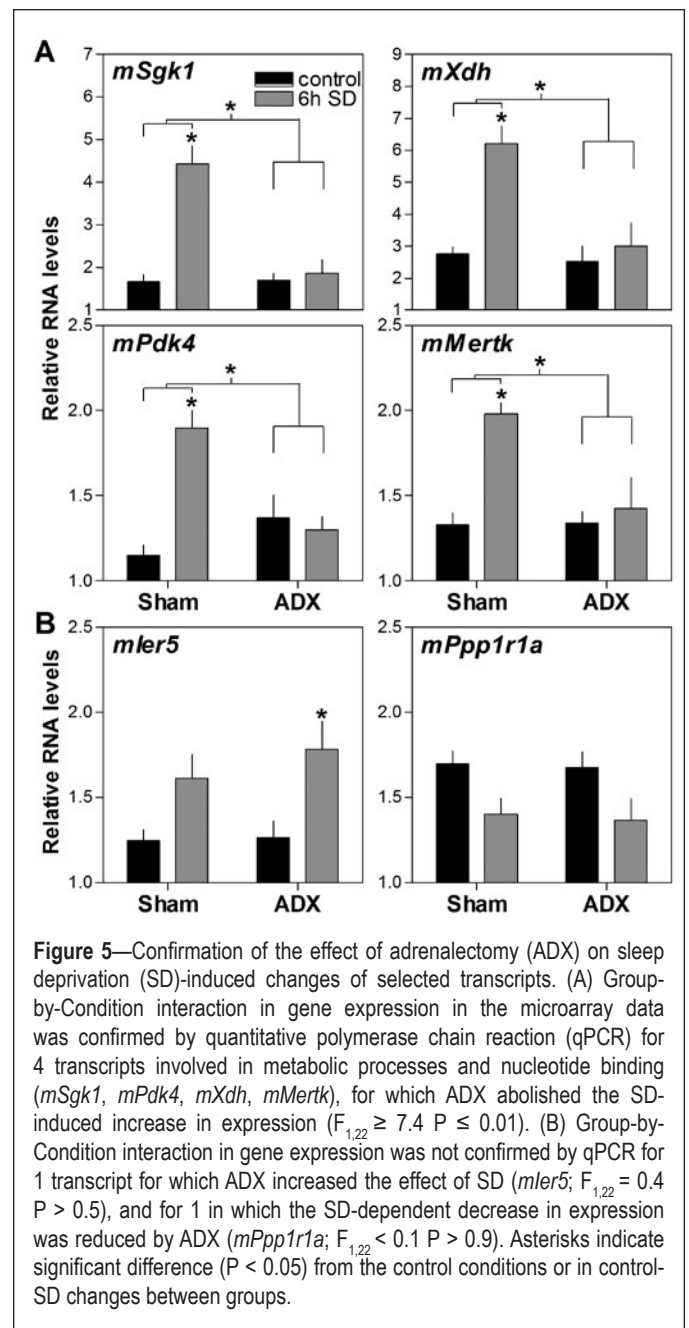


Figure 5—Confirmation of the effect of adrenalectomy (ADX) on sleep deprivation (SD)-induced changes of selected transcripts. (A) Group-by-Condition interaction in gene expression in the microarray data was confirmed by quantitative polymerase chain reaction (qPCR) for 4 transcripts involved in metabolic processes and nucleotide binding (*mSgk1*, *mPdk4*, *mXdh*, *mMertk*), for which ADX abolished the SD-induced increase in expression ($F_{1,22} \geq 7.4$, $P \leq 0.01$). (B) Group-by-Condition interaction in gene expression was not confirmed by qPCR for 1 transcript for which ADX increased the effect of SD (*mIer5*; $F_{1,22} = 0.4$, $P > 0.5$), and for 1 in which the SD-dependent decrease in expression was reduced by ADX (*mPpp1r1a*; $F_{1,22} < 0.1$, $P > 0.9$). Asterisks indicate significant difference ($P < 0.05$) from the control conditions or in control-SD changes between groups.

among the 297 genes that were represented by the 349 probe sets and that were present on both microarray platforms, more than one-quarter (i.e., 78) were similarly affected by sustained spontaneous wakefulness (Supplementary Table 4; Supplementary Figure 3). These 78 genes can be regarded as core molecular components of the sleep homeostatic response, as exemplified by the activity-induced transcript *Homer1a*.

The functional clusters not covered by the transcripts for which a significant interaction was observed (Supplementary Table 2) are also likely to encompass molecular correlates of sleep pressure independent of corticosterone signaling. These clusters include protein synthesis and folding, RNA posttranscriptional modification, and several molecular pathways, such as endoplasmic reticulum stress pathway, ERK/MAPK signaling, and the *Nrf2*-mediated oxidative stress response. MiRNAs have been implicated in the posttranscriptional control of cellular proliferation, development, and differentiation.³⁴ Indeed, we ob-

served 10 miRNAs for which the expression changed with sleep deprivation in sham-lesioned mice (Supplementary Table 1), 5 of which increased (*miR-410*, *-212*, *-29c*, *-29b-2*, and *-708*) and 5 decreased (*let-7e*, *miR-137*, *-22*, *-219-2*, and *-99a*) with sleep deprivation. A recent study in the rat also reported significant changes in *let-7e* and *miR-99a* expression after sleep deprivation, but, contrary to our findings, *let-7e* was increased by sleep deprivation in hippocampus and hypothalamus.³⁵ As in our study, *miR-99a* was decreased in prefrontal and somatosensory cortex and hypothalamus after sleep deprivation. Corticosterone appears to also target the transcriptional regulation of miRNAs because, of the 10 miRNA transcripts affected by sleep deprivation in sham-operated mice, only 3 reached transcriptome-wide statistical significance in ADX mice (*miR-410*, *-212*, and *-29c*; Supplementary Table 1), one of which, *miR-29c*, showed a significant interaction (Supplementary Table 3). In addition, we identified 1 miRNA, *miR-151*, that was increased by sleep deprivation in ADX mice (FDR 0.01 and 0.08 for ADX and sham, respectively). MiRNAs favor translational repression and/or destabilization of target mRNAs,³⁴ and we therefore verified for *miR-410*, *-212*, *-29c*, and *-151* whether the potential target transcripts of these miRNAs were among those affected by sleep deprivation. Among the 842 probes significantly decreased with sleep deprivation, we observed a significant enrichment of potential gene targets of miR-29c while among the 634 probes that increased with sleep deprivation, we observed a significant enrichment of potential targets of the 5' direction of miR-151 and a tendency for enrichment (P = 0.06) of miR-212 targets (Supplementary Table 5). No significant enrichment was found for the potential targets of *miR-410*. Hence, miRNA function in sleep and wakefulness deserves attention both in the context of sleep homeostasis as well as in corticosterone signaling.

DISCUSSION

In this study, we demonstrated that the corticosterone response to enforced wakefulness depends on genetic background in mice. Subsequently, using ADX, we aimed at assessing the contribution of the sleep deprivation-associated increase in plasma corticosterone levels to the molecular and electrophysiological response to sleep loss. Our results indicate that corticosterone greatly amplifies the molecular changes in the brain, which previously were attributed to extended wakefulness *per se*, resulting in a two-thirds reduction in the number of transcripts significantly affected by sleep deprivation. In contrast, delta power, a widely used electrophysiological marker of sleep pressure, proved to reliably follow the sleep-wake distribution independently of the changes in corticosterone under both baseline and sleep-deprivation conditions. The analyses also enabled us to identify 78 transcripts that, similar to delta power, varied with sleep and waking independent of changes in corticosterone.

Adrenalectomy and Delta Power

Abolishing the sleep-deprivation-dependent surge in corticosterone through ADX did not rescue the blunted delta power rebound in D2 mice. Although we cannot rule out other secondary effects of this intervention, this observation suggests that the increase in corticosterone does not contribute to the level of delta power reached after sleep deprivation. This result is consistent with that of a comparable study performed in rats³⁶ and

with the observation in mice that the duration of both spontaneous and enforced bouts of wakefulness equally predict delta power in subsequent sleep.³ As shown here, ADX eliminated the stress-induced increase in corticosterone secretion; ADX does, however, not eliminate the endocrine stress response at other levels of the HPA axis, such as elevated CRH (corticotrophin-releasing hormone) and ACTH (adrenocorticotrophic hormone) levels that might have contributed to the strain-specific sleep-deprivation-dependent changes in delta power. Although CRH and ACTH tend to modulate sleep duration, in particular that of REM sleep,^{37,38} the effect of CRH on delta power seems minor.³⁸ Overall, the data indicate that the strain differences in the delta-power rebound after sleep deprivation must be due to other (genetic) factors independent of the corticosterone component of the HPA-mediated stress response.

Adrenalectomy and Clock Genes

Numerous studies point to a close interrelationship between corticosterone signaling and *Per* expression. *Per1* transcription, in particular, has been shown to be directly controlled by corticosterone through glucocorticoid responsive elements (GRE) in its promoter.¹⁷ Our present results suggest that most of the sleep-deprivation-dependent increase in *Per1* expression is mediated through corticosterone signaling and not related to the increased time spent awake *per se*. Although *Per2* expression seems less affected by stress and corticosterone,³⁹ *PER2* protein levels were, nonetheless, found to be modulated by corticosterone,¹⁸ and, recently, a functional GRE sequence was also identified for *Per2*.⁴⁰ Based on observations made in *Npas2* knockout mice²⁴ and *Cryptochrome1,2* double-knockout mice⁴¹ that showed a reduced and an augmented increase, respectively, in *Per2* after sleep deprivation compared with wild-type mice, we concluded that the sleep-deprivation-dependent changes in *Per2* were mediated, in part, through the negative feedback loop made up of clock genes that underlie circadian-rhythm generation.⁷ Therefore, the reduced increase in *Per2* expression in ADX mice suggests that sleep deprivation activates both clock-gene and corticosterone-signaling pathways and that both pathways, in turn, affect *Per2* expression. These two closely associated pathways are both implicated in metabolism and are essential to cope with and anticipate energy demands.^{42,43} Because extended wakefulness is thought to represent a metabolic challenge to the brain, the sleep-wake-related changes in *Per2* in the forebrain underscore the notion that this molecule plays a role in homeostatic sleep need.⁷

Although our study focused on the sleep-deprivation-induced changes in corticosterone, it should be noted that HPA activation is only one of several mechanism affecting circulating corticosterone levels. The daily changes observed under undisturbed baseline conditions are controlled by various factors, including suprachiasmatic nucleus output, light, and circadian oscillations intrinsic to the adrenal.^{44,45} Also, these baseline variations in corticosterone, the amplitude of which approaches those reported here for the effect of sleep deprivation,⁴⁵ are accompanied by changes in clock-gene expression, and it has been proposed that increases in circulating corticosterone levels set the phase of circadian rhythms in the periphery.⁴⁴ Given the important role of corticosterone in normal physiology and in gene expression, it is surprising that the absence of circadian

changes in corticosterone in ADX mice did not affect the baseline expression of any of the transcripts, at least at this time of day when corticosterone was low in both experimental groups. Because corticosterone was supplemented in the experiment assessing delta power, levels of circulating corticosterone are likely to have followed the drinking rhythm.¹⁸

Adrenalectomy and the Brain Transcriptome

Corticosterone can bind and activate mineralocorticoid and glucocorticoid receptors in the brain. Both are highly expressed in forebrain areas such as the hippocampus and amygdala, which are involved in emotional regulation and in learning and memory processes.⁴⁶ These nuclear receptors, when ligand activated, can initiate transcription by binding to specific DNA sequences in the promoter regions of target genes or, by interacting with other transcription factors, can decrease transcription.^{16,46} Numerous transcripts in the brain, mainly concerning metabolism and neuronal function,⁴⁶ are affected by this signaling pathway. The importance of corticosterone in gene regulation is compellingly illustrated by our microarray results because the transcriptional response associated with sleep deprivation in the forebrain was greatly reduced after ADX. Although addressing a different question, the extensive 68% reduction in the number of transcripts affected by sleep deprivation is reminiscent of the 60% decrease in the number of transcripts that maintained circadian rhythmicity in the liver of ADX mice.³⁹ Similarly, we have previously established that 80% of the brain transcripts that were considered to be circadian because expression changed according to time of day were, in fact, sleep-wake driven.⁶ These studies illustrate the necessity of distinguishing between primary and consequent effects (e.g., sleep loss and corticosterone, or circadian and sleep-wake driven, respectively), especially when the influence of the latter exceeds those of the former.

The Molecular Wiring of Sleep Homeostasis

We assembled an exclusive list of 78 sleep homeostatic transcripts that responded to sleep loss independent of corticosterone and time of day. This list includes an important subset of immediate/activity-dependent genes linked to neuronal plasticity and memory (e.g., *Fos*, *Arc*, *Egr1*, *Egr3*, *Nr4a3*),⁴⁷⁻⁴⁹ which corroborates the proposed direct involvement of plastic neuronal changes in sleep homeostasis.¹ Also, genes associated with the ERK/MAPK pathway of intracellular signaling, which is closely linked to the immediate early gene response, are well represented in the 78 transcripts (e.g., *Dusp6*, *Dusp1*, *Dusp4*, *Trib2*). Maret et al.⁶ proposed a neuroprotective function for sleep, based on the role of *Homer1a* in intracellular calcium homeostasis. Also *Npas4* and *Nr4a1*, which feature among our set of 78, were recently found to be part of a gene program involved in neuroprotection, which is activated upon synaptic activity-induced calcium signaling,⁵⁰ further supporting such a role for sleep. Moreover, other transcripts on our list, such as *Egr1*, *Fos*, and *Nr4a3*, have also been involved in the molecular neuroprotective response triggered by ischemia,⁵¹ as is the case for *Hspa5*, *Xbp1*, *Hsp90b1*, and *Stip1*, which are responsive to cellular stress and implicated in the unfolded protein response,⁵²⁻⁵⁴ and *Bcl2*, a well-known apoptotic mediator.⁵⁵ Overall, these findings confirm that extended wakefulness ac-

tivates molecular pathways associated with the preservation of neuronal integrity and the modulation of neuronal connections.

Our list also contains *Nfil3* (or *E4bp4*), which drives circadian gene expression and is a molecular partner of PER2,⁵⁶ providing additional support for an involvement of specific clock components in homeostatic sleep regulation. Furthermore, in addition to the presence of RNA-binding proteins (*Cirbp*, *Rbm3*, *Rbm11*) in the list of homeostatic transcripts, our miRNA findings confirm a role for RNA posttranscriptional processing in sleep homeostasis.³⁵ Of the 10 miRNAs that changed with sleep deprivation in sham-operated mice, only *miR-410*, *-212*, and *-29c* did so independently of ADX. Thus, as for the entire transcriptome, again a two-third reduction occurred, indicating an important role for corticosterone in miRNA expression, which has not been demonstrated previously *in vivo*. Importantly, among the *miR-212* potential target genes, 5 feature on our list of homeostatic genes (i.e., *Npas4*, *Nfil3*, *Homer1*, *Ier5*, and *Hspa1a*). The relevance of *miR-212* to sleep homeostasis is a lead we are currently following up on. Thus, in addition to their relevance for circadian rhythms,^{57,58} our findings, which need to be confirmed using more-specific miRNA extraction protocols, show an additional role for miRNA in sleep regulation directly through sleep homeostasis.

CONCLUSIONS

We report on the central relationship between the molecular and physiological markers of sleep need and their response to one component of the stress response in mice. Also, in humans, sleep restriction can increase the level of the glucocorticoid cortisol.¹¹ Our EEG findings suggest that, at least for acute forms of stress, this effect does not have an important impact on the recuperative value of sleep, as indexed by delta power. Glucocorticoids mediate most of the central effects of stress, which is well documented for the hippocampus, where it affects energy metabolism, memory, synaptic plasticity, dendritic morphology, neurogenesis, and neurotoxicity.^{59,60} Several of these effects, such as the modulation of energy metabolism, the changes in synaptic plasticity, and the changes in mediators of cell death, have also been observed after sleep deprivation, where they have been attributed to sleep loss.⁵ At the molecular level, our findings support a large contribution of glucocorticoids, especially regarding the general regulation of various metabolic routes, an effect that has not been directly assessed previously. The analyses allowed for the identification of those transcripts that respond to sleep loss independent of glucocorticoids and time of day and suggest that sustained wakefulness activates a neuroprotective signaling pathway likely to be of direct relevance for sleep function.

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DISCLOSURE STATEMENT

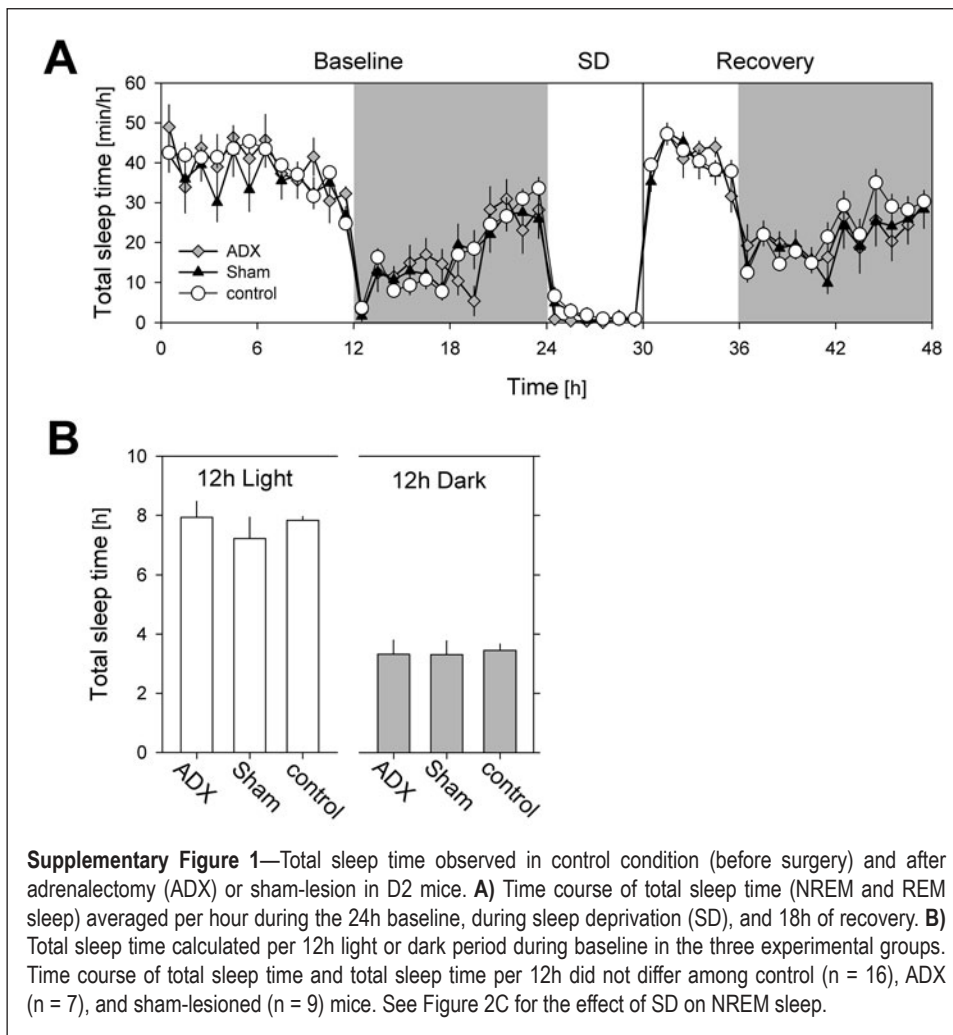
This was not an industry supported study. The authors have indicated no financial conflicts of interest.

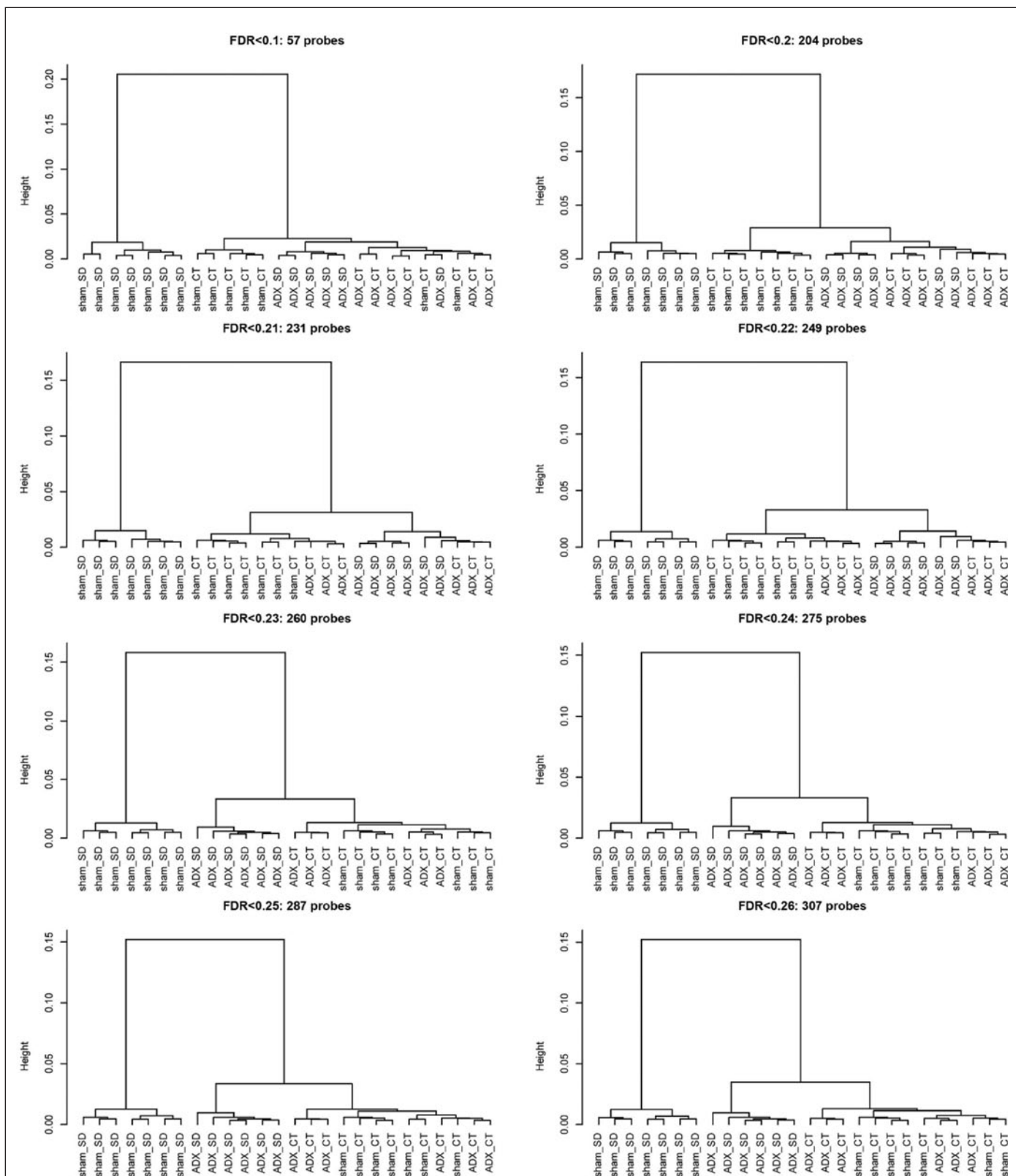
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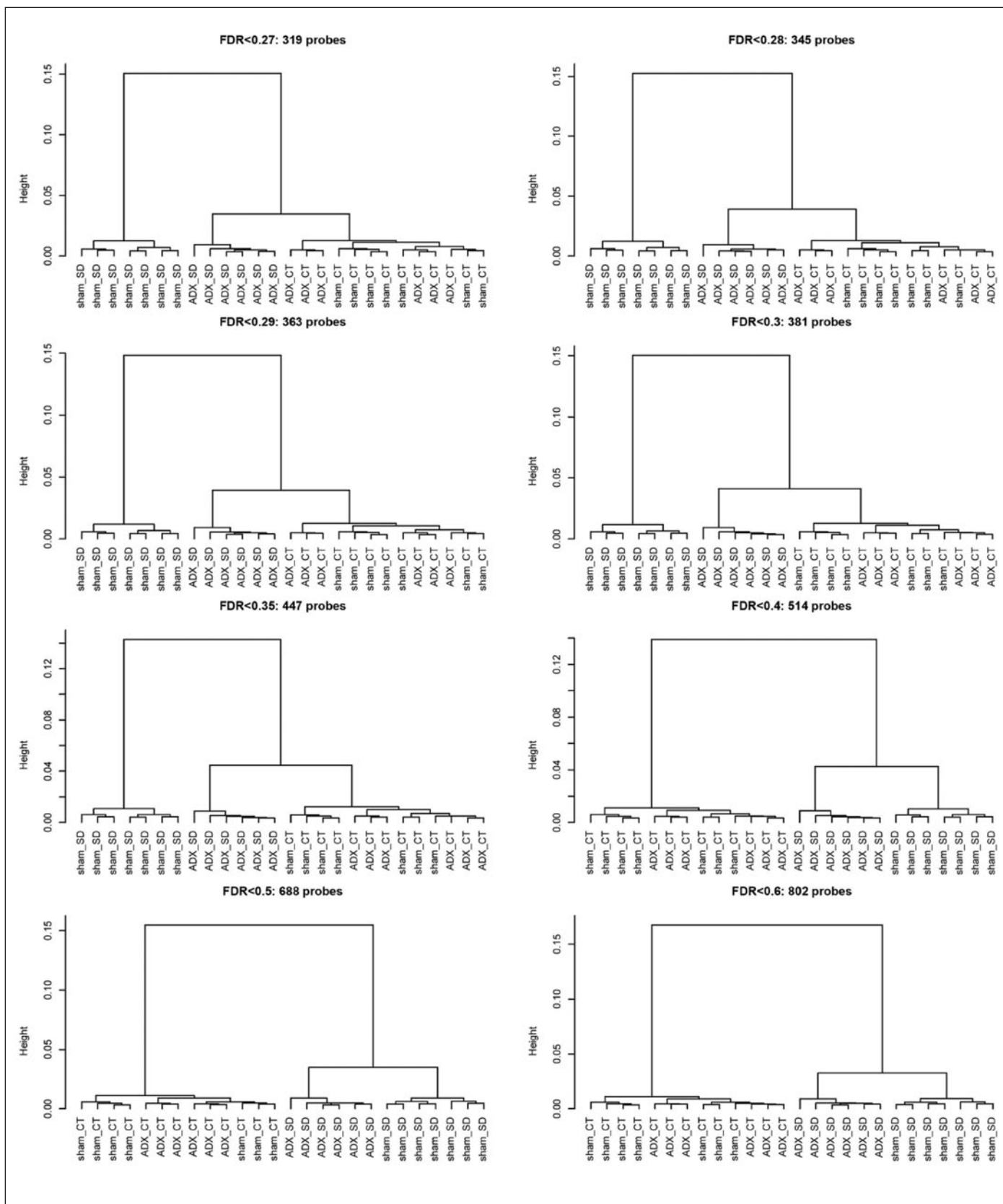
Supplementary Figures and Tables for Separating the Contribution of Glucocorticoids and Wakefulness to the Molecular and Electrophysiological Correlates of Sleep Homeostasis



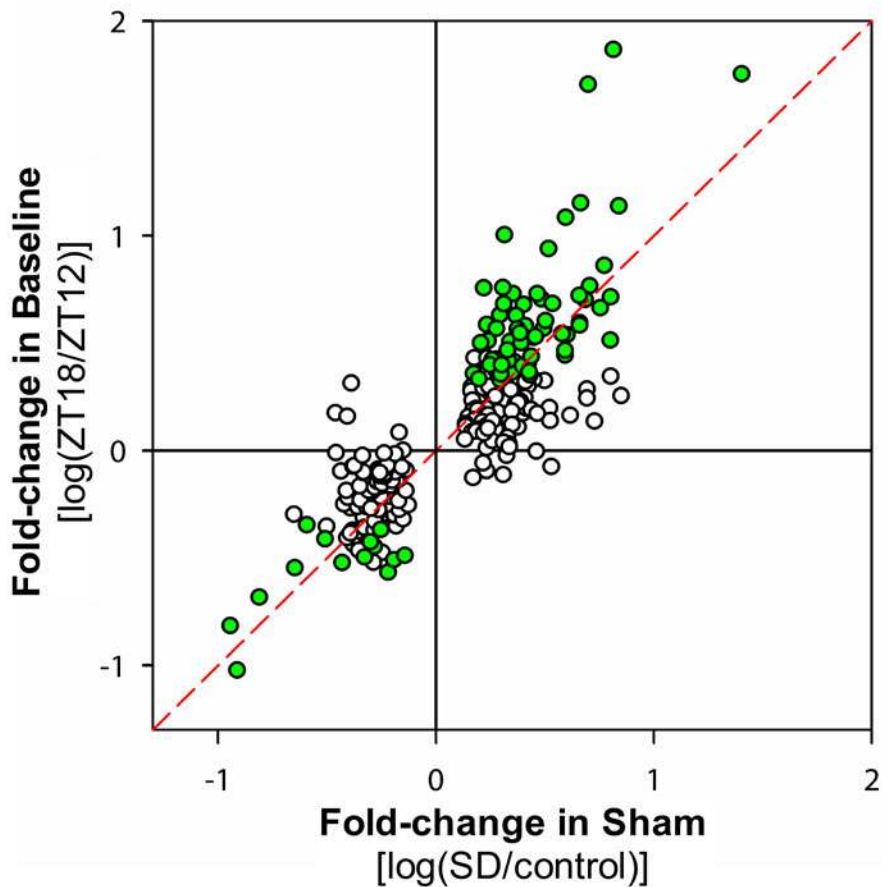


Supplementary Figure 2 continues on the following page

Supplementary Figure 2—Hierarchical clustering, using Ward's linkage method, of all 26 individual mice based on a variable number of probe sets displaying a significant interaction between the effects of ADX and of SD. This clustering approach was performed to delineate the genes for which the SD effect on expression was altered by ADX. In each graph an increasing FDR significance threshold was used (varying from 0.1 to 0.6; upper left – lower right) to assess the interaction. The lowest FDR threshold with which the Sham-SD, ADX-SD, and control (CT) groups could be separated was 0.23. This cut-off was subsequently used to evaluate probe sets for which a significant interaction between Group (sham vs. ADX) and Condition (CT vs. SD) was found among the 1476 probe sets affected by SD (See Supplementary Table 3). Using this approach, a significant interaction was found for 260 probe sets (see data points marked green in Figure 4B and the heatmap of Figure 4C). Pearson correlation was used as a distance metric for clustering analysis.



Supplementary Figure 2 (continued)—Hierarchical clustering, using Ward's linkage method, of all 26 individual mice based on a variable number of probe sets displaying a significant interaction between the effects of ADX and of SD. This clustering approach was performed to delineate the genes for which the SD effect on expression was altered by ADX. In each graph an increasing FDR significance threshold was used (varying from 0.1 to 0.6; upper left – lower right) to assess the interaction. The lowest FDR threshold with which the Sham-SD, ADX-SD, and control (CT) groups could be separated was 0.23. This cut-off was subsequently used to evaluate probe sets for which a significant interaction between Group (sham vs. ADX) and Condition (CT vs. SD) was found among the 1476 probe sets affected by SD (See Supplementary Table 3). Using this approach, a significant interaction was found for 260 probe sets (see data points marked green in Figure 4B and the heatmap of Figure 4C). Pearson correlation was used as a distance metric for clustering analysis.



Supplementary Figure 3—Scatter plot of the fold-change in expression induced by the sleep deprivation (SD) [$\log(\text{SD}/\text{control})$] in sham-lesioned animals plotted against the fold-change in expression between ZT18 and ZT12 in DBA/2J mice during baseline conditions [$\log(\text{ZT18}/\text{ZT12})$] (analysis of previously published micro-array data from Maret et al., 2007). The 297 gene sequences representing the 349 probe sets that were significantly modified by SD in both sham and ADX mice in the present study (Supplementary Table 1 and Figure 4A) were compared to the Maret et al. (2007) study to verify whether they were equally affected by a comparable extended period of spontaneous wakefulness. Among the 297 genes represented, 78 genes showed a significant and similar change between ZT18 and ZT12 (green symbols, see Supplementary Table 4). The 45 degree line of equality is indicated with a dashed red line.

Supplementary Table 1: Probes significantly affected by sleep deprivation (SD) in sham-operated D2 mice (1476 probe sets). The FDR of 5% for the ANOVA with factor SD was taken to adjust nominal P-values (Adj. P value). The direction indicates whether SD increased (up) or decreased (down) the expression of the transcript. The last two columns show the adjusted FDR P values calculated for sham and ADX mice separately. Gene symbols highlighted in **yellow** (378 probes) were also found to be affected by SD (ZT0 to -6) by Maret et al. (2007); gene symbols in **bold** (701 probes) have been reported to be affected by sleep and wakefulness by Mackiewicz et al. (2007). Probe sets affected by SD in ADX mice only (120) are listed at the end. ns: $p \geq 0.05$; * difference between studies terminology for Hrasls.

Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10471586	Hspa5	heat shock protein 5	NM_022310	up	1.49e-10	1.88e-08
10429491	Arc	activity regulated cytoskeletal-associated protein	NM_018790	up	1.52e-09	3.50e-08
10556113	Rbm3	RNA binding motif protein 3	ENSMUST0000115616	down	2.66e-09	2.73e-07
10358454	Rbm3	RNA binding motif protein 3	ENSMUST0000115616	down	2.66e-09	2.02e-07
10603469	Rbm3	RNA binding motif protein 3	NM_016809	down	2.66e-09	2.21e-07
10364712	Cirbp	cold inducible RNA binding protein	NM_007705	down	4.11e-09	1.57e-06
10394735	Pdia6	protein disulfide isomerase associated 6	NM_027959	up	5.99e-09	5.94e-07
10406626	Homer1	homer homolog 1 (Drosophila)	NM_147176	up	4.64e-08	4.08e-07
10435075	Tfrc	transferrin receptor	NM_011638	down	4.66e-08	3.75e-05
10426098	Creld2	cysteine-rich with EGF-like domains 2	NM_029720	up	4.66e-08	7.00e-06
10363350	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	NM_011030	up	8.47e-08	6.33e-05
10448471	Dnase1l2	deoxyribonuclease 1-like 2	NM_025718	up	9.46e-08	4.70e-05
10399680	Cys1	cystin 1	NM_138686	up	1.01e-07	0.008
10401743	4933437F05Rik	RIKEN cDNA 4933437F05 gene	BC125331	up	1.66e-07	3.75e-05
10535904	Hsph1	heat shock 105kDa/110kDa protein 1	NM_013559	up	1.91e-07	7.03e-05
10595324	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	NM_010482	up	2.55e-07	7.03e-05
10488048	Mkks	McKusick-Kaufman syndrome protein	NM_021527	up	2.55e-07	0.002
10544525	Pdia4	protein disulfide isomerase associated 4	NM_009787	up	2.55e-07	2.73e-05
10438098	Sdf2l1	stromal cell-derived factor 2-like 1	NM_022324	up	2.55e-07	3.75e-05
10401841	Dio2	deiodinase, iodothyronine, type II	NM_010050	up	2.55e-07	0.0004
10436552	Rbm11	RNA binding motif protein 11	NM_198302	down	2.55e-07	0.0002
10436945	Slc5a3	solute carrier family 5 (inositol transporters), member 3	NM_017391	up	3.04e-07	0.0001
10381474	Arl4d	ADP-ribosylation factor-like 4D	NM_025404	up	3.23e-07	0.02
10511580	Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	NM_001098230	up	7.60e-07	9.70e-05
10504218	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	NM_019874	up	7.60e-07	1.81e-05
10520862	Fosl2	fos-like antigen 2	NM_008037	up	7.60e-07	4.21e-05
10554863	Syt12	synaptotagmin-like 2	NM_001040085	down	7.61e-07	0.0001
10572271	Tm6sf2	transmembrane 6 superfamily member 2	NM_181540	up	7.75e-07	0.001
10606989	Tsc22d3	TSC22 domain family, member 3	NM_001077364	up	7.75e-07	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10596575	Armet	arginine-rich, mutated in early stage tumors	NM_029103	up	8.18e-07	0.0002
10371482	Hsp90b1	heat shock protein 90, beta (Grp94), member 1	NM_011631	up	9.40e-07	0.004
10362073	Sgk1	serum/glucocorticoid regulated kinase 1	NM_011361	up	1.42e-06	ns
10352918	---	MI0000577 Mus musculus miR-29c stem-loop	---	up	1.60e-06	0.007
10511136	B930041F14Rik	RIKEN cDNA B930041F14 gene	NM_178699	down	1.61e-06	ns
10459602	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	NM_001127177	up	1.61e-06	0.002
10352916	---	MI0000712 Mus musculus miR-29b-2 stem-loop	---	up	1.61e-06	ns
10478160	2310007D09Rik	RIKEN cDNA 2310007D09 gene	BC068129	up	2.26e-06	ns
10397346	Fos	FBJ osteosarcoma oncogene	NM_010234	up	2.32e-06	2.57e-06
10571824	EG547103	predicted gene, EG547103	ENSMUST0000098764	down	3.17e-06	0.0003
10357660	Mfsd4	major facilitator superfamily domain containing 4	NM_001114662	down	3.19e-06	7.03e-05
10544629	Tra2a	Transformer 2 alpha homolog (Drosophila)	NM_198102	up	3.42e-06	0.0001
10550605	Emi2	Echinoderm microtubule associated protein like 2	BC055476	down	3.42e-06	0.001
10584580	---	snoRNA, chromosome: NCBIM37: 9: 40612831: 40612920:1 gene:ENSMUSG00000064791	ENSMUST0000082857	up	3.42e-06	0.0002
10417013	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	NM_008929	up	3.42e-06	0.0008
10417034	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	NM_008929	up	3.42e-06	0.0008
10356601	Per2	period homolog 2 (Drosophila)	NM_011066	up	3.70e-06	ns
10385052	Ranbp17	RAN binding protein 17	NM_023146	down	3.95e-06	0.004
10352914	A330023F24Rik	RIKEN cDNA A330023F24 gene	AK171382	up	3.95e-06	0.005
10398442	---	MI0001161 Mus musculus miR-410 stem-loop	---	up	5.57e-06	9.38e-05
10498302	Gm410	gene model 410, (NCBI)	NM_001033349	up	5.83e-06	ns
10443463	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	NM_007669	up	5.93e-06	0.003
10485402	Fjx1	four jointed box 1 (Drosophila)	NM_010218	down	5.96e-06	ns
10467529	Opalin	oligodendrocytic myelin paranodal and inner loop protein	NM_153520	down	7.05e-06	0.04
10517005	Gpr3	G-protein coupled receptor 3	NM_008154	up	7.61e-06	0.0001
10366043	Dusp6	dual specificity phosphatase 6	NM_026268	up	7.61e-06	8.56e-05
10603860	Cfp	complement factor properdin	NM_008823	up	7.61e-06	0.004
10362372	9330159F19Rik	RIKEN cDNA 9330159F19 gene	AK034141	up	7.67e-06	ns
10524234	Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9	NM_198306	up	9.46e-06	0.0002
10541071	8430408G22Rik	RIKEN cDNA 8430408G22 gene	BC058515	up	9.71e-06	ns
10583347	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	NM_025844	up	1.01e-05	0.03
10426315	Lrrk2	leucine-rich repeat kinase 2	NM_025730	up	1.01e-05	0.0004
10580765	Pilp	plasma membrane proteolipid	NM_026385	down	1.01e-05	0.005
10580219	Calr	calreticulin	NM_007591	up	1.01e-05	0.0004

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10375735	Hnrnp1	heterogeneous nuclear ribonucleoprotein H1	NM_021510	up	1.01e-05	0.02
10464905	Npas4	neuronal PAS domain protein 4	NM_153553	up	1.17e-05	0.005
10505163	Zkscan16	zinc finger with KRAB and SCAN domains 16	NM_001099323	down	1.41e-05	0.0002
10571312	Dusp4	dual specificity phosphatase 4	NM_176933	up	1.43e-05	0.0002
10408928	Hspb1	heat shock protein 1	NM_013560	up	1.46e-05	4.84e-05
10561907	0610010E21Rik	RIKEN cDNA 0610010E21 gene	NM_001033140	down	1.61e-05	0.008
10486403	Pla2g4e	phospholipase A2, group IVE	NM_177845	down	1.61e-05	0.006
10532954	2410014A08Rik	RIKEN cDNA 2410014A08 gene	NM_175403	up	1.61e-05	0.004
10361250	Camk1g	calcium/calmodulin-dependent protein kinase I gamma	NM_144817	up	1.61e-05	0.01
10526410	Hspb1	heat shock protein 1	NM_013560	up	1.61e-05	3.75e-05
10474129	E430002G05Rik	RIKEN cDNA E430002G05 gene	NM_173749	down	1.61e-05	0.002
10427035	Nr4a1	nuclear receptor subfamily 4, group A, member 1	NM_010444	up	1.91e-05	0.0004
10431894	Slc38a2	solute carrier family 38, member 2	NM_175121	up	1.91e-05	0.005
10510668	Tnfrsf25	tumor necrosis factor receptor superfamily, member 25	NM_033042	up	1.91e-05	0.0001
10532944	2410014A08Rik	RIKEN cDNA 2410014A08 gene	NM_175403	up	1.97e-05	0.003
10584712	Hyou1	hypoxia up-regulated 1	NM_021395	up	2.07e-05	0.0001
10568873	Adam8	a disintegrin and metalloproteinase domain 8	NM_007403	up	2.09e-05	0.02
10505143	Akap2 // Palm2 // RP23-334A5.2	A kinase (PRKA) anchor protein 2 // paralemmin 2 // Palm2-Akap2 protein	ENSMUST0000107600	down	2.09e-05	0.002
10593225	Zbtb16	zinc finger and BTB domain containing 16	NM_001033324	up	2.09e-05	ns
10477286	Pofut1	protein O-fucosyltransferase 1	NM_080463	down	2.17e-05	0.002
10583992	Igsf9b	immunoglobulin superfamily, member 9B	NM_001129787	up	2.20e-05	0.0002
10536294	Peg10	paternally expressed 10	NM_001040611	up	2.21e-05	0.005
10408879	Gfod1	glucose-fructose oxidoreductase domain containing 1	NM_001033399	up	2.38e-05	3.75e-05
10439130	Umps	uridine monophosphate synthetase	NM_009471	up	2.45e-05	0.006
10596931	Wdr6	WD repeat domain 6	NM_031392	down	2.53e-05	0.005
10390283	Cdk5rap3	CDK5 regulatory subunit associated protein 3	NM_030248	down	2.60e-05	ns
10458461	Hdac3	histone deacetylase 3	NM_010411	down	2.94e-05	0.02
10514713	Wdr78	WD repeat domain 78	NM_146254	up	3.03e-05	0.003
10398356	---	---	AK049674	up	3.26e-05	0.0007
10567589	Usp31	ubiquitin specific peptidase 31	AK122466	up	3.49e-05	0.008
10504424	Reck	reversion-inducing-cysteine-rich protein with kazal motifs	NM_016678	down	3.78e-05	0.004
10374035	Xbp1	X-box binding protein 1	NM_013842	up	3.78e-05	0.0002
10560481	Fosb	FBJ osteosarcoma oncogene B	NM_008036	up	3.93e-05	0.0002
10489620	Ncoa5	nuclear receptor coactivator 5	NM_144892	up	3.94e-05	0.004
10358057	Shisa4	shisa homolog 4 (Xenopus laevis)	NM_175259	down	3.98e-05	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10516765	Serinc2	serine incorporator 2	NM_172702	up	4.12e-05	0.0002
10376074	P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	NM_011031	up	4.20e-05	0.03
10363144	EG547103	predicted gene, EG547103	ENSMUST0000098764	down	4.22e-05	0.006
10504838	Nr4a3	nuclear receptor subfamily 4, group A, member 3	NM_015743	up	4.22e-05	0.0001
10444066	Zbtb22	zinc finger and BTB domain containing 22	NM_020625	down	4.22e-05	0.01
10456184	Apcdd1	adenomatosis polyposis coli down-regulated 1	NM_133237	down	4.34e-05	ns
10443482	BC004004	cDNA sequence BC004004	BC058575	down	4.64e-05	0.01
10400405	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NM_010907	up	4.75e-05	ns
10479510	9230112E08Rik	RIKEN cDNA 9230112E08 gene	ENSMUST0000094214	up	4.83e-05	0.0009
10415319	Irf9	interferon regulatory factor 9	NM_008394	up	5.07e-05	0.008
10573198	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	NM_018808	up	5.12e-05	0.003
10409502	Dok3	docking protein 3	NM_013739	up	5.65e-05	0.0003
10449284	Dusp1	dual specificity phosphatase 1	NM_013642	up	6.25e-05	0.008
10606369	Iitm2a	integral membrane protein 2A	NM_008409	down	7.45e-05	ns
10508217	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	NM_023603	up	7.55e-05	0.02
10535458	Zdhhc4	zinc finger, DHHC domain containing 4	NM_028379	down	7.62e-05	ns
10474399	Bdnf	brain derived neurotrophic factor	NM_001048139	up	7.66e-05	0.0001
10475941	Zc3h6	zinc finger CCCH type containing 6	NM_178404	down	7.66e-05	0.001
10403743	Inhba	inhibin beta-A	NM_008380	up	7.73e-05	0.0003
10568982	BC066028	cDNA sequence BC066028	NM_001001180	down	8.00e-05	0.001
10503602	Fbx14	F-box and leucine-rich repeat protein 4	NM_172988	down	8.63e-05	0.008
10364841	9030607L17Rik	RIKEN cDNA 9030607L17 gene	NM_027829	down	8.75e-05	ns
10406229	Pcsk1	proprotein convertase subtilisin/kexin type 1	NM_013628	up	8.75e-05	0.0001
10521587	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	BC158024	up	9.38e-05	ns
10353871	Lman2l	lectin, mannose-binding 2-like	NM_001013374	up	9.50e-05	0.002
10514708	Insl5	insulin-like 5	NM_011831	up	9.93e-05	ns
10415095	1700123O20Rik	RIKEN cDNA 1700123O20 gene	BC011283	up	0.0001	0.006
10388254	Aspa	aspartoacylase	NM_023113	down	0.0001	0.02
10483624	Dlx1as	distal-less homeobox 1, antisense	NR_002854	up	0.0001	ns
10397966	Otub2	OTU domain, ubiquitin aldehyde binding 2	NM_026580	up	0.0001	0.001
10363901	---	cdna:Genscan chromosome: NCBIM37:10:71167116:71168033:1	GENSCAN0000000670	up	0.0001	6.33e-05
10489569	Pltp	phospholipid transfer protein	NM_011125	down	0.0001	ns
10526553	Vgf	VGF nerve growth factor inducible	NM_001039	up	0.0001	3.75e-05

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10541785	Acrbp	proacrosin binding protein	NM_016845	up	0.0001	0.005
10455942	A730017C20Rik	RIKEN cDNA A730017C20 gene	BC075669	down	0.0001	0.01
10480035	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	NM_133232	up	0.0001	0.001
10381697	Hexim1	hexamethylene bis-acetamide inducible 1	NM_138753	up	0.0001	0.003
10475946	Zc3h6	zinc finger CCCH type containing 6	NM_178404	down	0.0001	0.02
10436788	Hunk	hormonally upregulated Neu-associated kinase	NM_015755	down	0.0001	ns
10509218	Zfp46	zinc finger protein 46	NM_009557	down	0.0001	0.002
10540122	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	NM_009320	down	0.0001	0.03
10424370	Trib1	tribbles homolog 1 (Drosophila)	NM_144549	up	0.0001	ns
10454782	Egr1	early growth response 1	NM_007913	up	0.0002	0.001
10383993	Ccdc117	coiled-coil domain containing 117	NM_134033	up	0.0002	ns
10450367	Hspa1b	heat shock protein 1B	NM_010478	up	0.0002	0.02
10531201	Adams3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.0002	ns
10517540	Zbtb40	zinc finger and BTB domain containing 40	NM_198248	up	0.0002	0.005
10541873	Mrp151	mitochondrial ribosomal protein L51	NM_025595	up	0.0002	ns
10449741	Snf1lk	SNF1-like kinase	NM_010831	up	0.0002	ns
10543017	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	NM_013743	up	0.0002	ns
10531177	Adams3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.0002	0.009
10548996	Slco1a4	solute carrier organic anion transporter family, member 1a4	NM_030687	down	0.0002	0.001
10548194	Fkbp4	FK506 binding protein 4	NM_010219	up	0.0002	0.0003
10598771	Maoa	monoamine oxidase A	NM_173740	down	0.0002	0.01
10438293	Zdhhc8	zinc finger, DHHC domain containing 8	NM_172151	down	0.0002	ns
10600114	Pnma3	paraneoplastic antigen MA3	NM_153169	down	0.0002	0.004
10465604	Stip1	stress-induced phosphoprotein 1	NM_016737	up	0.0002	0.006
10437778	Parn	poly(A)-specific ribonuclease (deadenylation nuclease)	NM_028761	down	0.0002	0.007
10573626	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	NM_173866	up	0.0002	ns
10545417	Mat2a	methionine adenosyltransferase II, alpha	NM_145569	up	0.0002	ns
10346943	Creb1	cAMP responsive element binding protein 1	NM_133828	up	0.0002	ns
10417972	Camk2g	calcium/calmodulin-dependent protein kinase II gamma	NM_178597	down	0.0002	0.02
10434675	Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	NM_026400	up	0.0002	0.02
10505779	Asah3l	N-acylsphingosine amidohydrolase 3-like	NM_139306	up	0.0002	ns
10450006	Hnrrpm	heterogeneous nuclear ribonucleoprotein M	NM_029804	up	0.0002	ns
10547386	Adipor2	adiponectin receptor 2	NM_197985	up	0.0002	ns
10550509	Pglyrp1	peptidoglycan recognition protein 1	NM_009402	up	0.0003	ns
10494160	Tmod4	tropomodulin 4	NM_016712	up	0.0003	0.03
10467206	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	NM_016854	up	0.0003	0.002

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10532680	Sgsm1	small G protein signaling modulator 1	NM_172718	up	0.0003	0.0005
10352905	Cd34	CD34 antigen	NM_001111059	down	0.0003	0.03
10496872	Eltf1	EGF, latrophilin seven transmembrane domain containing 1	NM_133222	up	0.0003	ns
10441456	Synj2	synaptojanin 2	NM_011523	up	0.0003	0.002
10553092	Dbp	D site albumin promoter binding protein	NM_016974	down	0.0003	ns
10429573	Ly6c1	lymphocyte antigen 6 complex, locus C1	NM_010741	up	0.0003	ns
10462454	Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	NM_144873	up	0.0003	ns
10577528	AI316807	expressed sequence AI316807	BC048089	down	0.0003	0.003
10475910	---	snoRNA chromosome:NCBIM37.2: 128606112: 128606235:1 gene:ENSMUSG00000064937	ENSMUST0000083003	up	0.0003	ns
10582664	2310022B05Rik	RIKEN cDNA 2310022B05 gene	BC058626	down	0.0003	ns
10544660	Osbpl3	oxysterol binding protein-like 3	NM_027881	up	0.0003	0.01
10363735	Egr2	early growth response 2	NM_010118	up	0.0003	ns
10390299	Pnpo	pyridoxine 5'-phosphate oxidase	NM_134021	down	0.0003	ns
10479672	Tcea2	transcription elongation factor A (SII), 2	NM_009326	down	0.0003	0.02
10576073	Banp	BTG3 associated nuclear protein	NM_001110100	up	0.0003	0.0007
10544583	Gimap6	GTPase, IMAP family member 6	NM_153175	up	0.0003	ns
10586184	Tipin	timeless interacting protein	NM_025372	down	0.0003	0.02
10557399	Sbk1	SH3-binding kinase 1	NM_145587	up	0.0003	0.0004
10449487	Slc26a8	solute carrier family 26, member 8	NM_146076	down	0.0004	0.007
10577048	Ankrd10	ankyrin repeat domain 10	NM_133971	up	0.0004	0.005
10377439	Per1	period homolog 1 (Drosophila)	NM_011065	up	0.0004	ns
10475890	Mertk	c-mer proto-oncogene tyrosine kinase	NM_008587	up	0.0004	ns
10447938	Dact2	dapper homolog 2, antagonist of beta-catenin (xenopus)	NM_172826	down	0.0004	ns
10530201	Ugdh	UDP-glucose dehydrogenase	NM_009466	up	0.0004	ns
10397518	Ahsa1	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)	NM_146036	up	0.0004	0.009
10600017	Hmgb3	high mobility group box 3	NM_008253	down	0.0004	0.008
10546137	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	NM_030251	down	0.0004	ns
10492428	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	NM_178892	up	0.0004	ns
10429754	Nrbp2	nuclear receptor binding protein 2	NM_144847	down	0.0004	ns
10579219	Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	NM_001024922	down	0.0004	ns
10474671	Spred1	sprouty protein with EVH-1 domain 1, related sequence	NM_033524	up	0.0004	0.008
10464819	Rbm14	RNA binding motif protein 14	NM_019869	up	0.0004	0.04
10488655	Bcl2l1	BCL2-like 1	NM_009743	up	0.0004	ns
10585428	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	NM_021422	up	0.0005	0.003
10420413	Lats2	large tumor suppressor 2	NM_015771	up	0.0005	0.02
10345074	Cetn4	centrin 4	BC087905	down	0.0005	0.02

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10562548	C80913	expressed sequence C80913	NM_011274	down	0.0005	0.006
10398147	Papola	poly (A) polymerase alpha	NM_011112	up	0.0005	ns
10460591	Fibp	fibroblast growth factor (acidic) intracellular binding protein	NM_021438	down	0.0005	0.05
10378482	Mett10d	methyltransferase 10 domain containing	NM_026197	up	0.0005	0.02
10604505	6720401G13Rik	RIKEN cDNA 6720401G13 gene	BC066100	down	0.0005	ns
10470959	Phyhd1	phytanoyl-CoA dioxygenase domain containing 1	NM_172267	up	0.0005	ns
10394358	BC068281	cDNA sequence BC068281	BC068281	up	0.0005	0.02
10531183	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.0005	ns
10587878	---	snoRNA chromosome:NCBIM37:9:95524879: 95525030:1 gene:ENSMUSG00000065346	ENSMUST0000083412	down	0.0005	0.02
10406672	Arsb	arylsulfatase B	NM_009712	down	0.0005	0.007
10419691	Mettl3	methyltransferase-like 3	NM_019721	up	0.0005	ns
10437399	Coro7	coronin 7	NM_030205	down	0.0005	ns
10350516	Ptgs2	prostaglandin-endoperoxide synthase 2	NM_011198	up	0.0005	ns
10469936	Nrarp	Notch-regulated ankyrin repeat protein	NM_025980	down	0.0005	ns
10399470	Trib2	tribbles homolog 2 (Drosophila)	NM_144551	up	0.0005	0.004
10569848	Stxbp2	syntaxin binding protein 2	NM_011503	down	0.0005	ns
10510574	Errfi1	ERBB receptor feedback inhibitor 1	NM_133753	up	0.0005	ns
10357043	Bcl2	B-cell leukemia/lymphoma 2	NM_009741	up	0.0005	0.03
10488029	Zfand1	zinc finger, AN1-type domain 1	NM_025512	down	0.0005	0.01
10452815	Xdh	xanthine dehydrogenase	NM_011723	up	0.0005	ns
10576971	Irs2	insulin receptor substrate 2	NM_001081212	up	0.0006	0.03
10352954	Hmgb3	high mobility group box 3	ENSMUST0000072699	down	0.0006	0.004
10557816	Bckdk	branched chain ketoacid dehydrogenase kinase	NM_009739	down	0.0006	0.04
10490872	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	NM_028915	down	0.0006	0.002
10413559	Rft1	RFT1 homolog (S. cerevisiae)	NM_177815	down	0.0006	ns
10395129	Tmem18	transmembrane protein 18	NM_172049	down	0.0006	0.02
10358658	Hmcn1	hemacentin 1	NM_001024720	down	0.0006	ns
10520842	Bre	brain and reproductive organ-expressed protein	NM_181279	down	0.0006	0.01
10588927	1700102P08Rik	RIKEN cDNA 1700102P08 gene	BC061048	up	0.0006	0.01
10449018	Haghl	hydroxyacylglutathione hydrolase-like	NM_026897	down	0.0006	ns
10445992	Shd	src homology 2 domain-containing transforming protein D	NM_009168	down	0.0006	ns
10531187	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.0006	0.004
10355464	Pecr	peroxisomal trans-2-enoyl-CoA reductase	NM_023523	down	0.0006	ns
10497689	Gnb4	guanine nucleotide binding protein (G protein), beta 4	NM_013531	down	0.0006	0.02
10352110	EG545391	predicted gene, EG545391	BC147679	down	0.0006	0.01

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10350758	ENSMUSG00000066798	predicted gene, ENSMUSG00000066798	AK080751	up	0.0007	ns
10368484	ENSMUSG00000056316	predicted gene, ENSMUSG00000056316	ENSMUST0000070359	down	0.0007	0.008
10473690	Fnbp4	formin binding protein 4	NM_018828	down	0.0007	ns
10400157	Nova1	neuro-oncological ventral antigen 1	ENSMUST0000021438	down	0.0007	ns
10399725	Sox11	SRY-box containing gene 11	NM_009234	up	0.0007	ns
10417561	BC055107	cDNA sequence BC055107	NM_183187	up	0.0007	ns
10406364	2210408121Rik	RIKEN cDNA 2210408121 gene	BC157949	down	0.0007	0.01
10544150	Jhdm1d	jumonji C domain-containing histone demethylase 1 homolog D (<i>S. cerevisiae</i>)	NM_001033430	up	0.0007	ns
10500042	Zfp687	zinc finger protein 687	NM_030074	down	0.0007	0.02
10475335	Pdia3	protein disulfide isomerase associated 3	NM_007952	up	0.0007	0.03
10551736	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	NM_026731	down	0.0007	ns
10447190	Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	NM_177606	up	0.0007	ns
10409629	EG627648	predicted gene, EG627648	ENSMUST0000091583	up	0.0007	0.007
10350506	B830045N13Rik	RIKEN cDNA B830045N13 gene	NM_153539	down	0.0007	0.04
10390691	Nr1d1	nuclear receptor subfamily 1, group D, member 1	NM_145434	down	0.0007	ns
10405001	Bicd2	bicaudal D homolog 2 (<i>Drosophila</i>)	NM_001039179	up	0.0007	ns
10406614	LOC238771	similar to Metaxin 1	AK090249	down	0.0007	0.006
10585214	Cryab	crystallin, alpha B	NM_009964	up	0.0008	0.007
10411532	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	NM_030026	down	0.0008	0.02
10505954	Tek	endothelial-specific receptor tyrosine kinase	NM_013690	down	0.0008	ns
10475199	Snap23	synaptosomal-associated protein 23	NM_009222	up	0.0008	ns
10400866	Trim9	tripartite motif-containing 9	NM_053167	up	0.0008	0.02
10442968	Rgs11	regulator of G-protein signaling 11	NM_001081069	down	0.0008	ns
10468802	D19ErtD737e	DNA segment, Chr 19, ERATO Doi 737, expressed	BC061459	down	0.0008	ns
10429568	Ly6c1	lymphocyte antigen 6 complex, locus C1	NM_010741	up	0.0008	ns
10438460	Parl	presenilin associated, rhomboid-like	NM_001005767	down	0.0008	0.04
10420216	2310014G06Rik	RIKEN cDNA 2310014G06 gene	NM_001082975	down	0.0008	ns
10583732	Ldlr	low density lipoprotein receptor	NM_010700	down	0.0008	ns
10358619	Hmcn1	hemicentin 1	NM_001024720	down	0.0008	ns
10379044	Rab34	RAB34, member of RAS oncogene family	NM_033475	down	0.0008	ns
10567725	Zkscan2	zinc finger with KRAB and SCAN domains 2	NM_001081	down	0.0008	0.001

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10376216	Slc36a1	solute carrier family 36 (proton/amino acid symporter), member 1	329 NM_153139	up	0.0008	0.03
10426891	Mettl7a1	methyltransferase like 7A1	NM_027334	up	0.0009	ns
10428796	Fbxo32	F-box protein 32	NM_026346	down	0.0009	ns
10585068	D930028F11Rik	RIKEN cDNA D930028F11 gene	BC094249	down	0.0009	0.02
10591763	Zfp810	zinc finger protein 810	NM_145612	down	0.0009	ns
10478854	Slc9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	NM_148929	down	0.0009	0.01
10497300	Zfand1	zinc finger, AN1-type domain 1	NM_025512	down	0.0009	0.009
10521391	Acox3	acyl-Coenzyme A oxidase 3, pristanoyl	NM_030721	down	0.0009	0.01
10508089	Mrps15	mitochondrial ribosomal protein S15	NM_025544	down	0.0009	ns
10584674	Mcam	melanoma cell adhesion molecule	NM_023061	down	0.0009	ns
10556242	---	snoRNA chromosome:NCBIM37:7:117166724: 117166856:1 gene:ENSMUSG00000064600	ENSMUST0 0000082666	up	0.0009	ns
10584576	Hspa8	heat shock protein 8	M13967	up	0.0009	0.009
10517948	Spen	SPEN homolog, transcriptional regulator (Drosophila)	NM_019763	up	0.0009	0.04
10504849	Stx17	syntaxin 17	NM_026343	down	0.0009	0.004
10436941	Mrps6	mitochondrial ribosomal protein S6	NM_080456	up	0.0009	0.03
10556581	ENSMUSG0000 0073861	predicted gene, ENSMUSG00000073861	ENSMUST0 0000098096	up	0.0009	ns
10382271	Arsg	arylsulfatase G	NM_028710	down	0.0009	0.03
10531179	Adamts3	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081 401	down	0.0009	0.01
10472598	Klhl23	kelch-like 23 (Drosophila)	NM_177784	down	0.0009	0.04
10456046	Pdgfrb	platelet derived growth factor receptor, beta polypeptide	NM_008809	down	0.0009	ns
10387525	Mpdu1	mannose-P-dolichol utilization defect 1	NM_011900	down	0.001	ns
10354816	Clk1	CDC-like kinase 1	NM_001042 634	up	0.001	ns
10378857	Coro6	coronin, actin binding protein 6	NM_139128	down	0.001	ns
10379840	Myo19	myosin XIX	BC007156	up	0.001	0.004
10584578	Hspa8	heat shock protein 8	M13967	up	0.001	0.008
10476759	Rin2	Ras and Rab interactor 2	NM_028724	up	0.001	ns
10585206	Pih1d2	PIH1 domain containing 2	NM_028300	down	0.001	ns
10503334	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	NM_010276	up	0.001	ns
10419854	Slc7a8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	NM_016972	down	0.001	0.01
10562576	Plekhf1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	NM_024413	up	0.001	ns
10416251	Egr3	early growth response 3	NM_018781	up	0.001	0.0002
10375240	Hspd1	heat shock protein 1 (chaperonin)	NM_010477	up	0.001	ns
10503023	Cth	cystathionase (cystathionine gamma-lyase)	NM_145953	up	0.001	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10549760	Zfp580	zinc finger protein 580	BC066001	down	0.001	0.02
10520362	Insig1	insulin induced gene 1	NM_153526	down	0.001	ns
10376017	ENSMUSG00000054450	predicted gene, ENSMUSG00000054450	ENSMUST0000067523	up	0.001	ns
10478073	---	snoRNA chromosome:NCBIM37:2:158203958:158204090:1 gene:ENSMUSG00000065840	ENSMUST0000083906	down	0.001	ns
10426169	1300018J18Rik	RIKEN cDNA 1300018J18 gene	NM_027905	down	0.001	ns
10375880	Nola2	nucleolar protein family A, member 2	NM_026631	down	0.001	ns
10345183	Cdk10	cyclin-dependent kinase (CDC2-like) 10	NM_194446	down	0.001	ns
10383518	Hexdc	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	NM_001001333	down	0.001	0.04
10593430	Snf1lk2	SNF1-like kinase 2	NM_178710	up	0.001	0.002
10410709	Rfesd	Rieske (Fe-S) domain containing	NM_178916	down	0.001	ns
10532150	2900024C23Rik	RIKEN cDNA 2900024C23 gene	BC116683	down	0.001	ns
10458555	Spry4	sprouty homolog 4 (Drosophila)	NM_011898	up	0.001	0.004
10438478	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	NM_013790	up	0.001	0.03
10569203	Chid1	chitinase domain containing 1	NM_026522	down	0.001	ns
10491780	Hspa4l	heat shock protein 4 like	NM_011020	up	0.001	0.04
10550833	Zfp180	zinc finger protein 180	NM_001045486	up	0.001	0.04
10531185	Adamts3	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.001	0.006
10420366	Gjb6	gap junction protein, beta 6	NM_001010937	up	0.001	ns
10556381	Mical2	microtubule associated monooxygenase, calponin and LIM domain containing 2	NM_177282	up	0.001	0.005
10547100	Plxnd1	plexin D1	NM_026376	down	0.001	ns
10369290	Ddit4	DNA-damage-inducible transcript 4	NM_029083	up	0.001	ns
10449452	Fkbp5	FK506 binding protein 5	NM_010220	up	0.001	ns
10518957	Dffb	DNA fragmentation factor, beta subunit	NM_007859	down	0.001	ns
10455852	Prrc1	proline-rich coiled-coil 1	NM_028447	down	0.001	ns
10599192	Lonrf3	LON peptidase N-terminal domain and ring finger 3	NM_028894	up	0.001	ns
10359334	Cacybp	calcyclin binding protein	NM_009786	up	0.001	ns
10494467	Itga10	integrin, alpha 10	NM_001081053	up	0.001	ns
10450369	Hspa1a	heat shock protein 1A	NM_010479	up	0.001	0.04
10560329	Hif3a	hypoxia inducible factor 3, alpha subunit	NM_016868	up	0.001	ns
10411287	Btf3l4	basic transcription factor 3-like 4	ENSMUST0000102742	down	0.001	0.01
10385203	Odz2	odd Oz/ten-m homolog 2 (Drosophila)	NM_011856	down	0.001	ns
10381260	Tubg2	tubulin, gamma 2	NM_134028	down	0.001	ns

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10443108	Syngap1	synaptic Ras GTPase activating protein 1 homolog (rat)	XM_915205	down	0.001	ns
10457963	Gpr17	G protein-coupled receptor 17	NM_001025381	up	0.001	ns
10557843	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	NM_139149	down	0.001	ns
10481155	Rexo4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	NM_207234	up	0.001	ns
10372844	Rassf3	Ras association (RalGDS/AF-6) domain family member 3	NM_138956	down	0.001	ns
10360139	Klhdc9	kelch domain containing 9	NM_001033039	down	0.001	0.01
10558773	B4galnt4	beta-1,4-N-acetyl-galactosaminyl transferase 4	NM_177897	down	0.001	ns
10532803	Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	NM_198899	up	0.001	0.03
10451198	Vegfa	vascular endothelial growth factor A	NM_001025250	up	0.001	8.56e-05
10501235	Gstm4	glutathione S-transferase, mu 4	NM_026764	down	0.002	ns
10552622	2410002F23Rik	RIKEN cDNA 2410002F23 gene	BC059896	down	0.002	ns
10378024	Mis12	MIS12 homolog (yeast)	NM_025993	up	0.002	ns
10488472	2310001A20Rik	RIKEN cDNA 2310001A20 gene	AJ310638	down	0.002	0.04
10528021	Hspa8	heat shock protein 8	NM_031165	up	0.002	0.01
10559420	Tmc4	transmembrane channel-like gene family 4	NM_181820	up	0.002	ns
10381361	Aoc2	amine oxidase, copper containing 2 (retina-specific)	NM_178932	up	0.002	ns
10379615	Slnf5	schlafen 5	NM_183201	up	0.002	ns
10376555	ENSMUSG0000072890	predicted gene, ENSMUSG0000072890	AK144909	up	0.002	ns
10592830	Vps11	vacuolar protein sorting 11 (yeast)	NM_027889	down	0.002	0.04
10450796	EG667915	predicted gene, EG667915	XF_034307	down	0.002	ns
10552812	Irf3	interferon regulatory factor 3	NM_016849	up	0.002	0.003
10597493	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	NM_024222	up	0.002	ns
10349174	Serpib8	serine (or cysteine) peptidase inhibitor, clade B, member 8	NM_011459	up	0.002	ns
10379968	Tubd1	tubulin, delta 1	NM_019756	up	0.002	0.02
10361754	Epm2a	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	NM_010146	down	0.002	ns
10385790	Hspa4	heat shock protein 4	NM_008300	up	0.002	ns
10408490	Exoc2	exocyst complex component 2	NM_025588	down	0.002	0.02
10478615	Pcif1	PDX1 C-terminal inhibiting factor 1	NM_146129	down	0.002	ns
10400109	Zfp277	zinc finger protein 277	NM_172575	down	0.002	ns
10577882	Hgsnat	heparan-alpha-glucosaminide N-acetyltransferase	NM_029884	down	0.002	ns
10557508	Doc2a	double C2, alpha	NM_010069	down	0.002	ns
10451955	Sema6b	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	NM_013662	down	0.002	ns
10451974	Sema6b	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	NM_013662	down	0.002	ns
10556076	Olfml1	olfactomedin-like 1	NM_172907	down	0.002	ns

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10554269	Abhd2	Abhydrolase domain containing 2	NM_018811	down	0.002	ns
10378545	---	MI0000696 Mus musculus miR-212 stem-loop	---	up	0.002	0.009
10362394	Hddc2	HD domain containing 2	NM_027168	down	0.002	0.04
10515335	C530005A16Rik	RIKEN cDNA C530005A16 gene	AK039789	down	0.002	ns
10351769	Igsf8	immunoglobulin superfamily, member 8	NM_080419	down	0.002	ns
10531191	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.002	0.01
10505132	Akap2	A kinase (PRKA) anchor protein 2	NM_001035533	down	0.002	ns
10516529	Adc	arginine decarboxylase	NM_172875	down	0.002	ns
10489723	Prkcbp1	protein kinase C binding protein 1	NM_027230	up	0.002	0.03
10551989	Tmem149	transmembrane protein 149	NM_145580	up	0.002	0.02
10468639	Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	NM_018831	down	0.002	ns
10509838	Padi2	peptidyl arginine deiminase, type II	NM_008812	down	0.002	0.01
10460221	Chka	choline kinase alpha	NM_013490	up	0.002	ns
10487871	Cenpb	centromere protein B	NM_007682	down	0.002	ns
10382376	Ttyh2	tweety homolog 2 (Drosophila)	NM_053273	down	0.002	ns
10455588	Hspe1	heat shock protein 1 (chaperonin 10)	ENSMUST0000075242	up	0.002	ns
10382010	Wdr68	WD repeat domain 68	NM_027946	down	0.002	0.02
10529937	Kcnip4	Kv channel interacting protein 4	NM_030265	down	0.002	0.01
10534694	Ars2	arsenate resistance protein 2	NM_031405	up	0.002	0.009
10399208	Tmem196	transmembrane protein 196	ENSMUST0000058644	down	0.002	0.009
10474619	Fmn1	formin 1	NM_010230	down	0.002	ns
10565018	Iqgap1	IQ motif containing GTPase activating protein 1	NM_016721	up	0.002	ns
10371591	4930547N16Rik	RIKEN cDNA 4930547N16 gene	NM_029249	down	0.002	ns
10476252	Cdc25b	cell division cycle 25 homolog B (S. pombe)	NM_023117	down	0.002	ns
10462363	Jak2	Janus kinase 2	NM_008413	up	0.002	ns
10409278	Nfil3	nuclear factor, interleukin 3, regulated	NM_017373	up	0.002	0.005
10568897	Tubgcp2	tubulin, gamma complex associated protein 2	NM_133755	down	0.002	ns
10458843	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	NM_018744	down	0.002	ns
10491486	Atp11b	ATPase, class VI, type 11B	NM_029570	down	0.002	0.001
10376004	Gdf9	growth differentiation factor 9	NM_008110	up	0.002	ns
10461115	Slc22a8	solute carrier family 22 (organic anion transporter), member 8	NM_031194	down	0.002	ns
10407993	Fusip1	FUS interacting protein (serine-arginine rich) 1	NM_001080387	up	0.002	ns
10449061	Rhbdl1	rhomboid, veinlet-like 1 (Drosophila)	NM_144816	down	0.002	ns
10544148	Jhdm1d	jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)	NM_001033430	up	0.002	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10498620	Trim59	tripartite motif-containing 59	NM_025863	down	0.002	ns
10457665	4921533120Rik	Riken cDNA 4921533120 gene	AK076609	up	0.002	ns
10406817	Enc1	ectodermal-neural cortex 1	NM_007930	up	0.002	0.009
10363333	Sh3rf3	SH3 domain containing ring finger 3	NM_172788	up	0.002	ns
10424062	A930017M01Rik	RIKEN cDNA A930017M01 gene	XR_035330	down	0.002	ns
10361270	Cd46	CD46 antigen, complement regulatory protein	NM_010778	down	0.002	0.01
10482766	Rprm	reprimo, TP53 dependent G2 arrest mediator candidate	NM_023396	down	0.002	0.03
10420372	Cryl1	crystallin, lambda 1	NM_030004	down	0.002	ns
10556246	Zfp143	zinc finger protein 143	NM_009281	up	0.002	ns
10526559	Ache	acetylcholinesterase	NM_009599	down	0.002	ns
10543466	Gpr37	G protein-coupled receptor 37	NM_010338	down	0.002	ns
10385004	Mare	alpha globin regulatory element containing gene	NM_181569	down	0.002	ns
10388938	Wsb1	WD repeat and SOCS box-containing 1	NM_019653	down	0.002	ns
10451932	S3-12	plasma membrane associated protein, S3-12	NM_020568	up	0.002	ns
10346303	Hspe1	heat shock protein 1 (chaperonin 10)	NM_008303	up	0.002	ns
10451650	Nfya	nuclear transcription factor-Y alpha	NM_001110832	up	0.002	ns
10531645	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	NM_016690	down	0.002	ns
10344817	Cspp1	centrosome and spindle pole associated protein 1	NM_026493	down	0.002	0.001
10565775	Dgat2	diacylglycerol O-acyltransferase 2	NM_026384	down	0.002	ns
10495945	4930422G04Rik	RIKEN cDNA 4930422G04 gene	BC030185	down	0.002	ns
10504375	Npr2	natriuretic peptide receptor 2	NM_173788	down	0.003	ns
10533026	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	NM_031869	down	0.003	ns
10498952	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	NM_021896	down	0.003	0.02
10478291	Sfrs6	splicing factor, arginine/serine-rich 6	NM_026499	up	0.003	ns
10492774	Dchs2	dachsous 2 (Drosophila)	ENSMUST0000116329	down	0.003	0.004
10588326	Nphp3	nephronophthisis 3 (adolescent)	NM_028721	down	0.003	ns
10472630	Ubr3	ubiquitin protein ligase E3 component n-recognin 3	NM_001081548	down	0.003	0.01
10499438	Msto1	misato homolog 1 (Drosophila)	NM_144898	down	0.003	ns
10418604	Phf7	PHD finger protein 7	NM_027949	down	0.003	ns
10450845	Mog	myelin oligodendrocyte glycoprotein	NM_010814	down	0.003	ns
10581036	Tk2	thymidine kinase 2, mitochondrial	NM_021028	down	0.003	ns
10404885	Gmpr	guanosine monophosphate reductase	NM_025508	down	0.003	ns
10552656	Syt3	synaptotagmin III	NM_016663	down	0.003	ns
10399337	Klhl29	kelch-like 29 (Drosophila)	BC145748	up	0.003	0.03
10386636	Usp22	ubiquitin specific peptidase 22	NM_001004143	down	0.003	ns
10369704	Hnrmph3	heterogeneous nuclear ribonucleoprotein H3	NM_001079824	up	0.003	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10408755	Muted	muted	NM_139063	down	0.003	ns
10485282	Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	NM_026944	down	0.003	ns
10543737	Copg2	coatamer protein complex, subunit gamma 2	NM_017478	down	0.003	0.04
10345203	Paox	polyamine oxidase (exo-N4-amino)	NM_153783	down	0.003	ns
10397651	Spata7	spermatogenesis associated 7	NM_178914	down	0.003	ns
10547469	Hsn2	hereditary sensory neuropathy, type II	NM_001037155	down	0.003	0.05
10357814	Zc3h11a	zinc finger CCCH type containing 11A	NM_144530	up	0.003	ns
10579341	BC051227	cDNA sequence BC051227	BC051227	down	0.003	ns
10455092	Pcdhb12	protocadherin beta 12	NM_053137	down	0.003	0.01
10502823	Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	NM_025926	up	0.003	ns
10528102	Crot	carnitine O-octanoyltransferase	NM_023733	up	0.003	ns
10575598	Znrf1	zinc and ring finger 1	NM_133206	up	0.003	0.01
10561673	Spred3	sprouty-related, EVH1 domain containing 3	NM_182927	up	0.003	0.0009
10386455	Rasd1	RAS, dexamethasone-induced 1	NM_009026	up	0.003	0.04
10431463	1700027J05Rik	RIKEN cDNA 1700027J05 gene	NM_027081	down	0.003	ns
10347697	Slc4a3	solute carrier family 4 (anion exchanger), member 3	NM_009208	down	0.003	ns
10436282	Impg2	interphotoreceptor matrix proteoglycan 2	NM_174876	up	0.003	ns
10385239	Mat2b	methionine adenosyltransferase II, beta	NM_134017	down	0.003	ns
10347781	9430031J16Rik	RIKEN cDNA 9430031J16 gene	BC082310	down	0.003	ns
10359582	Fmo2	flavin containing monooxygenase 2	NM_018881	up	0.004	ns
10410477	Adamts16	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16	NM_172053	down	0.004	ns
10598138	Spry3	sprouty homolog 3 (Drosophila)	NM_001030293	up	0.004	ns
10549615	Leng8	leukocyte receptor cluster (LRC) member 8	NM_172736	down	0.004	ns
10535732	Gpr12	G-protein coupled receptor 12	NM_001010941	down	0.004	ns
10434880	Hrasls *	HRAS-like suppressor	NM_013751	down	0.004	ns
10478341	Ift52	intraflagellar transport 52 homolog (Chlamydomonas)	NM_172150	down	0.004	ns
10579508	Ano8	anoctamin 8	AK173222	down	0.004	ns
10590389	Nktr	natural killer tumor recognition sequence	NM_010918	up	0.004	ns
10350733	Rgs16	regulator of G-protein signaling 16	NM_011267	up	0.004	ns
10576258	Cdk10	cyclin-dependent kinase (CDC2-like) 10	NM_194446	down	0.004	ns
10586110	Cln6	ceroid-lipofuscinosis, neuronal 6	NM_001033175	down	0.004	0.01
10361007	Smyd2	SET and MYND domain containing 2	NM_026796	down	0.004	ns
10468990	Parl	presenilin associated, rhomboid-like	NM_001005767	down	0.004	0.0005
10561212	Ltbp4	latent transforming growth factor beta binding protein 4	NM_175641	down	0.004	ns
10492396	Vmn2r1	vomer nasal 2, receptor 1	NM_019918	down	0.004	ns

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10383289	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	NM_130862	up	0.004	0.008
10411882	Nln	neurolysin (metallopeptidase M3 family)	NM_029447	down	0.004	ns
10401900	Sei1l	sel-1 suppressor of lin-12-like (C. elegans)	NM_001039089	up	0.004	0.04
10381539	G6pc3	glucose 6 phosphatase, catalytic, 3	NM_175935	down	0.004	ns
10415052	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	NM_008608	down	0.004	ns
10601099	Med12	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	NM_021521	down	0.004	ns
10374590	Xpo1	exportin 1, CRM1 homolog (yeast)	NM_134014	up	0.004	ns
10448459	Tbc1d24	TBC1 domain family, member 24	NM_173186	down	0.004	ns
10583586	Slc44a2	solute carrier family 44, member 2	NM_152808	down	0.004	ns
10384672	Ahsa2	AHA1, activator of heat shock protein ATPase homolog 2 (yeast)	NM_172391	up	0.004	ns
10504918	Zfp189	zinc finger protein 189	NM_145547	up	0.004	ns
10546760	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	BC083059	down	0.004	ns
10429329	Eif2c2	eukaryotic translation initiation factor 2C, 2	NM_153178	up	0.004	ns
10531173	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.004	ns
10590245	Slc25a38	solute carrier family 25, member 38	NM_144793	up	0.004	0.01
10479884	OTTMUSG0000010878	predicted gene, OTTMUSG00000010878	ENSMUST0000071016	up	0.004	0.04
10478075	---	snoRNA chromosome:NCBIM37.2:158205270:158205402:1 gene:ENSMUSG00000064585	ENSMUST0000082651	down	0.004	0.03
10444936	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	NM_026987	up	0.004	0.02
10522160	N4bp2	NEDD4 binding protein 2	NM_001024917	up	0.004	ns
10548735	Dusp16	dual specificity phosphatase 16	NM_130447	down	0.004	ns
10495621	---	MI0000163 Mus musculus miR-137 stem-loop	---	down	0.004	ns
10441280	Prdm15	PR domain containing 15	BC046433	up	0.004	0.002
10525718	Arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4	NM_144509	down	0.005	ns
10363563	Slc25a16	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	NM_175194	down	0.005	ns
10489484	Sdc4	syndecan 4	NM_011521	up	0.005	ns
10529385	Zfyve28	zinc finger, FYVE domain containing 28	NM_001015039	down	0.005	ns
10530029	Lgi2	leucine-rich repeat LGI family, member 2	NM_144945	down	0.005	ns
10386394	BC050078	cDNA sequence BC050078	BC050078	down	0.005	ns
10577641	1810011O10Rik	RIKEN cDNA 1810011O10 gene	NM_026931	up	0.005	ns
10522250	Tmem33	transmembrane protein 33	NM_028975	up	0.005	ns
10517744	Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like	NM_172415	down	0.005	ns
10427816	Pdzd2	PDZ domain containing 2	NM_001081	up	0.005	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
			064			
10512915	2810432L12Rik	RIKEN cDNA 2810432L12 gene	BC013800	down	0.005	ns
10594426	Zwilch	Zwilch, kinetochore associated, homolog (Drosophila)	NM_026507	down	0.005	0.01
10601360	Atp7a	ATPase, Cu ⁺⁺ transporting, alpha polypeptide	NM_001109757	up	0.005	ns
10497417	Crh	corticotropin releasing hormone	NM_205769	up	0.005	ns
10571657	Acs11	acyl-CoA synthetase long-chain family member 1	NM_007981	down	0.005	ns
10564978	Blm	Bloom syndrome homolog (human)	NM_007550	down	0.005	ns
10490097	Cbln4	cerebellin 4 precursor protein	NM_175631	up	0.005	0.02
10607806	Ofd1	oral-facial-digital syndrome 1 gene homolog (human)	NM_177429	down	0.005	0.03
10521331	A930005I04Rik	RIKEN cDNA A930005I04 gene	BC116928	up	0.005	ns
10585874	Hexa	hexosaminidase A	NM_010421	up	0.005	0.02
10571274	Gsr	glutathione reductase	NM_010344	down	0.005	ns
10527332	Nptx2	neuronal pentraxin 2	NM_016789	up	0.005	0.006
10416279	Lgi3	leucine-rich repeat LGI family, member 3	NM_145219	down	0.005	ns
10597564	Cmc1	COX assembly mitochondrial protein homolog (S. cerevisiae)	ENSMUSTO000044220	down	0.005	ns
10392464	BC029169	cDNA sequence BC029169	BC029169	up	0.005	ns
10520154	Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	NM_029020	down	0.005	ns
10545629	Htra2	Htra serine peptidase 2	NM_019752	down	0.005	ns
10594645	Rab8b	RAB8B, member RAS oncogene family	NM_173413	up	0.005	ns
10584634	Usp2	ubiquitin specific peptidase 2	NM_198092	down	0.005	0.04
10395376	Ankmy2	ankyrin repeat and MYND domain containing 2	NM_146033	down	0.005	ns
10372342	Nav3	neuron navigator 3	NM_001081035	down	0.005	0.01
10388520	Glod4	glyoxalase domain containing 4	NM_026029	down	0.005	ns
10478897	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	NM_011201	up	0.005	0.03
10569134	Deaf1	deformed epidermal autoregulatory factor 1 (Drosophila)	NM_016874	down	0.005	ns
10468329	Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	NM_175360	down	0.005	ns
10582429	Cbfa2t3	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	NM_009824	up	0.005	0.005
10522303	Guf1	GUF1 GTPase homolog (S. cerevisiae)	NM_172711	down	0.005	ns
10568948	Sprn	shadow of prion protein	NM_183147	down	0.005	ns
10561004	Erf	Ets2 repressor factor	NM_010155	down	0.005	ns
10531166	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.005	0.02
10393620	Cbx4	chromobox homolog 4 (Drosophila Pc class)	NM_007625	down	0.005	ns
10559825	2810409K11Rik	RIKEN cDNA 2810409K11 gene	BC117497	up	0.005	ns
10578109	Ubxn8	UBX domain protein 8	NM_178648	down	0.005	ns
10596053	Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	NM_025835	down	0.005	ns
10453867	Rbbp8	retinoblastoma binding protein 8	NM_001081	down	0.005	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10584862	Scn4b	sodium channel, type IV, beta	223 NM_001013390	down	0.005	ns
10521626	Cc2d2a	coiled-coil and C2 domain containing 2A	NM_172274	down	0.005	ns
10507418	Eif2b3	eukaryotic translation initiation factor 2B, subunit 3	NM_001111277	down	0.006	ns
10600034	Gm1141	gene model 1141, (NCBI)	ENSMUST0000101495	up	0.006	ns
10378902	Nufip2	nuclear fragile X mental retardation protein interacting protein 2	NM_001024205	up	0.006	ns
10460359	Coro1b	coronin, actin binding protein 1B	NM_011778	down	0.006	ns
10416640	Mtrf1	mitochondrial translational release factor 1	NM_145960	down	0.006	ns
10377790	Slc16a11	solute carrier family 16 (monocarboxylic acid transporters), member 11	NM_153081	down	0.006	ns
10549552	Prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	NM_027328	down	0.006	ns
10589413	Nme6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	NM_018757	down	0.006	ns
10487945	Prei4	preimplantation protein 4	NM_028802	down	0.006	0.01
10424349	Sqle	squalene epoxidase	NM_009270	down	0.006	ns
10344713	Ahcy	S-adenosylhomocysteine hydrolase	L32836	down	0.006	ns
10558057	Brwd2	bromodomain and WD repeat domain containing 2	NM_172255	down	0.006	0.03
10479833	Optn	optineurin	NM_181848	down	0.006	ns
10604922	BC023829	cDNA sequence BC023829	NM_001033328	up	0.006	ns
10514000	Mpdz	multiple PDZ domain protein	NM_010820	up	0.006	ns
10430834	Naga	N-acetyl galactosaminidase, alpha	NM_008669	down	0.006	ns
10436830	Ifnar2	interferon (alpha and beta) receptor 2	NM_010509	down	0.006	ns
10513608	Alad	aminolevulinatase, delta-, dehydratase	NM_008525	down	0.006	ns
10397507	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	NM_010363	down	0.006	ns
10364194	Lss	lanosterol synthase	NM_146006	down	0.006	0.03
10368025	Hspa8	heat shock protein 8	NM_031165	up	0.006	0.04
10479026	Rae1	RAE1 RNA export 1 homolog (S. pombe)	NM_175112	down	0.006	ns
10595298	Filip1	filamin A interacting protein 1	NM_001081243	down	0.006	ns
10508490	Sfrs5	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	NM_001079694	down	0.006	0.005
10448016	Tcte3	t-complex-associated testis expressed 3	NM_011560	down	0.006	ns
10425207	H1f0	H1 histone family, member 0	NM_008197	down	0.006	ns
10578763	Sap30	sin3 associated polypeptide	NM_021788	up	0.006	ns
10460468	Ctsf	cathepsin F	NM_019861	down	0.006	ns
10487906	Slc23a2	solute carrier family 23 (nucleobase transporters), member 2	NM_018824	down	0.006	0.04
10448559	---	---	ENSMUST0	up	0.006	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
			0000084725			
10354374	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	NM_016917	down	0.006	ns
10414522	Apex1	apurinic/apyrimidinic endonuclease 1	NM_009687	down	0.006	ns
10483081	Fap	fibroblast activation protein	NM_007986	down	0.006	ns
10528120	Dmtf1	cyclin D binding myb-like transcription factor 1	NM_011806	up	0.007	ns
10580870	Zfp319	zinc finger protein 319	ENSMUST0000098479	up	0.007	ns
10430711	Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	NM_011399	down	0.007	ns
10577388	---	cdna:Genscan supercontig:NCBIM37:NT_166309:110939:130509:-1	GENSCAN0000018646	down	0.007	0.02
10394690	E2f6	E2F transcription factor 6	NM_033270	up	0.007	ns
10473125	Itga4	integrin alpha 4	NM_010576	down	0.007	0.02
10394331	Pfn4	profilin family, member 4	NM_028376	down	0.007	0.007
10597095	3000002C10Rik	RIKEN cDNA 3000002C10 gene	BC061210	down	0.007	0.03
10378453	1300001101Rik	RIKEN cDNA 1300001101 gene	BC072573	down	0.007	ns
10405211	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	NM_011817	up	0.007	ns
10404595	Ppp1r3g	protein phosphatase 1, regulatory (inhibitor) subunit 3G	XM_127272	up	0.007	ns
10518408	Plod1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	NM_011122	up	0.007	ns
10354432	Myo1b	myosin IB	NM_010863	down	0.007	0.008
10483809	Nfe2l2	nuclear factor, erythroid derived 2, like 2	NM_010902	up	0.007	ns
10533444	4930565B19Rik	RIKEN cDNA 4930565B19 gene	ENSMUST0000100746	up	0.007	ns
10360884	Iars2	isoleucine-tRNA synthetase 2, mitochondrial	NM_198653	down	0.007	ns
10575867	Mlycd	malonyl-CoA decarboxylase	NM_019966	up	0.007	0.005
10574087	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	NM_022331	up	0.007	0.04
10562152	Mag	myelin-associated glycoprotein	NM_010758	down	0.007	ns
10344807	Cspp1	centrosome and spindle pole associated protein 1	NM_026493	up	0.007	ns
10416533	Ccdc122	coiled-coil domain containing 122	NM_175369	down	0.007	ns
10386473	Sreb1	sterol regulatory element binding transcription factor 1	NM_011480	down	0.007	ns
10521090	Tacc3	transforming, acidic coiled-coil containing protein 3	NM_001040435	down	0.007	ns
10582477	Spata2L	spermatogenesis associated 2-like	NM_030176	up	0.007	0.01
10378848	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	NM_010480	up	0.007	ns
10578071	Wrn	Werner syndrome homolog (human)	NM_011721	down	0.007	0.01
10540028	Klf15	Kruppel-like factor 15	NM_023184	up	0.007	ns
10355205	D630023F18Rik	RIKEN cDNA D630023F18 gene	BC137870	down	0.007	0.02
10498367	P2ry13	purinergic receptor P2Y, G-protein coupled 13	NM_028808	down	0.007	ns
10354598	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	NM_001001883	down	0.007	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10505213	E130308A19Rik	RIKEN cDNA E130308A19 gene	NM_153158	up	0.007	ns
10380067	Sept4	septin 4	NM_011129	down	0.007	ns
10587627	Cyb5r4	cytochrome b5 reductase 4	NM_024195	up	0.007	ns
10545897	Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	NM_028099	up	0.007	0.01
10542872	Rps4y2	ribosomal protein S4, Y-linked 2	NR_003634	down	0.007	ns
10423745	Spag1	sperm associated antigen 1	NM_012031	up	0.007	ns
10519354	Pex1	peroxisome biogenesis factor 1	NM_027777	up	0.007	ns
10432439	Fmnl3	formin-like 3	NM_011711	down	0.008	ns
10516348	Eif2c3	eukaryotic translation initiation factor 2C, 3	NM_153402	up	0.008	ns
10402615	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	NM_010480	up	0.008	ns
10360912	EG677785	predicted gene, EG677785	XR_032381	down	0.008	ns
10556413	Mical1	MICAL C-terminal like	AB359922	up	0.008	ns
10401063	Zbtb25	zinc finger and BTB domain containing 25	NM_028356	down	0.008	ns
10557035	Polr3e	polymerase (RNA) III (DNA directed) polypeptide E	NM_025298	down	0.008	ns
10508115	Stk40	serine/threonine kinase 40	NM_028800	up	0.008	0.04
10591781	Anln	anillin, actin binding protein	NM_028390	up	0.008	ns
10416541	Enox1	ecto-NOX disulfide-thiol exchanger 1	NM_172813	up	0.008	ns
10444431	Prrt1	proline-rich transmembrane protein 1	NM_030890	up	0.008	0.004
10603387	Hdac6	histone deacetylase 6	NM_010413	down	0.008	ns
10378568	---	MI0000570 Mus musculus miR-22 stem-loop	---	down	0.008	ns
10408557	Serp1b1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	NM_025429	down	0.008	ns
10548105	Ccnd2	cyclin D2	NM_009829	up	0.008	ns
10362201	Ctgf	connective tissue growth factor	NM_010217	up	0.008	ns
10374430	Wdr92	WD repeat domain 92	NM_178909	up	0.008	ns
10449163	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	NM_011822	down	0.008	ns
10434934	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	NM_175177	down	0.008	ns
10596900	Tcta	T-cell leukemia translocation altered gene	NM_133986	down	0.008	ns
10480971	Snpc4	small nuclear RNA activating complex, polypeptide 4	NM_172339	down	0.008	ns
10495416	Vav3	vav 3 oncogene	NM_020505	up	0.008	ns
10602925	Phka2	phosphorylase kinase alpha 2	NM_172783	down	0.008	ns
10419261	Bmp4	bone morphogenetic protein 4	NM_007554	up	0.008	ns
10461191	Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	NM_016813	up	0.008	ns
10503995	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	NM_008298	up	0.008	ns
10603206	BC022960	cDNA sequence BC022960	ENSMUST0000052299	down	0.008	ns
10471154	Ass1	argininosuccinate synthetase 1	NM_007494	down	0.008	ns
10406434	Mef2c	myocyte enhancer factor 2C	NM_025282	down	0.008	0.04
10591537	Tmed1	transmembrane emp24 domain containing 1	NM_010744	down	0.008	ns
10544720	Hnrnpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	NM_016806	up	0.008	ns
10481378	---	MI0000741 Mus musculus miR-219-2 stem-loop	---	down	0.009	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10356628	Hdac4	histone deacetylase 4	NM_207225	up	0.009	ns
10580247	Mast1	microtubule associated serine/threonine kinase 1	NM_019945	down	0.009	ns
10461057	Rcor2	REST corepressor 2	NM_054048	down	0.009	ns
10560911	Rabac1	Rab acceptor 1 (prenylated)	NM_010261	down	0.009	ns
10539933	Txnrd3	thioredoxin reductase 3	NM_153162	down	0.009	ns
10560043	Zfp329	zinc finger protein 329	NM_026046	up	0.009	ns
10454564	Ercc3	excision repair cross-complementing rodent repair deficiency, complementation group 3	NM_133658	down	0.009	ns
10597883	Ano10	anoctamin 10	NM_133979	down	0.009	0.05
10557058	Polr3e	polymerase (RNA) III (DNA directed) polypeptide E	ENSMUST0000098072	up	0.009	ns
10462752	Btaf1	BTA1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, <i>S. cerevisiae</i>)	NM_001080706	up	0.009	ns
10509014	D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	BC043057	down	0.009	ns
10554521	Pde8a	phosphodiesterase 8A	NM_008803	down	0.009	ns
10398578	4930573119Rik	RIKEN cDNA 4930573119 gene	NM_001081057	down	0.009	ns
10497754	Dnajc19	DnaJ (Hsp40) homolog, subfamily C, member 19	NM_026332	down	0.009	ns
10488575	Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	NM_212446	down	0.009	ns
10429957	Fbxl6	F-box and leucine-rich repeat protein 6	NM_013909	down	0.009	ns
10590865	Cntn5	contactin 5	ENSMUST0000074133	down	0.009	0.04
10419049	Nrg3	neuregulin 3	NM_008734	down	0.009	0.05
10366476	Ptpnb	protein tyrosine phosphatase, receptor type, B	NM_029928	down	0.009	ns
10577441	Defb9	defensin beta 9	NM_139219	up	0.009	ns
10399465	Fam84a	family with sequence similarity 84, member A	NM_029007	up	0.009	ns
10526191	Gats	opposite strand transcription unit to Stag3	BC026208	up	0.009	ns
10512704	Exosc3	exosome component 3	NM_025513	up	0.009	ns
10508019	Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)	NM_145552	down	0.01	ns
10476633	Pcsk2	proprotein convertase subtilisin/kexin type 2	NM_008792	down	0.01	0.04
10540659	Ttl3	tubulin tyrosine ligase-like family, member 3	NM_133923	up	0.01	0.02
10467468	ENSMUSG00000074878	predicted gene, ENSMUSG00000074878	AK132080	up	0.01	ns
10351749	Wdr42a	WD repeat domain 42A	NM_153555	down	0.01	ns
10363541	Ass1	argininosuccinate synthetase 1	NM_007494	down	0.01	ns
10419825	Acin1	apoptotic chromatin condensation inducer 1	NM_023190	up	0.01	ns
10346882	Adam23	a disintegrin and metalloproteinase domain 23	NM_011780	down	0.01	0.05
10567229	2610207105Rik	RIKEN cDNA 2610207105 gene	NM_001031814	up	0.01	ns
10398618	Traf3	Tnf receptor-associated factor 3	NM_011632	up	0.01	ns
10458285	5133400G04Rik	RIKEN cDNA 5133400G04 gene	NM_029485	down	0.01	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10582008	2310061C15Rik	RIKEN cDNA 2310061C15 gene	NM_026844	up	0.01	ns
10606969	Rbm41	RNA binding motif protein 41	NM_153586	up	0.01	ns
10469954	C730025P13Rik	RIKEN cDNA C730025P13 gene	NM_177344	down	0.01	ns
10576403	AK122209	cDNA sequence AK122209	NM_001029876	up	0.01	ns
10445565	Mrp12	mitochondrial ribosomal protein L2	NM_025302	down	0.01	ns
10368997	C130030K03Rik	RIKEN cDNA C130030K03 gene	AK048022	down	0.01	ns
10421697	9030625A04Rik	RIKEN cDNA 9030625A04 gene	BC116748	down	0.01	ns
10571371	Tusc3	tumor suppressor candidate 3	NM_030254	down	0.01	ns
10421188	R3hcc1	R3H domain and coiled-coil containing 1	ENSMUST0000050569	down	0.01	ns
10521759	Slit2	slit homolog 2 (Drosophila)	NM_178804	down	0.01	ns
10407766	Lgals8	lectin, galactose binding, soluble 8	NM_018886	down	0.01	ns
10568001	Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	NM_133670	up	0.01	ns
10467425	Sorbs1	sorbin and SH3 domain containing 1	NM_178362	up	0.01	ns
10489253	Zhx3	zinc fingers and homeoboxes 3	NM_177263	up	0.01	ns
10486029	Atpbd4	ATP binding domain 4	NM_025675	down	0.01	ns
10456988	Pard6g	par-6 partitioning defective 6 homolog gamma (C. elegans)	NM_053117	down	0.01	ns
10360187	Vangl2	vang-like 2 (van gogh, Drosophila)	NM_033509	down	0.01	ns
10447036	---	rRNA chromosome:NCBIM37:17:79258276:79258390:1 gene:ENSMUSG00000064770	ENSMUST0000082836	down	0.01	ns
10434643	Psmb3	proteasome (prosome, macropain) subunit, beta type 3	NM_011971	down	0.01	ns
10588505	Abhd14b	abhydrolase domain containing 14b	NM_029631	down	0.01	ns
10404538	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	NM_013830	up	0.01	ns
10441718	Park2	parkin	NM_016694	down	0.01	ns
10475211	Cep27	centrosomal protein 27	NM_025475	down	0.01	ns
10463739	Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	NM_177342	up	0.01	ns
10560300	Fkrp	fukutin related protein	NM_173430	down	0.01	ns
10460085	Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)	NM_023149	down	0.01	ns
10522589	Srd5a3	steroid 5 alpha-reductase 3	NM_020611	down	0.01	ns
10422240	Slitrk1	SLIT and NTRK-like family, member 1	NM_199065	down	0.01	0.02
10429100	Lrrc6	leucine rich repeat containing 6 (testis)	NM_019457	down	0.01	ns
10433887	Pkp2	plakophilin 2	NM_026163	up	0.01	ns
10556266	Wee1	WEE 1 homolog (S. pombe)	NM_009516	up	0.01	ns
10549276	Bhlhb3	basic helix-loop-helix domain containing, class B3	NM_024469	down	0.01	ns
10381154	Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	NM_009923	down	0.01	ns
10448023	Tcte3	t-complex-associated testis expressed 3	NM_011560	down	0.01	ns
10531195	Adams3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.01	0.02
10503363	Rbm12b	RNA binding motif protein 12B	NM_028226	up	0.01	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10393387	Jmjd6	jumonji domain containing 6	NM_033398	up	0.01	0.005
10527801	Brca2	breast cancer 2	NM_001081001	down	0.01	ns
10578253	Sgcz	sarcoglycan zeta	NM_145841	down	0.01	ns
10541034	Anub1	AN1, ubiquitin-like, homolog (Xenopus laevis)	NM_001081317	down	0.01	ns
10345037	Paqr8	progesterone and adipoQ receptor family member VIII	NM_028829	up	0.01	ns
10364385	Ilvbl	ilvB (bacterial acetolactate synthase)-like	NM_173751	down	0.01	ns
10546349	Xpc	xeroderma pigmentosum, complementation group C	NM_009531	down	0.01	ns
10431017	Ttll1	tubulin tyrosine ligase-like 1	NM_178869	down	0.01	ns
10506170	Efcab7	EF-hand calcium binding domain 7	NM_145549	down	0.01	ns
10366163	Slc6a15	solute carrier family 6 (neurotransmitter transporter), member 15	NM_175328	down	0.01	ns
10451110	Hsp90ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1	NM_008302	up	0.01	0.04
10488033	Pak7	p21 (CDKN1A)-activated kinase 7	NM_172858	down	0.01	ns
10421817	Narg1l	NMDA receptor regulated 1-like	NM_025832	up	0.01	ns
10502655	Cyr61	cysteine rich protein 61	NM_010516	up	0.01	ns
10502830	Nexn	nexilin	NM_199465	down	0.01	ns
10459421	Atp8b1	ATPase, class I, type 8B, member 1	NM_001001488	down	0.01	ns
10393754	Actg1	actin, gamma, cytoplasmic 1	NM_009609	down	0.01	ns
10450640	Mrps18b	mitochondrial ribosomal protein S18B	NM_025878	down	0.01	ns
10426894	ENSMUSG00000058057	predicted gene, ENSMUSG00000058057	NM_001081471	up	0.01	ns
10405576	Fbxl21	F-box and leucine-rich repeat protein 21	NM_178674	down	0.01	ns
10525923	Tmem132b	transmembrane protein 132B	XM_915709	down	0.01	ns
10596583	Dock3	dedicator of cyto-kinesis 3	NM_153413	down	0.01	0.04
10345357	Imp4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	NM_178601	up	0.01	ns
10539472	Nagk	N-acetylglucosamine kinase	NM_019542	down	0.01	ns
10490169	Ppp4r1l	protein phosphatase 4, regulatory subunit 1-like	ENSMUST0000069669	down	0.01	ns
10484227	Sestd1	SEC14 and spectrin domains 1	NM_175465	down	0.01	ns
10537657	Ephb6	Eph receptor B6	NM_007680	down	0.01	ns
10397912	9030205A07Rik	RIKEN cDNA 9030205A07 Gene	AB257853	up	0.01	ns
10531181	Adams3	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.01	0.02
10595404	Fam46a	cDNA sequence BC023892	ENSMUST0000034802	up	0.01	0.003
10368277	Rps12	ribosomal protein S12	AF357393	up	0.01	ns
10476136	Vps16	vacuolar protein sorting 16 (yeast)	NM_030559	down	0.01	ns
10517141	Hmgn2	high mobility group nucleosomal binding domain 2	NM_016957	down	0.01	ns
10548729	Mansc1	MANSC domain containing 1	NM_026345	down	0.01	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10531197	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.01	ns
10400155	Nova1	neuro-oncological ventral antigen 1	ENSMUST0000066043	down	0.01	0.02
10525921	Tmem132b	transmembrane protein 132B	XM_915709	down	0.01	ns
10533131	1300012G16Rik	RIKEN cDNA 1300012G16 gene	NM_023625	down	0.01	ns
10396926	Sfrs5	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	NM_001079695	down	0.01	0.01
10355266	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1	NM_021295	down	0.01	ns
10538617	Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2	NM_133737	down	0.01	ns
10399299	A830093I24Rik	RIKEN cDNA A830093I24 gene	BC145648	down	0.01	ns
10434229	Cldn5	claudin 5	NM_013805	down	0.01	ns
10401684	Angel1	angel homolog 1 (Drosophila)	NM_144524	down	0.01	ns
10389245	Tada2l	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	NM_172562	down	0.01	ns
10444895	Flot1	flotillin 1	NM_008027	down	0.01	ns
10349809	Rbbp5	retinoblastoma binding protein 5	NM_172517	up	0.01	ns
10444008	Zfp414	zinc finger protein 414	NM_026712	down	0.01	ns
10541968	Ano2	anoctamin 2	NM_153589	down	0.01	0.01
10381683	Acbd4	acyl-Coenzyme A binding domain containing 4	NM_025988	down	0.01	ns
10440926	Dnajc28	DnaJ (Hsp40) homolog, subfamily C, member 28	NM_001099738	up	0.01	ns
10531189	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.01	ns
10358637	Hmcn1	hemicentin 1	NM_001024720	down	0.01	ns
10567316	Tmc7	transmembrane channel-like gene family 7	NM_172476	up	0.01	ns
10396694	Churc1	churchill domain containing 1	NM_206534	down	0.01	ns
10565456	Prss23	protease, serine, 23	NM_029614	up	0.01	ns
10390780	Krt222	keratin 222	BC079890	down	0.01	ns
10560434	Qpctl	glutamyl-peptide cyclotransferase-like	NM_026111	down	0.01	ns
10593421	1110032A03Rik	RIKEN cDNA 1110032A03 gene	CT010205	down	0.01	ns
10499839	Snapin	SNAP-associated protein	NM_133854	down	0.01	ns
10575578	4930402E16Rik	RIKEN cDNA 4930402E16 gene	NM_198308	down	0.01	ns
10446656	Lpin2	lipin 2	NM_022882	up	0.01	ns
10403511	Heatr1	HEAT repeat containing 1	NM_144835	up	0.01	ns
10516064	Mfsd2	major facilitator superfamily domain containing 2	NM_029662	up	0.01	ns
10511416	Tox	thymocyte selection-associated high mobility group box	NM_145711	down	0.01	ns
10455104	Pcdhb15	protocadherin beta 15	NM_053140	down	0.01	ns
10592891	Phldb1	pleckstrin homology-like domain, family B, member 1	NM_153537	down	0.01	ns
10450579	Ddr1	discoidin domain receptor family, member 1	NM_007584	down	0.01	ns
10383436	Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1	NM_026877	down	0.01	ns

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		(human)				
10390458	Pcgf2	polycomb group ring finger 2	NM_009545	down	0.01	ns
10396030	Fancm	Fanconi anemia, complementation group M	NM_178912	down	0.01	ns
10545658	Wdr54	WD repeat domain 54	NM_023790	down	0.01	ns
10423825	Fzd6	frizzled homolog 6 (Drosophila)	NM_008056	down	0.01	ns
10539592	Smyd5	SET and MYND domain containing 5	NM_144918	down	0.01	ns
10497548	Fndc3b	fibronectin type III domain containing 3B	NM_173182	up	0.01	ns
10495993	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	NM_130450	up	0.01	ns
10552075	Lgi4	leucine-rich repeat LGI family, member 4	NM_144556	down	0.01	ns
10544538	---	pseudogene chromosome:NCBIM37:6:47753957: 47754114:-1 gene:ENSMUSG00000045359	ENSMUST0000052129	up	0.01	ns
10506424	Actg1	actin, gamma, cytoplasmic 1	NM_009609	down	0.01	ns
10603087	Pir	pirin	NM_027153	down	0.01	ns
10352125	ENSMUSG00000055831	predicted gene, ENSMUSG00000055831	ENSMUST0000069568	up	0.01	ns
10509246	Luzp1	leucine zipper protein 1	NM_024452	up	0.01	0.04
10565057	Wdr73	WD repeat domain 73	ENSMUST0000026816	down	0.01	ns
10439249	Parp14	poly (ADP-ribose) polymerase family, member 14	NM_001039530	up	0.01	ns
10471062	Mettl11a	methyltransferase like 11A	ENSMUST0000041830	down	0.01	ns
10374464	Spred2	sprouty-related, EVH1 domain containing 2	BC040462	up	0.01	ns
10364093	Der13	Der1-like domain family, member 3	NM_024440	up	0.01	ns
10606475	Hdx	highly divergent homeobox	NM_001080549	down	0.01	ns
10478196	Top1	topoisomerase (DNA) I	NM_009408	up	0.01	ns
10431697	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	NM_011994	down	0.01	ns
10523277	9330159N05Rik	RIKEN cDNA 9330159N05 gene	AK034152	up	0.01	0.02
10410959	Atg10	autophagy-related 10 (yeast)	NM_025770	down	0.01	ns
10493770	Ilf2	interleukin enhancer binding factor 2	NM_026374	down	0.01	ns
10567591	---	Genscan chromosome:NCBIM37:7:128791698: 128850767:-1	GENSCAN0000018737	up	0.01	0.02
10432411	Mcrs1	microspherule protein 1	NM_016766	down	0.01	ns
10377938	Eno3	enolase 3, beta muscle	NM_007933	down	0.01	ns
10357888	Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	AK173053	down	0.01	ns
10401673	Tgfb3	transforming growth factor, beta 3	NM_009368	up	0.01	0.03
10472621	Ubr3	ubiquitin protein ligase E3 component n-recognin 3	NM_001081548	down	0.01	0.009
10593499	AI593442	expressed sequence AI593442	NM_178906	down	0.01	0.04

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10604375	Apln	apelin	NM_013912	up	0.01	ns
10375704	3010026O09Rik	RIKEN cDNA 3010026O09 gene	BC028428	down	0.01	ns
10504504	Grhpr	glyoxylate reductase/hydroxypyruvate reductase	NM_080289	down	0.01	ns
10366052	Kitl	kit ligand	NM_013598	up	0.01	0.05
10587604	Rwdd2a	RWD domain containing 2A	NM_027100	down	0.01	ns
10384423	Cobl	cordon-bleu	NM_172496	up	0.01	ns
10408870	Tbc1d7	TBC1 domain family, member 7	NM_025935	down	0.01	ns
10511099	A530082C11Rik	RIKEN cDNA A530082C11 gene	NM_177186	up	0.01	ns
10434446	Ece2	endothelin converting enzyme 2	NM_139293	down	0.01	ns
10592303	Robo3	roundabout homolog 3 (Drosophila)	AF060570	up	0.01	ns
10555777	---	GenScan chromosome:NCBIM37:7:110335117: 110384869:1	GENSCAN0000023102	up	0.01	ns
10381395	Rundc1	RUN domain containing 1	NM_172566	up	0.01	ns
10492671	Ppid	peptidylprolyl isomerase D (cyclophilin D)	NM_026352	up	0.01	ns
10538658	Herc3	hect domain and RLD 3	NM_028705	down	0.01	ns
10559312	Dhcr7	7-dehydrocholesterol reductase	NM_007856	down	0.01	ns
10558049	Ppapdc1a	phosphatidic acid phosphatase type 2 domain containing 1A	NM_001080963	up	0.01	ns
10424188	Mtbp	Mdm2, transformed 3T3 cell double minute p53 binding protein	NM_134092	down	0.01	ns
10358677	1200016B10Rik	RIKEN cDNA 1200016B10 gene	BC060204	up	0.01	ns
10499652	4632404H12Rik	RIKEN cDNA 4632404H12 gene	ENSMUST0000038450	down	0.01	ns
10379013	Flot2	flotillin 2	NM_008028	down	0.01	ns
10493235	Paqr6	progesterone and adipoQ receptor family member VI	NM_198410	down	0.01	ns
10572739	ENSMUSG0000060719	predicted gene, ENSMUSG0000060719	AK032580	up	0.01	ns
10407072	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	NM_029001	down	0.01	ns
10592140	Ddx25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	NM_013932	down	0.01	ns
10481349	Ntng2	netrin G2	NM_133501	down	0.01	ns
10360589	Ahctf1	AT hook containing transcription factor 1	NM_026375	up	0.01	ns
10599849	---	GenScan chromosome:NCBIM37:X:58500749: 58545291:1	GENSCAN0000033180	down	0.02	ns
10518132	Prdm2	PR domain containing 2, with ZNF domain	NM_001081355	up	0.02	ns
10578193	Thex1	three prime histone mRNA exonuclease 1	NM_026067	up	0.02	ns
10601551	LOC100039300	similar to enhancer of yellow 2 homolog (Drosophila)	ENSMUST0000055309	down	0.02	0.04
10441489	Gtf2h5	general transcription factor IIH, polypeptide 5	NM_181392	down	0.02	ns
10469425	Arl5b	ADP-ribosylation factor-like 5B	NM_029466	up	0.02	ns
10536541	St7	Suppression of tumorigenicity 7	NM_022332	up	0.02	ns
10526614	Actl6b	actin-like 6B	NM_031404	down	0.02	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10575184	Wwp2	WW domain containing E3 ubiquitin protein ligase 2	NM_025830	down	0.02	ns
10551981	U2af1l4	U2 small nuclear RNA auxiliary factor 1-like 4	NM_170760	up	0.02	ns
10491331	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	NM_008839	up	0.02	ns
10459844	Ccdc5	coiled-coil domain containing 5	NM_146089	down	0.02	ns
10442057	Riok2	RIO kinase 2 (yeast)	NM_025934	down	0.02	ns
10581378	Psmb10	proteasome (prosome, macropain) subunit, beta type 10	NM_013640	down	0.02	ns
10417579	4930452B06Rik	RIKEN cDNA 4930452B06 gene	BC064468	down	0.02	ns
10445239	EG546797	predicted gene, EG546797	ENSMUST0000071458	down	0.02	ns
10541098	Zfp239	zinc finger protein 239	NM_001001792	down	0.02	ns
10545130	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	NM_007836	up	0.02	0.05
10437210	Bace2	beta-site APP-cleaving enzyme 2	NM_019517	down	0.02	0.01
10544837	1200009O22Rik	RIKEN cDNA 1200009O22 gene	BC043099	down	0.02	ns
10364950	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	NM_008655	up	0.02	0.005
10444505	Rdbp	RD RNA-binding protein	NM_001045864	down	0.02	ns
10441038	Hlcs	holocarboxylase synthetase (biotin- [propionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	NM_139145	down	0.02	ns
10495854	Prss12	protease, serine, 12 neurotrypsin (motopsin)	NM_008939	down	0.02	ns
10560826	Zfp109	zinc finger protein 109	NM_020262	up	0.02	ns
10460706	Syvn1	synovial apoptosis inhibitor 1, synoviolin	NM_028769	up	0.02	0.02
10446013	Mpnd	MPN domain containing	NM_026530	down	0.02	ns
10539220	AW146020	expressed sequence AW146020	NM_177884	down	0.02	ns
10471171	Fubp3	far upstream element (FUSE) binding protein 3	NM_001033389	down	0.02	ns
10481272	1700007K13Rik	RIKEN cDNA 1700007K13 gene	BC099566	up	0.02	0.03
10549473	Caprin2	caprin family member 2	NM_181541	down	0.02	ns
10462091	Klf9	Kruppel-like factor 9	NM_010638	up	0.02	ns
10423963	Eny2	enhancer of yellow 2 homolog (Drosophila)	NM_175009	down	0.02	0.02
10582403	Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	NM_016722	down	0.02	ns
10401933	---	Mouse mammary tumor virus clone 66C env precursor and vSAG protein mRNA, complete cds.	AF043690	up	0.02	ns
10504759	---	Mouse mammary tumor virus clone 66C env precursor and vSAG protein mRNA, complete cds.	AF043690	up	0.02	ns
10387659	Nlgn2	neuroligin 2	NM_198862	down	0.02	ns
10417920	Usp54	ubiquitin specific peptidase 54	NM_030180	up	0.02	ns
10357381	Ysk4	Yeast Sps1/Ste20-related kinase 4 (S. cerevisiae)	XM_914055	up	0.02	ns
10573490	Hook2	hook homolog 2 (Drosophila)	NM_133255	down	0.02	ns
10380859	Crks	CDC2-related kinase, arginine/serine-rich	BC057057	down	0.02	ns
10415030	Oxa1l	oxidase assembly 1-like	NM_026936	down	0.02	ns

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10528145	Grm3	glutamate receptor, metabotropic 3	NM_181850	down	0.02	ns
10389627	Rad51c	Rad51 homolog c (<i>S. cerevisiae</i>)	NM_053269	up	0.02	ns
10581996	Cdyl2	chromodomain protein, Y chromosome-like 2	NM_029441	up	0.02	ns
10511865	Ptges3	prostaglandin E synthase 3 (cytosolic)	AF153479	up	0.02	ns
10480808	Gm996	gene model 996, (NCBI)	NM_001005424	down	0.02	ns
10483604	Slc25a12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	NM_172436	down	0.02	ns
10354677	Ankrd44	ankyrin repeat domain 44	NM_001081433	down	0.02	ns
10368380	L3mbt3	l(3)mbt-like 3 (<i>Drosophila</i>)	NM_172787	up	0.02	ns
10469609	OTTMUSG00000011664	predicted gene, OTTMUSG00000011664	ENSMUST0000100373	down	0.02	0.02
10376929	1810036I24Rik	RIKEN cDNA 1810036I24 gene	BC115504	up	0.02	ns
10578138	Dctn6	dynactin 6	NM_011722	down	0.02	ns
10588509	Pcbp4	poly(rC) binding protein 4	NM_021567	down	0.02	ns
10529953	EG625026	predicted gene, EG625026	AK036806	down	0.02	0.03
10436600	---	MI0000146 <i>Mus musculus</i> miR-99a stem-loop	---	down	0.02	ns
10451167	Tmem63b	transmembrane protein 63b	NM_198167	down	0.02	ns
10458834	Atg12	autophagy-related 12 (yeast)	NM_026217	up	0.02	ns
10549921	Vmn2r43	vomer nasal 2, receptor 43	NM_198961	up	0.02	ns
10363667	ENSMUSG00000062298	predicted gene, ENSMUSG00000062298	ENSMUST0000074437	down	0.02	ns
10539606	Cct7	chaperonin containing Tcp1, subunit 7 (eta)	NM_007638	up	0.02	ns
10423505	Cmb1	carboxymethylenebutenolidase-like (<i>Pseudomonas</i>)	NM_181588	down	0.02	ns
10484987	Nr1h3	nuclear receptor subfamily 1, group H, member 3	NM_013839	up	0.02	ns
10392560	Abca9	ATP-binding cassette, sub-family A (ABC1), member 9	NM_147220	up	0.02	ns
10381708	Fmn1	formin-like 1	NM_019679	up	0.02	0.0004
10570634	4930467E23Rik // EG665756	RIKEN cDNA 4930467E23 gene // predicted gene, EG665756	ENSMUST0000084046	down	0.02	0.05
10520638	0610007C21Rik	RIKEN cDNA 0610007C21 gene	NM_027855	down	0.02	ns
10507238	Lrrc41	leucine rich repeat containing 41	NM_153521	down	0.02	ns
10462281	Vldlr	very low density lipoprotein receptor	NM_013703	down	0.02	ns
10589889	Glb1	galactosidase, beta 1	NM_009752	down	0.02	ns
10522134	Lias	lipoic acid synthetase	NM_024471	down	0.02	0.03
10433389	Alg1	asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase)	NM_145362	down	0.02	ns
10353549	4921533L14Rik	RIKEN cDNA 4921533L14 gene	BC070446	down	0.02	0.04
10511156	Ccnl2	cyclin L2	NM_207678	up	0.02	0.04
10373756	Pla2g3	phospholipase A2, group III	NM_172791	up	0.02	ns
10472022	Lypd6b	LY6/PLAUR domain containing 6B	BC126943	down	0.02	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10473022	Plp2	proteolipid protein 2	NM_019755	down	0.02	ns
10545827	Rab11fip5	RAB11 family interacting protein 5 (class I)	NM_001003955	down	0.02	ns
10522802	Ythdc1	YTH domain containing 1	NM_177680	up	0.02	ns
10533993	Slc15a4	solute carrier family 15, member 4	NM_133895	up	0.02	ns
10359034	Qsox1	quiescin Q6 sulfhydryl oxidase 1	NM_001024945	down	0.02	ns
10508829	Map3k6	mitogen-activated protein kinase kinase kinase 6	NM_016693	up	0.02	ns
10566516	1500003O22Rik	RIKEN cDNA 1500003O22 gene	BC022923	up	0.02	ns
10439762	Ahcy	S-adenosylhomocysteine hydrolase	ENSMUST0000054607	down	0.02	ns
10438626	Etv5	ets variant gene 5	NM_023794	up	0.02	0.01
10353878	Ankrd23	ankyrin repeat domain 23	NM_153502	up	0.02	ns
10542319	Apold1	apolipoprotein L domain containing 1	NM_001109914	up	0.02	ns
10532896	2610524H06Rik	RIKEN cDNA 2610524H06 gene	NM_181075	down	0.02	ns
10583485	A230050P20Rik	RIKEN cDNA A230050P20 gene	NM_175687	down	0.02	ns
10599693	6330419J24Rik	RIKEN cDNA 6330419J24 gene	BC052359	down	0.02	ns
10483025	Rbms1	RNA binding motif, single stranded interacting protein 1	NM_020296	down	0.02	ns
10445544	Crip3	cysteine-rich protein 3	NM_053250	up	0.02	ns
10487040	Fbn1	fibrillin 1	NM_007993	down	0.02	ns
10455094	Pcdhb13	protocadherin beta 13	NM_053138	down	0.02	ns
10424060	A930017M01Rik	RIKEN cDNA A930017M01 gene	AK080719	down	0.02	ns
10462333	Cdc3711	cell division cycle 37 homolog (S. cerevisiae)-like 1	NM_025950	up	0.02	ns
10512165	Nol6	nucleolar protein family 6 (RNA-associated)	NM_139236	down	0.02	ns
10489784	BC067047	cDNA sequence BC067047	NM_177782	up	0.02	ns
10457886	ENSMUSG0000054990	predicted gene, ENSMUSG0000054990	ENSMUST0000068352	up	0.02	ns
10431558	2010001J22Rik	RIKEN cDNA 2010001J22 gene	BC087962	down	0.02	ns
10441422	Zdhhc14	zinc finger, DHHC domain containing 14	NM_146073	up	0.02	0.02
10484201	2610301F02Rik	RIKEN cDNA 2610301F02 gene	ENSMUST0000049544	up	0.02	ns
10377380	1500010J02Rik	RIKEN cDNA 1500010J02 gene	NM_026889	down	0.02	ns
10374455	Spred2	sprouty-related, EVH1 domain containing 2	NM_033523	up	0.02	0.03
10439424	4932425I24Rik	RIKEN cDNA 4932425I24 gene	NM_001081025	up	0.02	ns
10519578	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	NM_008830	down	0.02	ns
10431974	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	NM_144850	up	0.02	ns
10531610	Rasgef1b	RasGEF domain family, member 1B	NM_145839	down	0.02	ns
10558150	Htra1	HtrA serine peptidase 1	NM_019564	up	0.02	ns
10374564	Cct4	chaperonin containing Tcp1, subunit 4 (delta)	NM_009837	up	0.02	ns
10583291	2200002K05Rik	RIKEN cDNA 2200002K05 gene	BC055786	down	0.02	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10453887	Cables1	Cdk5 and Abl enzyme substrate 1	NM_022021	up	0.02	ns
10534002	Tmem132d	transmembrane protein 132D	NM_172885	down	0.02	ns
10506571	Dhcr24	24-dehydrocholesterol reductase	NM_053272	down	0.02	ns
10420730	Fdft1	farnesyl diphosphate farnesyl transferase 1	NM_010191	down	0.02	ns
10564877	Rccd1	RCC1 domain containing 1	NM_173445	down	0.02	ns
10601980	Mum11l	melanoma associated antigen (mutated) 1-like 1	NM_175541	up	0.02	ns
10533401	Cux2	cut-like homeobox 2	ENSMUST0000111752	down	0.02	ns
10411359	Plp2	proteolipid protein 2	NM_019755	down	0.02	ns
10437655	BC068110	cDNA sequence BC068110	BC068110	down	0.02	ns
10599530	Rab33a	RAB33A, member of RAS oncogene family	NM_011228	down	0.02	ns
10568221	Sephs2	selenophosphate synthetase 2	NM_009266	down	0.02	ns
10366346	Phlda1	pleckstrin homology-like domain, family A, member 1	NM_009344	up	0.02	ns
10505532	OTTMUSG0000000266	predicted gene, OTTMUSG0000000266	XR_033213	up	0.02	ns
10480459	Hnmt	histamine N-methyltransferase	NM_080462	down	0.02	ns
10484197	2610301F02Rik	RIKEN cDNA 2610301F02 gene	ENSMUST0000049544	up	0.02	ns
10471058	Cstad	CSA-conditional, T cell activation-dependent protein	NM_030137	down	0.02	ns
10455128	Pcdhb20	protocadherin beta 20	NM_053145	down	0.02	ns
10598467	Pim2	proviral integration site 2	NM_138606	up	0.02	ns
10582823	Rbm34	RNA binding motif protein 34	NM_172762	down	0.02	ns
10416406	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	NM_172812	up	0.02	ns
10457853	Ino80c	INO80 complex subunit C	BC060961	down	0.02	ns
10582330	Rnf166	ring finger protein 166	NM_001033142	up	0.02	ns
10412466	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	NM_145942	down	0.02	ns
10561247	Shkbp1	Sh3kbp1 binding protein 1	NM_138676	up	0.02	ns
10531348	Ppef2	protein phosphatase, EF hand calcium-binding domain 2	NM_011148	up	0.02	ns
10361156	Rcor3	REST corepressor 3	NM_144814	down	0.02	ns
10424979	Gpt	glutamic pyruvic transaminase, soluble	NM_182805	up	0.02	ns
10387922	Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	NM_024211	down	0.02	ns
10470283	Egfl7	EGF-like domain 7	NM_198724	down	0.02	ns
10450533	Vars2	valyl-tRNA synthetase 2, mitochondrial (putative)	NM_175137	down	0.02	ns
10591022	4931406C07Rik	RIKEN cDNA 4931406C07 gene	BC016078	down	0.02	0.03
10378754	2310047D13Rik	RIKEN cDNA 2310047D13 gene	NM_027773	down	0.02	ns
10438738	Bcl6	B-cell leukemia/lymphoma 6	NM_009744	up	0.02	ns
10530910	Uba6	ubiquitin-like modifier activating enzyme 6	NM_172712	up	0.02	ns
10400510	Clec14a	C-type lectin domain family 14, member a	NM_025809	down	0.02	ns
10388884	Nik	nemo like kinase	NM_008702	up	0.02	ns

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10448136	---	pseudogene chromosome:NCBIM37:17:18613394: 18613645:-1 gene:ENSMUSG00000051878	ENSMUST0000078796	down	0.02	ns
10368101	D10Bwg1379e	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	NM_001033258	down	0.02	ns
10465263	Dpf2	D4, zinc and double PHD fingers family 2	NM_011262	up	0.02	ns
10377508	Trappc1	trafficking protein particle complex 1	NM_001024206	down	0.02	ns
10439976	2310061J03Rik	RIKEN cDNA 2310061J03 gene	BC017620	down	0.02	0.02
10385747	Phf15	PHD finger protein 15	NM_199299	up	0.02	ns
10436678	Gabpa	GA repeat binding protein, alpha	NM_008065	up	0.02	ns
10600504	Fundc2	FUN14 domain containing 2	NM_026126	down	0.02	ns
10519203	A230069A22Rik	RIKEN cDNA A230069A22 gene	BC147318	down	0.02	ns
10379652	Al450353	expressed sequence Al450353	AJ007734	up	0.02	ns
10360648	Psen2	presenilin 2	NM_011183	down	0.02	ns
10405372	Zfp346	zinc finger protein 346	NM_012017	down	0.02	ns
10519140	Mmp23	matrix metalloproteinase 23	NM_011985	up	0.02	ns
10410919	EG435373	predicted gene, EG435373	XR_034009	down	0.02	ns
10539649	Ptges3	prostaglandin E synthase 3 (cytosolic)	AY281130	up	0.02	ns
10598723	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	NM_010028	down	0.02	ns
10487969	Trmt6	tRNA methyltransferase 6 homolog (S. cerevisiae)	NM_175113	down	0.02	ns
10526897	Unc84a	unc-84 homolog A (C. elegans)	NM_024451	down	0.02	ns
10469505	Commd3	COMM domain containing 3	NM_147778	down	0.02	ns
10572747	Tpm4	tropomyosin 4	NM_001001491	up	0.02	ns
10603346	Plp2	proteolipid protein 2	NM_019755	down	0.02	ns
10366938	Stac3	SH3 and cysteine rich domain 3	NM_177707	up	0.02	ns
10513020	Ikbpap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	NM_026079	down	0.02	ns
10394812	EG245297	predicted gene, EG245297	BC030401	down	0.02	ns
10406417	Actg1	actin, gamma, cytoplasmic 1	NM_009609	down	0.02	ns
10475544	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	NM_172537	down	0.02	ns
10587942	Xrm1	5'-3' exoribonuclease 1	NM_011916	down	0.02	ns
10399555	Kcnf1	potassium voltage-gated channel, subfamily F, member 1	NM_201531	up	0.02	ns
10383395	Slc25a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	NM_013770	down	0.02	ns
10379363	Atad5	ATPase family, AAA domain containing 5	NM_001029856	down	0.02	ns
10563314	Dhdh	dihydrodiol dehydrogenase (dimeric)	NM_027903	down	0.02	ns
10358660	Hmnc1	hemicentin 1	NM_001024720	down	0.02	ns

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10601091	Foxo4	forkhead box O4	NM_018789	up	0.02	ns
10408113	Hist1h4i	histone cluster 1, H4i	NM_175656	up	0.02	ns
10440918	Tmem50b	transmembrane protein 50B	NM_030018	up	0.02	ns
10497920	Ankrd50	ankrin repeat domain 50	NM_001033198	up	0.02	ns
10499643	Chrn2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	NM_009602	down	0.02	ns
10586039	Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	NM_001083927	up	0.02	ns
10482434	Gtdc1	glycosyltransferase-like domain containing 1	NM_172662	down	0.02	ns
10543697	Zc3hc1	zinc finger, C3HC type 1	NM_172735	down	0.02	ns
10524941	Fbxo21	F-box protein 21	NM_145564	down	0.02	ns
10471443	Pip5k1l	phosphatidylinositol-4-phosphate 5-kinase-like 1	NM_198191	down	0.02	ns
10491091	Tnfrsf10	tumor necrosis factor (ligand) superfamily, member 10	NM_009425	down	0.02	ns
10455088	Pcdhb11	protocadherin beta 11	NM_053136	down	0.02	ns
10400057	Arl4a	ADP-ribosylation factor-like 4A	NM_001039515	down	0.02	0.02
10426284	Acr	acrosin prepropeptide	NM_013455	down	0.02	ns
10545835	1700040I03Rik	RIKEN cDNA 1700040I03 gene	BC115452	down	0.02	ns
10583834	9530077C05Rik	RIKEN cDNA 9530077C05 gene	BC054761	up	0.02	ns
10376685	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	NM_172943	up	0.02	ns
10501555	Amy1	amylase 1, salivary	NM_007446	down	0.02	0.002
10488816	Ahcy	S-adenosylhomocysteine hydrolase	NM_016661	down	0.02	ns
10528482	BC050254	cDNA sequence BC050254	BC050254	up	0.02	ns
10458340	Hbegf	heparin-binding EGF-like growth factor	NM_010415	up	0.02	0.02
10355785	Glb1l	galactosidase, beta 1-like	BC021773	down	0.02	ns
10519224	Pusl1	pseudouridylate synthase-like 1	ENSMUST0000097737	down	0.02	ns
10393970	Fasn	fatty acid synthase	NM_007988	down	0.03	ns
10604735	Rbmx	RNA binding motif protein, X chromosome	NM_011252	down	0.03	ns
10571329	Gm501	gene model 501, (NCBI)	XM_146277	down	0.03	ns
10358648	Hmcn1	hemicentin 1	NM_001024720	down	0.03	ns
10547288	Ankrd26	ankyrin repeat domain 26	NM_001081112	up	0.03	ns
10554156	Fam174b	family with sequence similarity 174, member B	BC034069	up	0.03	ns
10346224	5330401P04Rik	RIKEN cDNA 5330401P04 gene	ENSMUST0000087708	down	0.03	ns
10544563	Zfp467	zinc finger protein 467	NM_020589	down	0.03	ns
10365302	A230046K03Rik	RIKEN cDNA A230046K03 gene	NM_001033375	up	0.03	ns
10447675	Rnaset2a	ribonuclease T2A	NM_001083938	down	0.03	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10560035	Zscan18	zinc finger and SCAN domain containing 18	BC094341	down	0.03	ns
10396919	4933426M11Rik	RIKEN cDNA 4933426M11 gene	BC040401	up	0.03	ns
10572253	Sf4	splicing factor 4	NM_027481	down	0.03	0.05
10430956	Cyb5r3	cytochrome b5 reductase 3	NM_029787	down	0.03	ns
10444978	Gna-rs1	guanine nucleotide binding protein, related sequence 1	NM_008136	down	0.03	ns
10463836	Gsto1	glutathione S-transferase omega 1	NM_010362	down	0.03	ns
10414612	Slc39a2	solute carrier family 39 (zinc transporter), member 2	NM_001039676	up	0.03	ns
10544689	4921507P07Rik	RIKEN cDNA 4921507P07 gene	BC055110	down	0.03	ns
10556962	Vwa3a	von Willebrand factor A domain containing 3A	NM_177697	down	0.03	ns
10576010	Gse1	genetic suppressor element 1	NM_198671	up	0.03	ns
10515716	BC059842	cDNA sequence BC059842	ENSMUST0000075406	down	0.03	ns
10573115	Rnf150	ring finger protein 150	NM_177378	up	0.03	ns
10345882	Mrps9	mitochondrial ribosomal protein S9	NM_023514	down	0.03	ns
10579406	Arrdc2	arrestin domain containing 2	NM_027560	up	0.03	ns
10542104	ENSMUSG0000059659	predicted gene, ENSMUSG0000059659	ENSMUST0000082030	up	0.03	ns
10586128	---	snRNA chromosome:NCBIM37:9:63290126: 63290267:1 gene:ENSMUSG0000065679	ENSMUST0000083745	up	0.03	ns
10469951	Rnf208	ring finger protein 208	NM_176834	down	0.03	ns
10576857	Timm44	translocase of inner mitochondrial membrane 44	NM_011592	down	0.03	ns
10538290	Snx10	sorting nexin 10	NM_028035	down	0.03	ns
10592629	Grik4	glutamate receptor, ionotropic, kainate 4	NM_175481	down	0.03	ns
10589494	Cspg5	chondroitin sulfate proteoglycan 5	NM_013884	down	0.03	ns
10434436	EG328644	predicted gene, EG328644	BC125016	down	0.03	ns
10579659	Hmgn2	high mobility group nucleosomal binding domain 2	NM_016957	down	0.03	ns
10492522	Schip1	schwannomin interacting protein 1	NM_001113421	up	0.03	0.04
10542714	Lym5	LYR motif containing 5	NM_133688	down	0.03	ns
10399224	1110002L01Rik	RIKEN cDNA 1110002L01 gene	ENSMUST0000095903	up	0.03	ns
10591773	Hmgn2	high mobility group nucleosomal binding domain 2	NM_016957	down	0.03	ns
10533323	Adam1a	a disintegrin and metallopeptidase domain 1a	NM_172126	up	0.03	ns
10384192	Tbrg4	transforming growth factor beta regulated gene 4	NM_134011	down	0.03	ns
10433163	Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	NM_021391	down	0.03	ns
10388784	Rpl23a	ribosomal protein L23a	AF357367	down	0.03	ns
10369661	Ccar1	cell division cycle and apoptosis regulator 1	NM_026201	up	0.03	ns
10423577	Mtdh	Metadherin	NM_026002	down	0.03	ns
10532984	Dynll1	dynein light chain LC8-type 1	NM_019682	up	0.03	ns
10607116	Ammecr1	Alport syndrome, mental retardation, midface hypoplasia and	NM_019496	down	0.03	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
		elliptocytosis chromosomal region gene 1 homolog (human)				
10397189	Ptgr2	prostaglandin reductase 2	NM_029880	down	0.03	ns
10572679	Glt25d1	glycosyltransferase 25 domain containing 1	NM_146211	down	0.03	ns
10526055	Gbas	glioblastoma amplified sequence	NM_008095	down	0.03	ns
10439442	Pla1a	phospholipase A1 member A	NM_134102	up	0.03	ns
10377612	Plscr3	phospholipid scramblase 3	NM_023564	down	0.03	ns
10458033	Stard4	StAR-related lipid transfer (START) domain containing 4	NM_133774	down	0.03	ns
10472418	OTTMUSG0000013098	predicted gene, OTTMUSG00000013098	AK039017	down	0.03	ns
10529260	6030436E02Rik	RIKEN cDNA 6030436E02 gene	ENSMUST0000094889	up	0.03	ns
10579054	4930467E23Rik // EG665756	RIKEN cDNA 4930467E23 gene // predicted gene, EG665756	ENSMUST0000084046	down	0.03	0.04
10364030	Adora2a	adenosine A2a receptor	NM_009630	down	0.03	ns
10502205	Hadh	hydroxyacyl-Coenzyme A dehydrogenase	NM_008212	down	0.03	ns
10597758	Axud1	AXIN1 up-regulated 1	NM_153287	up	0.03	ns
10408047	OTTMUSG0000018077	predicted gene, OTTMUSG00000018077	AK132930	down	0.03	ns
10438445	Kih16	kelch-like 6 (Drosophila)	NM_183390	down	0.03	ns
10591164	---	known chromosome:NCBIM37:9:18265539: 18282707:-1 gene:ENSMUSG00000074500	ENSMUST0000034646	down	0.03	ns
10441055	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	NM_019543	down	0.03	ns
10378038	Wscd1	WSC domain containing 1	NM_177618	down	0.03	ns
10596568	Rbm15b	RNA binding motif protein 15B	ENSMUST0000098424	up	0.03	ns
10560551	Sfrs16	splicing factor, arginine/serine-rich 16	NM_016680	down	0.03	ns
10358565	Hmcn1	hemicentin 1	NM_001024720	down	0.03	ns
10584208	Cdon	cell adhesion molecule-related/down-regulated by oncogenes	NM_021339	down	0.03	ns
10448707	Tbl3	transducin (beta)-like 3	NM_145396	down	0.03	ns
10354031	Tsga10	testis specific 10	NM_207228	up	0.03	ns
10471519	Tor2a	torsin family 2, member A	NM_152800	down	0.03	ns
10528090	Rundc3b	RUN domain containing 3B	NM_198620	down	0.03	ns
10403945	Hist1h4j	histone cluster 1, H4j	NM_178210	up	0.03	0.008
10577808	Tacc1	transforming, acidic coiled-coil containing protein 1	NM_177089	up	0.03	ns
10365123	Dohh	deoxyhypusine hydroxylase/monooxygenase	AK080664	up	0.03	ns
10417275	---	novel chromosome:NCBIM37:14:20434352: 20436596:1 gene:ENSMUSG00000068776	ENSMUST0000090639	up	0.03	ns
10387936	Spag7	sperm associated antigen 7	NM_172561	down	0.03	ns
10587012	Ccpg1	cell cycle progression 1	NM_001114328	up	0.03	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10566668	LOC675799	similar to suppressor of cytokine signaling 6	XR_032694	up	0.03	ns
10380087	Mttr4	myotubularin related protein 4	NM_133215	up	0.03	0.04
10596521	Grm2	glutamate receptor, metabotropic 2	BC115866	down	0.03	ns
10347427	Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	NM_175031	up	0.03	ns
10445688	Ccnd3	cyclin D3	NM_001081636	up	0.03	ns
10420516	Cdadcl1	cytidine and dCMP deaminase domain containing 1	NM_027986	up	0.03	ns
10493798	S100a16	S100 calcium binding protein A16	NM_026416	down	0.03	ns
10413542	Tkt	transketolase	NM_009388	down	0.03	ns
10581499	5830457O10Rik	RIKEN cDNA 5830457O10 gene	NM_145412	up	0.03	ns
10351063	---	GENSCAN chromosome:NCBIM37:1:163081124: 163167441:1	GENSCAN0000035901	up	0.03	ns
10443421	Brpf3	bromodomain and PHD finger containing, 3	NM_001081315	down	0.03	ns
10366546	Cpm	carboxypeptidase M	NM_027468	up	0.03	ns
10467802	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	NM_019424	down	0.03	ns
10415980	Fbxo16	F-box protein 16	NM_015795	down	0.03	ns
10415282	Psme1	proteasome (prosome, macropain) 28 subunit, alpha	NM_011189	down	0.03	ns
10469987	Man1b1	mannosidase, alpha, class 1B, member 1	NM_001029983	down	0.03	ns
10523647	Aff1	AF4/FMR2 family, member 1	NM_001080798	up	0.03	ns
10481111	---	GENSCAN chromosome:NCBIM37:2:26519054: 26578485:-1	GENSCAN0000007465	up	0.03	ns
10600324	Rpl3	ribosomal protein L3	NM_013762	down	0.03	ns
10407192	Slc38a9	solute carrier family 38, member 9	NM_178746	up	0.03	ns
10358559	Hmcn1	hemicentin 1	NM_001024720	down	0.03	ns
10491455	Fxr1	fragile X mental retardation gene 1, autosomal homolog	NM_001113188	up	0.03	ns
10444352	Notch4	Notch gene homolog 4 (Drosophila)	NM_010929	up	0.03	ns
10490559	Chrna4	cholinergic receptor, nicotinic, alpha polypeptide 4	NM_015730	down	0.03	ns
10406536	---	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330419F14.	AK134580	down	0.03	ns
10355960	Scg2	secretogranin II	NM_009129	up	0.03	0.05
10395922	Rps2	ribosomal protein S2	NM_008503	down	0.03	ns
10490946	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	NM_010480	up	0.03	ns
10434942	Dlg1	discs, large homolog 1 (Drosophila)	NM_007862	up	0.03	ns
10571978	Cbr4	carbonyl reductase 4	NM_145595	down	0.03	ns
10430201	Myh9	myosin, heavy polypeptide 9, non-muscle	NM_022410	up	0.03	ns
10568296	---	---	AK034940	up	0.03	ns
10398360	---	Mus musculus mRNA, MBII-343 snoRNA.	AB076245	up	0.03	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10442240	Zfp760	zinc finger protein 760	NM_001008501	up	0.03	ns
10439766	Pvrl3	poliovirus receptor-related 3	NM_021496	down	0.03	ns
10505623	D4Bwg0951e	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	BC030404	up	0.03	ns
10576118	9330133O14Rik	RIKEN cDNA 9330133O14 gene	BC094355	down	0.03	ns
10462702	Hectd2	HECT domain containing 2	NM_172637	up	0.03	ns
10443021	Atp6v0e	ATPase, H+ transporting, lysosomal V0 subunit E	NM_025272	up	0.03	ns
10365845	Fgd6	FYVE, RhoGEF and PH domain containing 6	NM_053072	up	0.03	ns
10495134	100043129	predicted gene, 100043129	XM_001479553	down	0.03	ns
10502696	Spata1	spermatogenesis associated 1	NM_027617	up	0.03	ns
10396421	Hif1a	hypoxia inducible factor 1, alpha subunit	NM_010431	down	0.03	ns
10418905	3110001K24Rik	RIKEN cDNA 3110001K24 gene	NM_029389	down	0.03	ns
10601857	Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	NM_009750	down	0.03	ns
10472277	March7	membrane-associated ring finger (C3HC4) 7	NM_020575	down	0.03	ns
10601569	Pcdh11x	protocadherin 11 X-linked	NM_001081385	down	0.03	ns
10427255	Tarbp2	TAR (HIV) RNA binding protein 2	NM_009319	down	0.03	ns
10465314	Capn1	calpain 1	NM_007600	down	0.03	ns
10373027	Tspan31	tetraspanin 31	NM_025982	up	0.03	ns
10457546	Osbp1a	oxysterol binding protein-like 1A	NM_207530	down	0.03	0.03
10560983	Dedd2	death effector domain-containing DNA binding protein 2	NM_207677	up	0.03	ns
10472514	Nostrin	nitric oxide synthase trafficker	NM_181547	up	0.03	ns
10571705	Irf2	interferon regulatory factor 2	NM_008391	up	0.03	ns
10357875	Btg2	B-cell translocation gene 2, anti-proliferative	NM_007570	up	0.03	ns
10365219	EG237412	predicted gene, EG237412	DQ459435	down	0.03	ns
10443817	Pknx1	Pbx/knotted 1 homeobox	NM_016670	up	0.03	ns
10413897	Ercc6	excision repair cross-complementing rodent repair deficiency, complementation group 6	NM_001081221	up	0.03	ns
10413220	ENSMUSG0000072684	predicted gene, ENSMUSG0000072684	ENSMUST0000100823	up	0.03	ns
10565250	Mesdc1	mesoderm development candidate 1	NM_030705	up	0.03	ns
10445796	AI314976	expressed sequence AI314976	BC022574	down	0.03	ns
10542397	H2afj	H2A histone family, member J	NM_177688	up	0.03	ns
10535979	Rfc3	replication factor C (activator 1) 3	NM_027009	down	0.03	ns
10524338	Crybb1	crystallin, beta B1	NM_023695	up	0.03	ns
10512499	Tpm2	tropomyosin 2, beta	NM_009416	down	0.03	ns
10490569	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	NM_010611	up	0.03	ns
10523766	Lrrc8c	leucine rich repeat containing 8 family, member C	NM_133897	up	0.03	ns
10457225	Map3k8	mitogen-activated protein kinase kinase kinase 8	NM_007746	up	0.03	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10362717	Wasf1	WASP family 1	NM_031877	down	0.03	ns
10574743	Plekhh4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	NM_001081333	up	0.03	ns
10358627	Hmcn1	hemicentin 1	NM_001024720	down	0.03	ns
10597823	Lyzl4	lysozyme-like 4	NM_026915	up	0.03	ns
10556812	Lym1	LYR motif containing 1	NM_029610	down	0.03	ns
10607752	Bmx	BMX non-receptor tyrosine kinase	NM_009759	down	0.03	ns
10524889	Ksr2	kinase suppressor of ras 2	NM_001114545	down	0.03	ns
10358605	Hmcn1	hemicentin 1	NM_001024720	down	0.03	ns
10565794	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	NM_009825	up	0.03	ns
10490706	Znf512b	zinc finger protein 512B	ENSMUST0000108789	down	0.03	ns
10533849	Rilpl1	Rab interacting lysosomal protein-like 1	NM_021430	up	0.03	ns
10576152	Trappc2l	trafficking protein particle complex 2-like	NM_021502	down	0.03	ns
10522467	Rasl11b	RAS-like, family 11, member B	NM_026878	down	0.03	ns
10460926	Sf1	splicing factor 1	NM_001110791	up	0.03	ns
10424909	Hsf1	heat shock factor 1	NM_008296	up	0.03	ns
10422946	Ranbp3l	RAN binding protein 3-like	NM_198024	down	0.03	ns
10532616	Myo18b	myosin XVIIIb	XM_912851	up	0.03	ns
10395807	1110008L16Rik	RIKEN cDNA 1110008L16 gene	BC034876	down	0.03	ns
10470788	Odf2	outer dense fiber of sperm tails 2	NM_001113213	down	0.03	ns
10437432	Nmral1	NmrA-like family domain containing 1	NM_026393	down	0.03	ns
10404069	Hist1h1a	histone cluster 1, H1a	NM_030609	down	0.03	ns
10576581	Kcnk1	potassium channel, subfamily K, member 1	NM_008430	up	0.03	ns
10448506	Ccnf	cyclin F	NM_007634	up	0.03	ns
10418766	Ankrd28	ankyrin repeat domain 28	NM_001024604	down	0.03	ns
10430725	St13	suppression of tumorigenicity 13	NM_133726	up	0.03	ns
10550915	Cadm4	cell adhesion molecule 4	NM_153112	down	0.03	ns
10358654	Hmcn1	hemicentin 1	NM_001024720	down	0.03	ns
10381304	Vps25	vacuolar protein sorting 25 (yeast)	NM_026776	down	0.03	ns
10387483	Efnb3	ephrin B3	NM_007911	down	0.03	ns
10478285	9430021M05Rik	RIKEN cDNA 9430021M05 gene	ENSMUST0000067526	down	0.03	ns
10421922	---	Genscan chromosome:NCBIM37:14:93001677: 93003616:-1	GENSCAN0000018713	up	0.03	0.005
10430929	Tbrg3	transforming growth factor beta regulated gene 3	BC095996	up	0.03	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10543273	Cttnbp2	cortactin binding protein 2	NM_080285	up	0.03	ns
10479596	Zgpat	zinc finger, CCCH-type with G patch domain	NM_001048148	up	0.03	0.004
10448307	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	NM_013749	up	0.03	ns
10582474	Chmp1a	chromatin modifying protein 1A	NM_145606	down	0.03	ns
10564849	2610034B18Rik	RIKEN cDNA 2610034B18 gene	BC031379	down	0.04	ns
10536746	Arf5	ADP-ribosylation factor 5	NM_007480	down	0.04	ns
10594631	Aph1b	anterior pharynx defective 1b homolog (<i>C. elegans</i>)	NM_177583	up	0.04	ns
10398678	Eif5	eukaryotic translation initiation factor 5	NM_173363	down	0.04	ns
10446235	Trip10	thyroid hormone receptor interactor 10	NM_134125	up	0.04	ns
10480714	Uap1l1	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	NM_001033293	down	0.04	ns
10600480	4930408F14Rik	RIKEN cDNA 4930408F14 gene	BC117726	up	0.04	ns
10603230	4930408F14Rik	RIKEN cDNA 4930408F14 gene	BC117726	up	0.04	ns
10605353	4930408F14Rik	RIKEN cDNA 4930408F14 gene	BC117726	up	0.04	ns
10555262	Xrra1	X-ray radiation resistance associated 1	BC151014	down	0.04	ns
10433702	Mpv17l	Mpv17 transgene, kidney disease mutant-like	NM_033564	down	0.04	ns
10572527	EG665858	predicted gene, EG665858	ENSMUST0000110075	down	0.04	0.02
10388954	Omg	oligodendrocyte myelin glycoprotein	NM_019409	down	0.04	ns
10607475	Prdx4	peroxiredoxin 4	NM_016764	down	0.04	ns
10576439	Cog2	component of oligomeric golgi complex 2	NM_029746	down	0.04	ns
10479514	Col20a1	collagen, type XX, alpha 1	BC016112	up	0.04	ns
10474096	Lrrc4c	leucine rich repeat containing 4C	NM_178725	down	0.04	ns
10561461	Samd4b	sterile alpha motif domain containing 4B	NM_175021	up	0.04	ns
10590479	Zfp167	zinc finger protein 167	BC119591	down	0.04	ns
10564573	Chd2	chromodomain helicase DNA binding protein 2	NM_001081345	up	0.04	ns
10490352	Taf4a	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	NM_001081092	up	0.04	ns
10350188	Tmem9	transmembrane protein 9	NM_025439	down	0.04	ns
10593492	Zc3h12c	zinc finger CCCH type containing 12C	AK220416	up	0.04	ns
10345368	D1Ert448e	DNA segment, Chr 1, ERATO Doi 448, expressed	ENSMUST0000097783	up	0.04	ns
10369932	Susd2	sushi domain containing 2	NM_027890	down	0.04	ns
10486616	Ubr1	ubiquitin protein ligase E3 component n-recognin 1	NM_009461	down	0.04	ns
10507250	Pomgnt1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	NM_026651	down	0.04	ns
10497481	2810416G20Rik	RIKEN cDNA 2810416G20 gene	ENSMUST0000057404	down	0.04	ns
10558285	Zranb1	zinc finger, RAN-binding domain containing 1	NM_207302	down	0.04	0.01
10413598	Tmem110	transmembrane protein 110	NM_028839	down	0.04	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10427436	C7	complement component 7	XM_356827	down	0.04	ns
10442083	---	MI0000561 Mus musculus let-7e stem-loop	---	down	0.04	ns
10481734	Lrsam1	leucine rich repeat and sterile alpha motif containing 1	NM_199302	down	0.04	ns
10586011	Larp6	La ribonucleoprotein domain family, member 6	NM_026235	down	0.04	ns
10373367	Coq10a	coenzyme Q10 homolog A (yeast)	NM_001081040	down	0.04	ns
10511084	Nadk	NAD kinase	NM_138671	up	0.04	ns
10428983	0910001A06Rik	RIKEN cDNA 0910001A06 gene	BC011343	down	0.04	ns
10512739	Xpa	xeroderma pigmentosum, complementation group A	NM_011728	down	0.04	ns
10424945	Kifc2	kinesin family member C2	NM_010630	down	0.04	ns
10411927	Sdccag10	serologically defined colon cancer antigen 10	NM_026072	down	0.04	ns
10556208	D930014E17Rik	RIKEN cDNA D930014E17 gene	NM_020616	down	0.04	ns
10586405	Spg21	spastic paraplegia 21 homolog (human)	NM_138584	down	0.04	ns
10481508	Asb6	ankyrin repeat and SOCS box-containing 6	NM_133346	up	0.04	ns
10507594	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	NM_011400	up	0.04	ns
10358978	Ier5	immediate early response 5	NM_010500	up	0.04	3.96e-06
10571653	Actg1	actin, gamma, cytoplasmic 1	NM_009609	down	0.04	ns
10456836	St8sia5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	NM_153124	up	0.04	0.005
10543785	AB041803	cDNA sequence AB041803	ENSMUST0000115107	up	0.04	ns
10595402	BC023892	cDNA sequence BC023892	ENSMUST0000098501	up	0.04	ns
10458251	Sil1	endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	NM_030749	down	0.04	ns
10488231	Rps2	ribosomal protein S2	NM_008503	down	0.04	ns
10515220	Faah	fatty acid amide hydrolase	NM_010173	down	0.04	ns
10442643	Nme3	non-metastatic cells 3, protein expressed in	NM_019730	down	0.04	ns
10468200	Cuedc2	CUE domain containing 2	NM_024192	down	0.04	ns
10499309	Apoa1bp	apolipoprotein A-I binding protein	NM_144897	down	0.04	ns
10454514	Lims2	LIM and senescent cell antigen like domains 2	NM_144862	up	0.04	ns
10451093	Spats1	spermatogenesis associated, serine-rich 1	NM_027649	down	0.04	ns
10599841	C230004F18Rik	RIKEN cDNA C230004F18 gene	AK082088	up	0.04	ns
10400357	Baz1a	bromodomain adjacent to zinc finger domain 1A	NM_013815	up	0.04	ns
10453102	Sfrs7	splicing factor, arginine/serine-rich 7	NM_146083	up	0.04	ns
10605222	Irak1	interleukin-1 receptor-associated kinase 1	NM_008363	down	0.04	ns
10404061	Hist1h2bb	histone cluster 1, H2bb	NM_175664	up	0.04	ns
10572949	Nr3c2	nuclear receptor subfamily 3, group C, member 2	NM_001083906	down	0.04	0.02
10572533	Myo9b	myosin IXb	NM_015742	up	0.04	ns
10468916	Fam171a1	family with sequence similarity 171, member A1	NM_001081161	up	0.04	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10511510	Ints8	integrator complex subunit 8	NM_178112	up	0.04	ns
10403558	Ero11b	ERO1-like beta (<i>S. cerevisiae</i>)	NM_026184	up	0.04	ns
10346562	Cflar	CASP8 and FADD-like apoptosis regulator	NM_207653	up	0.04	ns
10577999	Unc5d	unc-5 homolog D (<i>C. elegans</i>)	NM_153135	down	0.04	ns
10555009	---	MI0004692 Mus musculus miR-708 stem-loop	---	up	0.04	ns
10604564	Gpc4	glypican 4	NM_008150	down	0.04	ns
10474526	Lpcat4	lysophosphatidylcholine acyltransferase 4	NM_207206	down	0.04	ns
10378555	Smyd4	SET and MYND domain containing 4	NM_001102611	down	0.04	ns
10461369	Ahnak	AHNAK nucleoprotein (desmoyokin)	NM_009643	up	0.04	ns
10395719	Npas3	neuronal PAS domain protein 3	NM_013780	down	0.04	ns
10561927	Aplp1	amyloid beta (A4) precursor-like protein 1	NM_007467	down	0.04	ns
10569707	Myadm	myeloid-associated differentiation marker	NM_001093765	up	0.04	ns
10572838	Sin3b	transcriptional regulator, SIN3B (yeast)	NM_009188	up	0.04	ns
10382022	Ccdc44	coiled-coil domain containing 44	NM_027346	up	0.04	ns
10392449	Wipi1	WD repeat domain, phosphoinositide interacting 1	NM_145940	down	0.04	ns
10576216	Rpl13	ribosomal protein L13	AF357327	down	0.04	ns
10525733	Setd8	SET domain containing (lysine methyltransferase) 8	NM_030241	up	0.04	ns
10404928	C78339	expressed sequence C78339	NM_001033192	up	0.04	ns
10481383	Wdr34	WD repeat domain 34	NM_001008498	down	0.04	ns
10580010	Pkn1	protein kinase N1	NM_177262	down	0.04	ns
10356172	5033414K04Rik	RIKEN cDNA 5033414K04 gene	BC080290	up	0.04	ns
10506843	Cc2d1b	coiled-coil and C2 domain containing 1B	NM_177045	down	0.04	ns
10572580	Use1	unconventional SNARE in the ER 1 homolog (<i>S. cerevisiae</i>)	NM_025917	down	0.04	ns
10581538	Nqo1	NAD(P)H dehydrogenase, quinone 1	NM_008706	down	0.04	ns
10473224	Dusp19	dual specificity phosphatase 19	NM_024438	up	0.04	ns
10509228	Hnrnpr	heterogeneous nuclear ribonucleoprotein R	NM_028871	down	0.04	ns
10355401	Acp1	acid phosphatase 1, soluble	ENSMUST0000074038	down	0.04	ns
10410766	Nr2f1	nuclear receptor subfamily 2, group F, member 1	NM_010151	down	0.04	ns
10379204	Poldip2	polymerase (DNA-directed), delta interacting protein 2	NM_026389	down	0.04	ns
10449608	Mdga1	MAM domain containing glycosylphosphatidylinositol anchor 1	NM_001081160	up	0.04	ns
10490370	Psmg7	proteasome (prosome, macropain) subunit, alpha type 7	NM_011969	down	0.04	ns
10526923	1110007L15Rik	RIKEN cDNA 1110007L15 gene	BC019557	down	0.04	ns
10420155	Dhrs1	dehydrogenase/reductase (SDR family) member 1	NM_026819	down	0.04	ns
10605999	---	snoRNA chromosome:NCBIM37:X:98336772:98336891:-1 gene:ENSMUSG00000065180	ENSMUST0000083246	up	0.04	ns
10578557	Ccdc111	coiled-coil domain containing 111	NM_001001	down	0.04	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
			184			
10456405	Slmo1	slowmo homolog 1 (Drosophila)	NM_144867	down	0.04	ns
10522596	Tmem165	transmembrane protein 165	NM_011626	down	0.04	ns
10506254	Raver2	ribonucleoprotein, PTB-binding 2	NM_183024	up	0.04	ns
10453318	Abcg5	ATP-binding cassette, sub-family G (WHITE), member 5	NM_031884	up	0.04	ns
10568939	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NM_053119	down	0.04	ns
10506154	Alg6	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase)	NM_001081264	down	0.04	ns
10567095	Calca	calcitonin/calcitonin-related polypeptide, alpha	NM_007587	up	0.04	ns
10394245	Dnajc27	DnaJ (Hsp40) homolog, subfamily C, member 27	NM_153082	down	0.04	ns
10578964	1810029B16Rik	RIKEN cDNA 1810029B16 gene	BC016246	up	0.04	ns
10374790	---	Genscan chromosome.NCBIM37:11:28646529:28857608:1	GENSCAN0000027048	up	0.04	ns
10543428	Iqub	IQ motif and ubiquitin domain containing	NM_172535	up	0.04	ns
10361110	Dtl	denticleless homolog (Drosophila)	NM_029766	down	0.04	ns
10395142	Sh3yl1	Sh3 domain YSC-like 1	NM_013709	down	0.04	ns
10579663	Eps15l1	epidermal growth factor receptor pathway substrate 15-like 1	NM_007944	down	0.04	ns
10497944	Mfsd8	major facilitator superfamily domain containing 8	NM_028140	up	0.04	ns
10533176	1110008J03Rik	RIKEN cDNA 1110008J03 gene	BC021365	up	0.04	ns
10454369	Fhod3	formin homology 2 domain containing 3	NM_175276	down	0.04	ns
10562911	Tbc1d17	TBC1 domain family, member 17	NM_001042655	down	0.04	ns
10494821	Tspan2	tetraspanin 2	NM_027533	down	0.04	0.02
10380137	Bzrap1	benzodiazapine receptor associated protein 1	NM_172449	down	0.04	ns
10393879	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	AK047224	up	0.04	ns
10458046	D0H4S114	DNA segment, human D4S114	NM_053078	down	0.04	ns
10499988	2310007A19Rik	RIKEN cDNA 2310007A19 gene	BC107021	down	0.04	ns
10511042	C030017K20Rik	RIKEN cDNA C030017K20 gene	BC113168	up	0.04	ns
10494227	Lass2	LAG1 homolog, ceramide synthase 2	NM_029789	down	0.04	ns
10456392	Cidea	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	NM_007702	down	0.04	ns
10515700	BC059842	cDNA sequence BC059842	ENSMUST0000075406	down	0.04	ns
10374012	Rasl10a	RAS-like, family 10, member A	NM_145216	up	0.04	0.01
10404059	Hist1h1c	histone cluster 1, H1c	NM_015786	down	0.04	ns
10438530	Clcn2	chloride channel 2	NM_009900	down	0.04	ns
10368486	Rnf146	ring finger protein 146	NM_001110197	down	0.04	ns
10347748	AcsI3	acyl-CoA synthetase long-chain family member 3	NM_028817	up	0.04	ns
10458424	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-	NM_175770	up	0.04	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
		associated factor				
10531193	Adamts3	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	down	0.04	ns
10383575	Tbcd	tubulin-specific chaperone d	NM_029878	down	0.04	ns
10467688	Exosc1	exosome component 1	NM_025644	down	0.04	ns
10511901	Ankrd6	ankyrin repeat domain 6	NM_001012450	up	0.04	ns
10459138	Slc6a7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	NM_201353	down	0.04	ns
10531987	Gbp4	guanylate binding protein 4	NM_008620	down	0.04	ns
10517250	Extl1	exostoses (multiple)-like 1	NM_019578	down	0.04	ns
10394843	---	Genscan chromosome:NCBIM37:12:20274447: 20283883:1	GENSCAN0000015114	down	0.04	ns
10435714	Tmem39a	transmembrane protein 39a	NM_026407	up	0.04	ns
10437687	Litaf	LPS-induced TN factor	NM_019980	down	0.04	ns
10574676	Nol3	nucleolar protein 3 (apoptosis repressor with CARD domain)	NM_030152	down	0.04	ns
10538100	Repin1	replication initiator 1	NM_001079901	down	0.04	ns
10565152	9330120H11Rik	RIKEN cDNA 9330120H11 gene	ENSMUST0000098326	up	0.04	ns
10541522	Rps2	ribosomal protein S2	NM_008503	down	0.04	ns
10365601	Gnptab	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	NM_001004164	up	0.04	ns
10428052	Cct5	chaperonin containing Tcp1, subunit 5 (epsilon)	NM_007637	up	0.04	ns
10348000	2810459M11Rik	RIKEN cDNA 2810459M11 gene	BC137675	down	0.04	ns
10376263	Mfap3	microfibrillar-associated protein 3	NM_145426	up	0.04	ns
10553788	Atp10a	ATPase, class V, type 10A	NM_009728	up	0.04	ns
10430770	Tob2	transducer of ERBB2, 2	NM_020507	up	0.04	ns
10578623	Wwc2	WW, C2 and coiled-coil domain containing 2	NM_133791	down	0.04	ns
10350753	Glu1	glutamate-ammonia ligase (glutamine synthetase)	NM_008131	up	0.04	ns
10358982	Mr1	major histocompatibility complex, class I-related	NM_008209	down	0.04	ns
10438376	Rps2	ribosomal protein S2	NM_008503	down	0.04	ns
10501827	A730020M07Rik	RIKEN cDNA A730020M07 gene	ENSMUST0000050571	up	0.04	ns
10553015	Bcat2	branched chain aminotransferase 2, mitochondrial	NM_009737	up	0.04	ns
10427538	Nipbl	Nipped-B homolog (Drosophila)	NM_201232	up	0.04	ns
10412559	Slbp	stem-loop binding protein	NM_009193	down	0.04	ns
10351056	Ankrd45	ankyrin repeat domain 45	BC049713	up	0.04	ns
10582094	Mbtps1	membrane-bound transcription factor peptidase, site 1	NM_019709	down	0.04	ns
10369792	Arid5b	AT rich interactive domain 5B (MRF1-like)	NM_023598	up	0.04	ns
10460312	Cdk2ap2	CDK2-associated protein 2	NM_026373	up	0.04	0.05
10451547	LOC100043385	similar to high mobility group nucleosomal binding domain 2	ENSMUST0	down	0.04	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10579060	4930467E23Rik // EG665756	RIKEN cDNA 4930467E23 gene // predicted gene, EG665756	0000116100 ENSMUST0 0000084046	down	0.04	ns
10494509	Pias3	protein inhibitor of activated STAT 3	NM_146135	down	0.04	ns
10508711	Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	NM_025579	up	0.04	0.02
10560945	Grik5	glutamate receptor, ionotropic, kainate 5 (gamma 2)	NM_008168	down	0.04	ns
10420659	6330409N04Rik	RIKEN cDNA 6330409N04 gene	BC037015	down	0.04	ns
10378988	Phf12	PHD finger protein 12	NM_174852	down	0.04	ns
10439016	4930444G20Rik	RIKEN cDNA 4930444G20 gene	NM_053264	up	0.05	ns
10520234	2010209O12Rik	RIKEN cDNA 2010209O12 gene	NM_133913	down	0.05	ns
10526181	Gats	opposite strand transcription unit to Stag3	NM_030719	up	0.05	0.03
10465424	OTTMUSG0000018617	predicted gene, OTTMUSG00000018617	ENSMUST0 0000063955	down	0.05	ns
10501860	Fnbp1l	formin binding protein 1-like	NM_001114 665	up	0.05	ns
10547282	Zfp9	zinc finger protein 9	NM_011763	down	0.05	ns
10350146	Phlda3	pleckstrin homology-like domain, family A, member 3	NM_013750	down	0.05	ns
10488156	Kif16b	kinesin family member 16B	NM_001081 133	down	0.05	ns
10482772	Nr4a2	nuclear receptor subfamily 4, group A, member 2	NM_013613	up	0.05	ns
10575021	Zfp90	zinc finger protein 90	NM_011764	down	0.05	ns
10375439	Med7	mediator complex subunit 7	NM_025426	up	0.05	ns
10519857	Hgf	hepatocyte growth factor	NM_010427	down	0.05	ns
10579852	Mmaa	methylmalonic aciduria (cobalamin deficiency) type A	NM_133823	up	0.05	ns
10542395	Atf7ip	activating transcription factor 7 interacting protein	ENSMUST0 0000066689	down	0.05	ns
10398362	Rian	RNA imprinted and accumulated in nucleus	AF357355	up	0.05	ns
10570418	Upf3a	UPF3 regulator of nonsense transcripts homolog A (yeast)	NM_025924	down	0.05	ns
10468292	ENSMUSG00000071525	predicted gene, ENSMUSG00000071525	AK086428	up	0.05	ns
10361375	Fbxo5	F-box protein 5	NM_025995	down	0.05	0.05
10590821	9230110C19Rik	RIKEN cDNA 9230110C19 gene	BC115525	up	0.05	ns
10597960	Slc6a20a	solute carrier family 6 (neurotransmitter transporter), member 20A	NM_139142	down	0.05	0.04
10410452	Srd5a1	steroid 5 alpha-reductase 1	NM_175283	down	0.05	ns
10453166	Cdkl4	cyclin-dependent kinase-like 4	NM_001033 443	down	0.05	ns
10406663	Arsb	arylsulfatase B	NM_009712	down	0.05	ns
10464504	Lrp5	low density lipoprotein receptor-related protein 5	NM_008513	up	0.05	ns
10358583	Hmcn1	hemicentin 1	NM_001024 720	down	0.05	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10381018	4121402D02Rik	RIKEN cDNA 4121402D02 gene	NM_028722	up	0.05	ns
10346260	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	NM_028091	down	0.05	ns
10415159	Thtpa	thiamine triphosphatase	NM_153083	down	0.05	0.04
10447602	Ezr	ezrin	NM_009510	up	0.05	ns
10449258	Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	NM_008113	down	0.05	ns
10507218	Mknk1	MAP kinase-interacting serine/threonine kinase 1	NM_021461	down	0.05	0.007
10567564	Cdr2	cerebellar degeneration-related 2	NM_007672	up	0.05	ns
10461423	Fads3	fatty acid desaturase 3	NM_021890	down	0.05	ns
10495675	F3	coagulation factor III	NM_010171	up	0.05	ns
10377927	Rnf167	ring finger protein 167	NM_027445	down	0.05	ns
10402314	Rps2	ribosomal protein S2	NM_008503	down	0.05	ns
10501649	Rtcd1	RNA terminal phosphate cyclase domain 1	NM_025517	down	0.05	ns
10365983	Lum	lumican	NM_008524	down	0.05	ns
10523772	Lrrc8d	leucine rich repeat containing 8D	NM_178701	down	0.05	ns
10604424	Zfp280c	zinc finger protein 280c	NM_153532	down	0.05	ns
10368893	Lace1	lactation elevated 1	NM_145743	up	0.05	ns
10476886	Sstr4	somatostatin receptor 4	NM_009219	up	0.05	ns
10373577	Ormdl2	ORM1-like 2 (S. cerevisiae)	NM_024180	up	0.05	ns
10487382	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	NM_029629	down	0.05	ns
10472199	Upp2	uridine phosphorylase 2	NM_029692	down	0.05	ns
10594353	Map2k5	mitogen-activated protein kinase kinase 5	NM_011840	down	0.05	ns
10585328	4930510E17Rik	RIKEN cDNA 4930510E17 gene	ENSMUSTO0000034550	up	0.05	ns
10498064	Setd7	SET domain containing (lysine methyltransferase) 7	NM_080793	up	0.05	ns
10477604	Itch	itchy, E3 ubiquitin protein ligase	NM_008395	up	0.05	ns
10362538	Lama4	laminin, alpha 4	NM_010681	down	0.05	ns
10430997	Paccin2	protein kinase C and casein kinase substrate in neurons 2	NM_011862	up	0.05	ns
10551215	Rnf170	ring finger protein 170	ENSMUSTO0000014022	down	0.05	ns
10467139	Lipa	lysosomal acid lipase A	NM_021460	up	0.05	ns
10412562	Flnb	filamin, beta	NM_134080	down	0.05	ns
10364702	Midn	midnolin	NM_021565	up	0.05	0.0006
10469867	Pnpla7	patatin-like phospholipase domain containing 7	NM_146251	up	0.05	ns
10495316	Psrc1	proline/serine-rich coiled-coil 1	NM_019976	up	0.05	ns
10446341	4930505H01Rik	RIKEN cDNA 4930505H01 gene	AK132847	up	0.05	ns
10439881	5330426P16Rik	RIKEN cDNA 5330426P16 gene	ENSMUSTO0000089395	up	0.05	ns
10505526	---	Mouse LLRep3 protein mRNA, complete cds	M20632	down	0.05	ns
10477929	1110008F13Rik	RIKEN cDNA 1110008F13 gene	NM_026124	up	0.05	ns
10494069	Tnrc4	trinucleotide repeat containing 4	NM_172434	down	0.05	ns
10582743	Pcnx12	pecanex-like 2 (Drosophila)	NM_175561	down	0.05	ns

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10383767	Osbp2	oxysterol binding protein 2	NM_152818	down	0.05	ns
10484440	Zdhhc5	zinc finger, DHHC domain containing 5	NM_144887	up	0.05	ns
10488797	Pxmp4	peroxisomal membrane protein 4	NM_021534	down	0.05	ns
10500327	Hist2h3c2	histone cluster 2, H3c2	NM_054045	up	0.05	ns
10385599	Canx	calnexin	NM_007597	up	0.05	ns
10595109	Lrrc1	leucine rich repeat containing 1	NM_172528	up	0.05	ns
10438262	Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	NM_153150	down	0.05	ns
10534889	Hrbl	HIV-1 Rev binding protein-like	NM_178162	down	0.05	ns
10496892	Fubp1	far upstream element (FUZE) binding protein 1	NM_057172	up	0.05	ns
10428370	Abra	actin-binding Rho activating protein	NM_175456	up	0.05	ns
10414433	6720456H20Rik	RIKEN cDNA 6720456H20 gene	NM_172600	up	0.05	ns
10566132	Rhog	ras homolog gene family, member G	NM_019566	down	0.05	ns
10505747	Rraga	Ras-related GTP binding A	NM_178376	down	0.05	ns
10455118	Pcdhb18	protocadherin beta 18	NM_053143	down	0.05	ns
10491885	Pcdh10	protocadherin 10	NM_001098171	down	0.05	ns
10447224	Dync2li1	dynein cytoplasmic 2 light intermediate chain 1	NM_172256	down	0.05	ns
10508099	1810007P19Rik	RIKEN cDNA 1810007P19 gene	NM_172701	down	0.05	ns
10511703	Ripk2	receptor (TNFRSF)-interacting serine-threonine kinase 2	NM_138952	down	0.05	ns
10399308	Fkbp1b	FK506 binding protein 1b	NM_016863	down	0.05	ns
10428302	Kif10	Kruppel-like factor 10	NM_013692	up	ns	0.001
10431410	Mapk11	mitogen-activated protein kinase 11	NM_011161	up	ns	0.004
10376019	OTTMUSG00000005637	predicted gene, OTTMUSG00000005637	XM_910917	up	ns	0.004
10410166	Cntnap3	contactin associated protein-like 3	NM_001081129	down	ns	0.005
10580282	Junb	Jun-B oncogene	NM_008416	up	ns	0.006
10489406	Rims4	regulating synaptic membrane exocytosis 4	NM_183023	up	ns	0.007
10413229	Anxa11	annexin A11	NM_013469	up	ns	0.008
10432986	Aaas	achalasia, adrenocortical insufficiency, alacrimia	NM_153416	down	ns	0.008
10518069	Efhd2	EF hand domain containing 2	NM_025994	up	ns	0.008
10427026	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	NM_019518	up	ns	0.009
10393662	Nptx1	neuronal pentraxin 1	NM_008730	up	ns	0.009
10587085	BC031353	cDNA sequence BC031353	NM_001113283	down	ns	0.009
10501762	Snx7	sorting nexin 7	NM_029655	down	ns	0.01
10469070	Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	NM_016918	up	ns	0.01
10485594	OTTMUSG0000	predicted gene, OTTMUSG00000014964	BC147362	up	ns	0.01

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
	0014964					
10429385	---	MI0000173 Mus musculus miR-151 stem-loop	---	up	ns	0.01
10528877	Lmbr1	limb region 1	NM_020295	down	ns	0.01
10425364	Atf4	activating transcription factor 4	NM_009716	up	ns	0.01
10574220	Cx3cl1	chemokine (C-X3-C motif) ligand 1	NM_009142	up	ns	0.01
10492538	ENSMUSG00000074573	predicted gene, ENSMUSG00000074573	ENSMUST0000099064	down	ns	0.01
10363845	Ccdc6	coiled-coil domain containing 6	NM_001111121	up	ns	0.01
10574727	Slc9a5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	NM_001081332	up	ns	0.01
10515797	Tmem125	transmembrane protein 125	NM_172383	down	ns	0.01
10421418	Epb4.9	erythrocyte protein band 4.9	NM_013514	up	ns	0.01
10451363	Srf	serum response factor	NM_020493	up	ns	0.02
10461152	Snhg1	small nucleolar RNA host gene (non-protein coding) 1	AK051045	down	ns	0.02
10461158	Snhg1	small nucleolar RNA host gene (non-protein coding) 1	AK051045	down	ns	0.02
10607738	Car5b	carbonic anhydrase 5b, mitochondrial	NM_181315	down	ns	0.02
10390560	Stac2	SH3 and cysteine rich domain 2	NM_146028	up	ns	0.02
10385709	C330016O10Rik	RIKEN cDNA C330016O10 gene	NM_145974	up	ns	0.02
10601595	3110007F17Rik	RIKEN cDNA 3110007F17 gene	BC027572	down	ns	0.02
10548038	Ntf3	neurotrophin 3	NM_008742	down	ns	0.02
10479607	Lime1	Lck interacting transmembrane adaptor 1	NM_023684	up	ns	0.02
10524310	Ttc28	tetratricopeptide repeat domain 28	BC002262	down	ns	0.02
10356403	Kcnj13	potassium inwardly-rectifying channel, subfamily J, member 13	NM_001110227	up	ns	0.02
10404038	Hist1h3d	histone cluster 1, H3d	NM_178204	up	ns	0.02
10515168	Cyp4x1	cytochrome P450, family 4, subfamily x, polypeptide 1	NM_001003947	down	ns	0.02
10452188	Mllt1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	NM_022328	up	ns	0.02
10430660	Pdgfb	platelet derived growth factor, B polypeptide	NM_011057	up	ns	0.02
10421351	Polr3d	polymerase (RNA) III (DNA directed) polypeptide D	NM_025945	up	ns	0.02
10571111	Zfp703	zinc finger protein 703	NM_001101502	up	ns	0.02
10371379	Nuak1	NUAK family, SNF1-like kinase, 1	NM_001004363	up	ns	0.02
10440238	Nsun3	NOL1/NOP2/Sun domain family member 3	NM_178925	down	ns	0.02
10368585	Nkain2	Na ⁺ /K ⁺ transporting ATPase interacting 2	NM_001013411	down	ns	0.02
10582719	Sipa1l2	signal-induced proliferation-associated 1 like 2	NM_001081337	up	ns	0.02
10491732	Fat4	FAT tumor suppressor homolog 4 (Drosophila)	NM_183221	down	ns	0.02

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10527268	Pms2	postmeiotic segregation increased 2 (S. cerevisiae)	NM_008886	down	ns	0.02
10511808	4930528A17Rik	RIKEN cDNA 4930528A17 gene	ENSMUST0000062777	down	ns	0.02
10603627	Bcor	BCL6 interacting corepressor	NM_175045	up	ns	0.03
10429222	1700010C24Rik	RIKEN cDNA 1700010C24 gene	BC125645	up	ns	0.03
10539211	Lrrtm4	leucine rich repeat transmembrane neuronal 4	NM_178731	down	ns	0.03
10430941	Rrp7a	ribosomal RNA processing 7 homolog A (S. cerevisiae)	BC012523	up	ns	0.03
10451303	Ttbk1	tau tubulin kinase 1	BC059249	up	ns	0.03
10531484	Ankrd56	ankyrin repeat domain 56	NM_175270	up	ns	0.03
10579373	Mast3	microtubule associated serine/threonine kinase 3	BC024265	up	ns	0.03
10468795	Rab11fip2	RAB11 family interacting protein 2 (class I)	NM_001033172	down	ns	0.03
10600317	Opn1mw	opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)	NM_008106	up	ns	0.03
10462442	Il33	interleukin 33	NM_133775	down	ns	0.03
10601598	3110007F17Rik	RIKEN cDNA 3110007F17 gene	BC027572	down	ns	0.03
10506569	Usp24	ubiquitin specific peptidase 24	BC030081	down	ns	0.03
10601771	Armxc1	armadillo repeat containing, X-linked 1	NM_030066	down	ns	0.03
10481634	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	NM_146118	up	ns	0.03
10369474	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	NM_010124	up	ns	0.03
10362450	---	cdna:novel chromosome:NCBIM37:10:33062878:33194324:1 gene:ENSMUSG00000071344	---	up	ns	0.03
10389238	Dusp14	dual specificity phosphatase 14	NM_019819	up	ns	0.03
10391744	ENSMUSG00000075516	predicted gene, ENSMUSG00000075516	AK135410	up	ns	0.03
10491056	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	NM_030732	down	ns	0.03
10545528	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	BC061116	down	ns	0.03
10386582	Top3a	topoisomerase (DNA) III alpha	NM_009410	down	ns	0.03
10484683	Olf1134	olfactory receptor 1134	NM_147030	down	ns	0.03
10412517	ENSMUSG00000057445	predicted gene, ENSMUSG00000057445	ENSMUST0000090647	down	ns	0.03
10387372	Jmjd3	jumonji domain containing 3	NM_001017426	up	ns	0.03
10499168	Kirrel	kin of IRRE like (Drosophila)	NM_130867	up	ns	0.03
10455080	Pcdhb9	protocadherin beta 9	NM_053134	down	ns	0.03
10482500	Rnd3	Rho family GTPase 3	NM_028810	up	ns	0.03
10565627	Aqp11	aquaporin 11	NM_175105	down	ns	0.03
10524955	Tesc	tescalcin	NM_021344	up	ns	0.03
10397085	Rbm25	RNA binding motif protein 25	NM_027349	down	ns	0.04
10541246	Il17ra	interleukin 17 receptor A	NM_008359	up	ns	0.04

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10413482	Wnt5a	wingless-related MMTV integration site 5A	NM_009524	down	ns	0.04
10382341	Sstr2	somatostatin receptor 2	NM_009217	up	ns	0.04
10498146	Nhlrc3	NHL repeat containing 3	NM_172501	down	ns	0.04
10574718	Tmem208	transmembrane protein 208	NM_025486	up	ns	0.04
10352957	Rgs20	regulator of G-protein signaling 20	NM_021374	up	ns	0.04
10601588	3110007F17Rik	RIKEN cDNA 3110007F17 gene	BC027572	down	ns	0.04
10440993	Rcan1	regulator of calcineurin 1	NM_001081549	up	ns	0.04
10515399	Plk3	polo-like kinase 3 (Drosophila)	NM_013807	up	ns	0.04
10534405	Wbscr22	Williams Beuren syndrome chromosome region 22	NM_025375	up	ns	0.04
10544062	D630045J12Rik	RIKEN cDNA D630045J12 gene	ENSMUST0000078942	up	ns	0.04
10403943	Hist1h2bm	histone cluster 1, H2bm	NM_178200	up	ns	0.04
10377695	Phf23	PHD finger protein 23	NM_030064	up	ns	0.04
10368409	Lama2	laminin, alpha 2	NM_008481	down	ns	0.04
10479560	Rtel1	regulator of telomere elongation helicase 1	NM_001001882	down	ns	0.04
10404772	ENSMUSG0000074927	predicted gene, ENSMUSG00000074927	ENSMUST0000099561	down	ns	0.04
10504203	4930578G10Rik	RIKEN cDNA 4930578G10 gene	AK006581	down	ns	0.04
10570982	Fgfr1	fibroblast growth factor receptor 1	NM_010206	up	ns	0.04
10511298	9430015G10Rik	RIKEN cDNA 9430015G10 gene	BC004010	up	ns	0.04
10436304	Abi3bp	ABI gene family, member 3 (NESH) binding protein	NM_001014423	down	ns	0.04
10603066	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	NM_027286	down	ns	0.04
10587854	Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	NM_177909	down	ns	0.04
10436106	C330027C09Rik	RIKEN cDNA C330027C09 gene	NM_172616	down	ns	0.04
10473473	Olf1022	olfactory receptor 1022	NM_146589	up	ns	0.04
10589061	Dalrd3	DALR anticodon binding domain containing 3	NM_026378	up	ns	0.04
10459837	8030462N17Rik	RIKEN cDNA 8030462N17 gene	BC120889	up	ns	0.04
10603870	Elk1	ELK1, member of ETS oncogene family	NM_007922	up	ns	0.04
10451893	Stap2	signal transducing adaptor family member 2	NM_145934	up	ns	0.04
10521068	4933407H18Rik	RIKEN cDNA 4933407H18 gene	NM_001081101	down	ns	0.04
10493498	---	Mus musculus mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library, clone:G830001D04 product:hypothetical protein, full insert sequence.	---	down	ns	0.04
10514510	Cyp2j6	cytochrome P450, family 2, subfamily j, polypeptide 6	NM_010008	down	ns	0.04
10438220	Car15	carbonic anhydrase 15	NM_030558	up	ns	0.04
10409190	Cenpp	centromere protein P	NM_025495	down	ns	0.04
10606376	2610002M06Rik	RIKEN cDNA 2610002M06 gene	BC016070	down	ns	0.04
10528880	Lmbr1	limb region 1	NM_020295	down	ns	0.05

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Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Direction	Sham Adj. P value	ADX Adj. P value
10404913	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	NM_026056	up	ns	0.05
10605143	Arhgap4	Rho GTPase activating protein 4	NM_138630	up	ns	0.05
10595094	2310046A06Rik	RIKEN cDNA 2310046A06 gene	BC089626	down	ns	0.05
10375501	---	ncrna:snoRNA chromosome:NCBIM37:11:48616641:48616708:1 gene:ENSMUSG00000064780	---	down	ns	0.05
10415408	BC030046	cDNA sequence BC030046	ENSMUST0000100529	down	ns	0.05
10535659	Cyp3a16	cytochrome P450, family 3, subfamily a, polypeptide 16	NM_007820	up	ns	0.05
10543709	Tmem209	transmembrane protein 209	NM_178625	down	ns	0.05

Supplementary Table 2: Functional clustering of probe sets significantly affected by sleep deprivation (SD) in sham-operated D2 mice (Ingenuity Pathways Analysis; Ingenuity Systems). Indicated for each functional cluster are the range of P values based on all 1476 probes significantly affected by SD and the number of probes decreased (down) or increased (up) by SD. Clusters for which probes are mostly down or up have been highlighted in yellow. Last column presents the results of the functional clustering of the 260 probes showing interaction (see text and gene list in Supplementary Table 3). Clusters lacking a significant number of transcripts with interaction could depend less on corticosterone signaling and are highlighted in yellow. ns: $p \geq 0.05$.

Class	Functional Clusters	P values (for all)	N of Down probes	N of Up probes	N of probes with INTERACTION
Molecular and cellular functions	Post-translational modification	$1.3E^{-8} - 2.1E^{-2}$	3	73	14
	Protein folding	$1.3E^{-8} - 1.9E^{-6}$	ns	18	ns
	Cellular compromise	$3.6E^{-8} - 2.3E^{-2}$	13	58	7
	Cellular function and maintenance	$1.1E^{-7} - 2.3E^{-2}$	20	18	15
	Small molecule biochemistry	$4.7E^{-6} - 2.1E^{-2}$	63	59	37
	RNA post-transcriptional modification	$4.8E^{-6} - 1.7E^{-4}$	12	11	ns
	Drug metabolism	$5.5E^{-6} - 2.1E^{-2}$	12	13	10
	Lipid metabolism	$5.5E^{-6} - 1.8E^{-2}$	35	9	17
	Cell death	$1.1E^{-5} - 2.3E^{-2}$	16	136	27
	Cell cycle	$1.8E^{-5} - 2.3E^{-2}$	13	75	21
	Neurological disease	$2.0E^{-5} - 2.3E^{-2}$	189	159	21
	Cancer	$6.5E^{-5} - 2.3E^{-2}$	75	163	37
	Cellular growth and proliferation	$6.5E^{-5} - 2.3E^{-2}$	9	134	13
	Respiratory disease	$6.5E^{-5} - 2.1E^{-2}$	3	48	13
	Gene expression	$8.7E^{-5} - 2.3E^{-2}$	5	102	9
	Genetic disorder	$1.3E^{-4} - 2.3E^{-2}$	306	259	29
	Skeletal and muscular disorders	$1.3E^{-4} - 2.3E^{-2}$	44	125	30
	Cell morphology	$2.8E^{-4} - 2.3E^{-2}$	21	63	13
	Cellular assembly and organization	$2.8E^{-4} - 1.8E^{-2}$	38	34	17
	Reproductive system disease	$3.2E^{-4} - 2.3E^{-2}$	20	85	16
	Connective tissue disorders	$3.7E^{-4} - 2.3E^{-2}$	2	97	6
	Immunological disease	$3.7E^{-4} - 2.3E^{-2}$	4	115	9
	Inflammatory disease	$3.7E^{-4} - 2.2E^{-2}$	1	109	6
	DNA replication, recombination and repair	$4.9E^{-4} - 2.9E^{-2}$	26	37	4
	Nucleic acid metabolism	$4.9E^{-4} - 1.2E^{-2}$	9	8	3
	Gastrointestinal disease	$4.9E^{-4} - 2.3E^{-2}$	35	54	15
	Cell signalling	$5.1E^{-4} - 2.3E^{-2}$	1	11	2
	Cellular development	$5.1E^{-4} - 2.3E^{-2}$	6	87	13
	Tissue morphology	$5.1E^{-4} - 2.3E^{-2}$	12	50	15
	Molecular transport	$2.5E^{-3} - 2.3E^{-2}$	34	33	19
Amino acid metabolism	$2.5E^{-3} - 2.1E^{-2}$	7	33	15	
Behavior	$3.7E^{-3} - 2.3E^{-2}$	16	26	2	
Cellular movement	$4.3E^{-3} - 2.2E^{-2}$	18	53	13	
Cell-to-cell signaling and interaction	$4.3E^{-3} - 2.3E^{-2}$	30	7	14	
Protein degradation	$6.1E^{-3} - 6.4E^{-3}$	25	ns	10	

Class	Functional Clusters	P values (for all)	N of Down probes	N of Up probes	N of probes with INTERACTION
System development and function	Protein synthesis	6.4E ⁻³	37	ns	ns
	Metabolic disease	1.1E ⁻²	117	ns	3
	Carbohydrate metabolism	1.2E ⁻² - 2.3E ⁻²	9	11	13
	Endocrine system development and function	4.7E ⁻⁶ - 1.2E ⁻²	6	23	9
	Connective tissue development and function	8.7E ⁻⁵ - 2.3E ⁻²	11	13	9
	Nervous system development and function	2.8E ⁻⁴ - 2.3E ⁻²	47	39	14
	Organ development	3.2E ⁻⁴ - 1.2E ⁻²	5	19	11
	Organismal development	3.4E ⁻⁴ - 2.3E ⁻²	17	60	3
	Skeletal and muscular system development and function	4.2E ⁻⁴ - 2.3E ⁻²	19	20	19
	Cardiovascular system development and function	5.1E ⁻⁴ - 2.3E ⁻²	15	32	14
	Hepatic system development and function	5.1E ⁻⁴	1	5	2
	Hematological system development and function	1.8E ⁻³ - 2.2E ⁻²	12	61	15
Cell-mediated immune response	4.3E ⁻³ - 2.3E ⁻²	1	56	14	
Canonical pathways	Biosynthesis of steroids	5.8E ⁻³	6	ns	ns
	Glucocorticoid receptor signaling	1.0E ⁻²	ns	24	5
	Glutamate metabolism	2.2E ⁻²	3	ns	3
	Phenylalanine metabolism	2.5E ⁻²	4	ns	ns
	Endoplasmic reticulum stress pathway	2.7E ⁻²	ns	3	ns
	Cell cycle: G1/S checkpoint regulation	2.8E ⁻²	ns	6	ns
	LXR/RXR activation	3.2E ⁻²	6	ns	3
	Aldosterone signalling in epithelial cells	3.3E ⁻²	ns	7	ns
	Aryl hydrocarbon receptor signaling	3.5E ⁻²	ns	10	ns
	Fatty acid biosynthesis	3.9E ⁻²	3	ns	ns
	Aminosugars metabolism	4.1E ⁻²	6	ns	ns
	ERK/MAPK signaling	0.35	ns	10	ns
Toxicity pathways	Cholesterol biosynthesis and metabolism	2.8E ⁻³	5	ns	2
	Oxidative stress response mediated by Nrf2	4.0E ⁻³	ns	17	ns
	Mechanism of gene regulation by peroxisome proliferators via PPAR α	4.6E ⁻²	ns	9	3
	p53 signaling	5.8E ⁻²	ns	8	ns

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Supplementary Table 3: Listing of the 260 probe sets showing Group (sham vs. ADX) by Condition (control vs. SD) interaction (FDR < 0.23; see Supplementary text and Supplementary Figure 1) among the 1476 probes affected by sleep deprivation (SD) (see Supplementary Table 1). With the exception of two probe sets (**highlighted**), ADX caused an attenuation of the effect of SD both for probe sets that were increased and that were decreased by SD in sham operated mice. Probes in **bold** have been evaluated by qPCR analysis.

Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Adjusted P value
10478160	2310007D09Rik	RIKEN cDNA 2310007D09 gene	BC068129	0.0006
10362073	Sgk1	serum/glucocorticoid regulated kinase 1	NM_011361	0.0009
10543017	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	NM_013743	0.009
10606989	Tsc22d3	TSC22 domain family, member 3	NM_001077364	0.01
10358619	Hmcn1	hemicentin 1	NM_001024720	0.02
10358978	Ier5	immediate early response 5	NM_010500	0.02
10541071	8430408G22Rik	RIKEN cDNA 8430408G22 gene	BC058515	0.02
10505779	Asah3l	N-acylsphingosine amidohydrolase 3-like	NM_139306	0.02
10593225	Zbtb16	zinc finger and BTB domain containing 16	NM_001033324	0.03
10585328	4930510E17Rik	RIKEN cDNA 4930510E17 gene	ENSMUST0000034550	0.03
10475910	---	snoRNA chromosome:NCBIM37:2:128606112:128606235:1 gene:ENSMUSG00000064937	ENSMUST0000083003	0.03
10452815	Xdh	xanthine dehydrogenase	NM_011723	0.03
10433163	Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	NM_021391	0.04
10572739	ENSMUSG00000060719	predicted gene, ENSMUSG00000060719	AK032580	0.05
10369290	Ddit4	DNA-damage-inducible transcript 4	NM_029083	0.05
10552075	Lgi4	leucine-rich repeat LGI family, member 4	NM_144556	0.05
10400405	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NM_010907	0.05
10511136	B930041F14Rik	RIKEN cDNA B930041F14 gene	NM_178699	0.05
10399680	Cys1	cystin 1	NM_138686	0.05
10434643	Psmb3	proteasome (prosome, macropain) subunit, beta type 3	NM_011971	0.06
10352916	---	MI0000712 Mus musculus miR-29b-2 stem-loop	---	0.06
10359582	Fmo2	flavin containing monooxygenase 2	NM_018881	0.06
10539592	Smyd5	SET and MYND domain containing 5	NM_144918	0.06
10381474	Arl4d	ADP-ribosylation factor-like 4D	NM_025404	0.06
10475890	Mertk	c-mer proto-oncogene tyrosine kinase	NM_008587	0.06
10557058	Polr3e	polymerase (RNA) III (DNA directed) polypeptide E	ENSMUST0000098072	0.06
10450533	Vars2	valyl-tRNA synthetase 2, mitochondrial (putative)	NM_175137	0.06
10471519	Tor2a	torsin family 2, member A	NM_152800	0.06
10358658	Hmcn1	hemicentin 1	NM_001024720	0.06
10531348	Ppef2	protein phosphatase, EF hand calcium-binding domain 2	NM_011148	0.06
10600480	4930408F14Rik	RIKEN cDNA 4930408F14 gene	BC117726	0.06
10603230	4930408F14Rik	RIKEN cDNA 4930408F14 gene	BC117726	0.06
10605353	4930408F14Rik	RIKEN cDNA 4930408F14 gene	BC117726	0.06
10498302	Gm410	gene model 410, (NCBI)	NM_001033349	0.06
10484201	2610301F02Rik	RIKEN cDNA 2610301F02 gene	ENSMUST0000049544	0.06
10461057	Rcor2	REST corepressor 2	NM_054048	0.06
10457665	4921533I20Rik	Riken cDNA 4921533I20 gene	AK076609	0.06
10447036	---	rRNA chromosome:NCBIM37:17:79258276:	ENSMUST0000082836	0.06

Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Adjusted P value
		79258390:1 gene:ENSMUSG00000064770		
10568001	Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	NM_133670	0.07
10447938	Dact2	dapper homolog 2, antagonist of beta-catenin (xenopus)	NM_172826	0.07
10588509	Pcbp4	poly(rC) binding protein 4	NM_021567	0.07
10578964	1810029B16Rik	RIKEN cDNA 1810029B16 gene	BC016246	0.07
10362372	9330159F19Rik	RIKEN cDNA 9330159F19 gene	AK034141	0.07
10469936	Nrarp	Notch-regulated ankyrin repeat protein	NM_025980	0.08
10505532	OTTMUSG0000000266	predicted gene, OTTMUSG00000000266	XR_033213	0.08
10387525	Mpdu1	mannose-P-dolichol utilization defect 1	NM_011900	0.08
10358648	Hmcn1	hemacentin 1	NM_001024720	0.08
10449452	Fkbp5	FK506 binding protein 5	NM_010220	0.08
10467468	ENSMUSG00000074878	predicted gene, ENSMUSG00000074878	AK132080	0.08
10547386	Adipor2	adiponectin receptor 2	NM_197985	0.09
10470959	Phyhd1	phytanoyl-CoA dioxygenase domain containing 1	NM_172267	0.09
10589413	Nme6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	NM_018757	0.09
10376017	ENSMUSG00000054450	predicted gene, ENSMUSG00000054450	ENSMUST0000067523	0.09
10350758	ENSMUSG00000066798	predicted gene, ENSMUSG00000066798	AK080751	0.09
10577641	1810011O10Rik	RIKEN cDNA 1810011O10 gene	NM_026931	0.10
10582664	2310022B05Rik	RIKEN cDNA 2310022B05 gene	BC058626	0.10
10417275	---	novel chromosome:NCBIM37:14:20434352:20436596:1 gene:ENSMUSG00000068776	ENSMUST0000090639	0.10
10581378	Psmb10	proteasome (prosome, macropain) subunit, beta type 10	NM_013640	0.10
10516529	Adc	arginine decarboxylase	NM_172875	0.10
10515700	BC059842	cDNA sequence BC059842	ENSMUST0000075406	0.10
10556242	---	snoRNA chromosome:NCBIM37:7:117166724:117166856:1 gene:ENSMUSG00000064600	ENSMUST0000082666	0.10
10350146	Phlda3	pleckstrin homology-like domain, family A, member 3	NM_013750	0.10
10356601	Per2	period homolog 2 (Drosophila)	NM_011066	0.10
10373756	Pla2g3	phospholipase A2, group III	NM_172791	0.10
10431558	2010001J22Rik	RIKEN cDNA 2010001J22 gene	BC087962	0.10
10584674	Mcam	melanoma cell adhesion molecule	NM_023061	0.10
10513608	Alad	aminolevulinic acid, delta-, dehydratase	NM_008525	0.10
10446013	Mpnd	MPN domain containing	NM_026530	0.10
10404885	Gmpr	guanosine monophosphate reductase	NM_025508	0.11
10496872	Eltf1	EGF, latrophilin seven transmembrane domain containing 1	NM_133222	0.11
10523647	Aff1	AF4/FMR2 family, member 1	NM_001080798	0.11
10505954	Tek	endothelial-specific receptor tyrosine kinase	NM_013690	0.11
10526923	1110007L15Rik	RIKEN cDNA 1110007L15 gene	BC019557	0.11
10555777	---	cdna:Genscan chromosome:NCBIM37:7:110335117:110384869:1	GENSCAN0000023102	0.11
10469425	Arl5b	ADP-ribosylation factor-like 5B	NM_029466	0.11
10475199	Snap23	synaptosomal-associated protein 23	NM_009222	0.11
10583485	A230050P20Rik	RIKEN cDNA A230050P20 gene	NM_175687	0.11
10378754	2310047D13Rik	RIKEN cDNA 2310047D13 gene	NM_027773	0.11
10439249	Parp14	poly (ADP-ribose) polymerase family, member 14	NM_001039	0.11

Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Adjusted P value
			530	
10358057	Shisa4	shisa homolog 4 (<i>Xenopus laevis</i>)	NM_175259	0.11
10457963	Gpr17	G protein-coupled receptor 17	NM_001025381	0.11
10493798	S100a16	S100 calcium binding protein A16	NM_026416	0.11
10560329	Hif3a	hypoxia inducible factor 3, alpha subunit	NM_016868	0.12
10485402	Fjx1	four jointed box 1 (<i>Drosophila</i>)	NM_010218	0.12
10381260	Tubg2	tubulin, gamma 2	NM_134028	0.12
10375880	Nola2	nucleolar protein family A, member 2	NM_026631	0.12
10561004	Erf	Ets2 repressor factor	NM_010155	0.12
10345183	Cdk10	cyclin-dependent kinase (CDC2-like) 10	NM_194446	0.12
10553788	Atp10a	ATPase, class V, type 10A	NM_009728	0.12
10410452	Srd5a1	steroid 5 alpha-reductase 1	NM_175283	0.12
10366546	Cpm	carboxypeptidase M	NM_027468	0.12
10495675	F3	coagulation factor III	NM_010171	0.12
10508829	Map3k6	mitogen-activated protein kinase kinase kinase 6	NM_016693	0.12
10456046	Pdgfrb	platelet derived growth factor receptor, beta polypeptide	NM_008809	0.12
10573626	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	NM_173866	0.12
10378453	1300001I01Rik	RIKEN cDNA 1300001I01 gene	BC072573	0.12
10488048	Mkks	McKusick-Kaufman syndrome protein	NM_021527	0.12
10447190	Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	NM_177606	0.12
10358565	Hmcn1	hemicentin 1	NM_001024720	0.13
10555009	---	MI0004692 <i>Mus musculus</i> miR-708 stem-loop	---	0.13
10579406	Arrdc2	arrestin domain containing 2	NM_027560	0.13
10549921	Vmn2r43	vomer nasal 2, receptor 43	NM_198961	0.13
10437399	Coro7	coronin 7	NM_030205	0.13
10429957	Fbxl6	F-box and leucine-rich repeat protein 6	NM_013909	0.13
10445992	Shd	src homology 2 domain-containing transforming protein D	NM_009168	0.13
10562576	Plekhf1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	NM_024413	0.13
10461423	Fads3	fatty acid desaturase 3	NM_021890	0.13
10499643	Chrn2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	NM_009602	0.13
10376004	Gdf9	growth differentiation factor 9	NM_008110	0.13
10575021	Zfp90	zinc finger protein 90	NM_011764	0.13
10451932	S3-12	plasma membrane associated protein, S3-12	NM_020568	0.13
10545827	Rab11fip5	RAB11 family interacting protein 5 (class I)	NM_001003955	0.13
10576439	Cog2	component of oligomeric golgi complex 2	NM_029746	0.13
10408047	OTTMUSG0000018077	predicted gene, OTTMUSG00000018077	AK132930	0.13
10547100	Plxnd1	plexin D1	NM_026376	0.13
10544563	Zfp467	zinc finger protein 467	NM_020589	0.13
10417920	Usp54	ubiquitin specific peptidase 54	NM_030180	0.13
10514708	InsI5	insulin-like 5	NM_011831	0.13
10467529	Opalin	oligodendrocytic myelin paranodal and inner loop protein	NM_153520	0.13
10448559	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130072E10 product: hypothetical protein, full insert sequence gene:ENSMUSG00000073437	ENSMUST00000084725	0.13
10520234	2010209O12Rik	RIKEN cDNA 2010209O12 gene	NM_133913	0.13
10456988	Pard6g	par-6 partitioning defective 6 homolog gamma	NM_053117	0.13

Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Adjusted P value
		(C. elegans)		
10582474	Chmp1a	chromatin modifying protein 1A	NM_145606	0.13
10576403	AK122209	cDNA sequence AK122209	NM_001029 876	0.14
10530201	Ugdh	UDP-glucose dehydrogenase	NM_009466	0.14
10583732	Ldlr	low density lipoprotein receptor	NM_010700	0.14
10441055	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	NM_019543	0.14
10561212	Ltbp4	latent transforming growth factor beta binding protein 4	NM_175641	0.14
10484987	Nr1h3	nuclear receptor subfamily 1, group H, member 3	NM_013839	0.14
10489569	Pltp	phospholipid transfer protein	NM_011125	0.14
10414433	6720456H20Rik	RIKEN cDNA 6720456H20 gene	NM_172600	0.14
10424370	Trib1	tribbles homolog 1 (Drosophila)	NM_144549	0.14
10469867	Pnpla7	patatin-like phospholipase domain containing 7	NM_146251	0.14
10552656	Syt3	synaptotagmin III	NM_016663	0.15
10446341	4930505H01Rik	RIKEN cDNA 4930505H01 gene	AK132847	0.15
10389627	Rad51c	Rad51 homolog c (S. cerevisiae)	NM_053269	0.15
10571274	Gsr	glutathione reductase	NM_010344	0.15
10603387	Hdac6	histone deacetylase 6	NM_010413	0.15
10551736	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	NM_026731	0.16
10489484	Sdc4	syndecan 4	NM_011521	0.16
10492428	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	NM_178892	0.16
10390691	Nr1d1	nuclear receptor subfamily 1, group D, member 1	NM_145434	0.16
10576216	Rpl13	ribosomal protein L13	AF357327	0.16
10567095	Calca	calcitonin/calcitonin-related polypeptide, alpha	NM_007587	0.16
10449061	Rhbdl1	rhomboid, veinlet-like 1 (Drosophila)	NM_144816	0.16
10408755	Muted	muted	NM_139063	0.16
10541873	Mrpl51	mitochondrial ribosomal protein L51	NM_025595	0.16
10562911	Tbc1d17	TBC1 domain family, member 17	NM_001042 655	0.16
10442083	---	MI0000561 Mus musculus let-7e stem-loop	---	0.16
10352918	---	MI0000577 Mus musculus miR-29c stem-loop	---	0.16
10365123	Dohh	deoxyhypusine hydroxylase/monooxygenase	AK080664	0.16
10606369	Itm2a	integral membrane protein 2A	NM_008409	0.17
10504504	Grhpr	glyoxylate reductase/hydroxypyruvate reductase	NM_080289	0.17
10566516	1500003O22Rik	RIKEN cDNA 1500003O22 gene	BC022923	0.17
10470283	Egfl7	EGF-like domain 7	NM_198724	0.17
10516064	Mfsd2	major facilitator superfamily domain containing 2	NM_029662	0.17
10387659	Nlgn2	neuroligin 2	NM_198862	0.17
10436282	Impg2	interphotoreceptor matrix proteoglycan 2	NM_174876	0.18
10384192	Tbrg4	transforming growth factor beta regulated gene 4	NM_134011	0.18
10382376	Ttyh2	tweety homolog 2 (Drosophila)	NM_053273	0.18
10536746	Arf5	ADP-ribosylation factor 5	NM_007480	0.18
10380137	Bzrap1	benzodiazapine receptor associated protein 1	NM_172449	0.18
10502696	Spata1	spermatogenesis associated 1	NM_027617	0.18
10434229	Cldn5	claudin 5	NM_013805	0.18
10591537	Tmed1	transmembrane emp24 domain containing 1	NM_010744	0.18
10503334	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	NM_010276	0.18
10444008	Zfp414	zinc finger protein 414	NM_026712	0.18
10546137	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	NM_030251	0.18
10512499	Tpm2	tropomyosin 2, beta	NM_009416	0.18
10586128	---	ncrna:snRNA chromosome:NCBIM37:9: 63290126:63290267:1 gene:ENSMUSG00000065679	ENSMUST0 0000083745	0.18

Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Adjusted P value
10371482	Hsp90b1	heat shock protein 90, beta (Grp94), member 1	NM_011631	0.18
10504918	Zfp189	zinc finger protein 189	NM_145547	0.18
10475544	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	NM_172537	0.18
10404069	Hist1h1a	histone cluster 1, H1a	NM_030609	0.18
10547288	Ankrd26	ankyrin repeat domain 26	NM_001081112	0.18
10526559	Ache	acetylcholinesterase	NM_009599	0.18
10428370	Abra	actin-binding Rho activating protein	NM_175456	0.18
10561927	Aplp1	amyloid beta (A4) precursor-like protein 1	NM_007467	0.18
10488655	Bcl2l1	BCL2-like 1	NM_009743	0.18
10464504	Lrp5	low density lipoprotein receptor-related protein 5	NM_008513	0.18
10518957	Dffb	DNA fragmentation factor, beta subunit	NM_007859	0.18
10545417	Mat2a	methionine adenosyltransferase II, alpha	NM_145569	0.18
10442643	Nme3	non-metastatic cells 3, protein expressed in	NM_019730	0.18
10583347	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	NM_025844	0.18
10432439	Fmnl3	formin-like 3	NM_011711	0.18
10540028	Klf15	Kruppel-like factor 15	NM_023184	0.18
10535458	Zdhhc4	zinc finger, DHHC domain containing 4	NM_028379	0.18
10542872	Rps4y2	ribosomal protein S4, Y-linked 2	NR_003634	0.18
10517250	Extl1	exostoses (multiple)-like 1	NM_019578	0.18
10483624	Dlx1as	distal-less homeobox 1, antisense	NR_002854	0.18
10450579	Ddr1	discoidin domain receptor family, member 1	NM_007584	0.18
10476759	Rin2	Ras and Rab interactor 2	NM_028724	0.18
10350188	Tmem9	transmembrane protein 9	NM_025439	0.18
10601980	Mum11	melanoma associated antigen (mutated) 1-like 1	NM_175541	0.18
10530029	Lgi2	leucine-rich repeat LGI family, member 2	NM_144945	0.18
10572679	Glt25d1	glycosyltransferase 25 domain containing 1	NM_146211	0.18
10390299	Pnpo	pyridoxine 5'-phosphate oxidase	NM_134021	0.18
10364702	Midn	midnolin	NM_021565	0.18
10462454	Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	NM_144873	0.19
10469987	Man1b1	mannosidase, alpha, class 1B, member 1	NM_001029983	0.19
10378024	Mis12	MIS12 homolog (yeast)	NM_025993	0.19
10358660	Hmcn1	hemicentin 1	NM_001024720	0.19
10450006	Hnrnmp	heterogeneous nuclear ribonucleoprotein M	NM_029804	0.19
10418604	Phf7	PHD finger protein 7	NM_027949	0.20
10438530	Clcn2	chloride channel 2	NM_009900	0.20
10415282	Psme1	proteasome (prosome, macropain) 28 subunit, alpha	NM_011189	0.20
10544583	Gimap6	GTPase, IMAF family member 6	NM_153175	0.20
10390283	Cdk5rap3	CDK5 regulatory subunit associated protein 3	NM_030248	0.20
10420366	Gjb6	gap junction protein, beta 6	NM_001010937	0.20
10432411	Mcrs1	microspherule protein 1	NM_016766	0.20
10517744	Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like	NM_172415	0.20
10550509	Pglyrp1	peptidoglycan recognition protein 1	NM_009402	0.20
10461369	Ahnak	AHNAK nucleoprotein (desmoyokin)	NM_009643	0.20
10512165	Nol6	nucleolar protein family 6 (RNA-associated)	NM_139236	0.21
10594645	Rab8b	RAB8B, member RAS oncogene family	NM_173413	0.21
10438293	Zdhhc8	zinc finger, DHHC domain containing 8	NM_172151	0.21
10603206	BC022960	cDNA sequence BC022960	ENSMUST0000052299	0.21
10375735	Hnrnph1	heterogeneous nuclear ribonucleoprotein H1	NM_021510	0.21

Affymetrix ID	Gene Symbol	Gene or mRNA Description	Accession	Adjusted P value
10507594	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	NM_011400	0.21
10394812	EG245297	predicted gene, EG245297	BC030401	0.21
10597823	Lyzl4	lysozyme-like 4	NM_026915	0.21
10419261	Bmp4	bone morphogenetic protein 4	NM_007554	0.21
10507238	Lrrc41	leucine rich repeat containing 41	NM_153521	0.21
10498367	P2ry13	purinergic receptor P2Y, G-protein coupled 13	NM_028808	0.21
10498620	Trim59	tripartite motif-containing 59	NM_025863	0.21
10399725	Sox11	SRY-box containing gene 11	NM_009234	0.21
10430770	Tob2	transducer of ERBB2, 2	NM_020507	0.21
10358605	Hmcn1	hemicentin 1	NM_001024720	0.21
10531201	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	NM_001081401	0.21
10439442	Pla1a	phospholipase A1 member A	NM_134102	0.21
10439424	4932425I24Rik	RIKEN cDNA 4932425I24 gene	NM_001081025	0.21
10519140	Mmp23	matrix metallopeptidase 23	NM_011985	0.21
10429573	Ly6c1	lymphocyte antigen 6 complex, locus C1	NM_010741	0.21
10371591	4930547N16Rik	RIKEN cDNA 4930547N16 gene	NM_029249	0.21
10576258	Cdk10	cyclin-dependent kinase (CDC2-like) 10	NM_194446	0.21
10462333	Cdc37I1	cell division cycle 37 homolog (S. cerevisiae)-like 1	NM_025950	0.21
10453867	Rbbp8	retinoblastoma binding protein 8	NM_001081223	0.21
10595109	Lrrc1	leucine rich repeat containing 1	NM_172528	0.21
10439016	4930444G20Rik	RIKEN cDNA 4930444G20 gene	NM_053264	0.21
10543697	Zc3hc1	zinc finger, C3HC type 1	NM_172735	0.21
10462363	Jak2	Janus kinase 2	NM_008413	0.21
10401841	Dio2	deiodinase, iodothyronine, type II	NM_010050	0.21
10532616	Myo18b	myosin XVIIIb	XM_912851	0.21
10393620	Cbx4	chromobox homolog 4 (Drosophila Pc class)	NM_007625	0.21
10548735	Dusp16	dual specificity phosphatase 16	NM_130447	0.21
10497944	Mfsd8	major facilitator superfamily domain containing 8	NM_028140	0.21
10358637	Hmcn1	hemicentin 1	NM_001024720	0.21
10576152	Trappc2l	trafficking protein particle complex 2-like	NM_021502	0.22
10478615	Pcif1	PDX1 C-terminal inhibiting factor 1	NM_146129	0.22
10468639	Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	NM_018831	0.22
10572271	Tm6sf2	transmembrane 6 superfamily member 2	NM_181540	0.22
10481734	Lrsam1	leucine rich repeat and sterile alpha motif containing 1	NM_199302	0.22
10496892	Fubp1	far upstream element (FUSE) binding protein 1	NM_057172	0.22
10519224	Pus1	pseudouridylate synthase-like 1	ENSMUST0000097737	0.22
10577441	Defb9	defensin beta 9	NM_139219	0.22
10472514	Nostrin	nitric oxide synthase trafficker	NM_181547	0.23
10443421	Brpf3	bromodomain and PHD finger containing, 3	NM_001081315	0.23
10506170	Efcab7	EF-hand calcium binding domain 7	NM_145549	0.23
10505623	D4Bwg0951e	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	BC030404	0.23
10404059	Hist1h1c	histone cluster 1, H1c	NM_015786	0.23

Supplementary Table 4: List of the 78 genes showing a significant effect of sleep deprivation (SD) in both sham and ADX mice of the present micro-array and a significant effect of spontaneous wakefulness (from an analysis of the difference between baseline ZT18 and ZT12 micro-array data of Maret et al., 2007). Log fold-change (logFC) and FDR adjusted P values are shown for sham-lesioned mice between sleep deprivation (SD) and baseline (BL) and for DBA/2J mice between ZT18 and ZT12. The direction indicates whether SD and ZT18 timing increased (up) or decreased (down) the expression of the transcripts.

Gene Symbol	Sham SD/BL logFC	Sham SD/BL Adj. P value	ZT18/ZT12 logFC	ZT18/ZT12 Adj. P value	Direction
Hspa1b	0.81	0.0002	1.87	1.45e-05	up
Arc	1.40	1.52e-09	1.75	6.81e-05	up
Egr1	0.59	0.0002	1.09	0.0001	up
Egr3	0.31	0.001	1.00	0.0006	up
Hspa5	0.77	1.49e-10	0.86	0.0009	up
Cirbp	-0.91	4.11e-09	-1.02	0.001	down
P4ha1	0.70	8.47e-08	0.77	0.001	up
Cryab	0.35	0.0008	0.73	0.001	up
Fam46a	0.22	0.01	0.76	0.001	up
Fos	0.70	2.32e-06	1.70	0.001	up
Chordc1	0.68	1.01e-05	0.70	0.001	up
Dusp6	0.48	7.61e-06	0.71	0.002	up
Npas4	0.66	1.17e-05	1.15	0.002	up
Nr4a1	0.84	1.91e-05	1.14	0.002	up
Sfpq	0.31	7.55e-05	0.76	0.002	up
Nr4a3	0.46	4.22e-05	0.73	0.002	up
Mkks	0.40	2.55e-07	0.68	0.003	up
Sdf2l1	0.80	2.55e-07	0.71	0.003	up
Rbm3	-0.81	2.66e-09	-0.68	0.003	down
Trim9	0.29	0.0008	0.63	0.003	up
Etv5	0.31	0.02	0.68	0.005	up
Cys1	0.49	1.01e-07	0.57	0.005	up
Tra2a	0.50	3.42e-06	0.60	0.005	up
Dusp1	0.66	6.25e-05	0.72	0.006	up
Dio2	0.75	2.55e-07	0.66	0.007	up
Spred1	0.37	0.0004	0.63	0.007	up
Usp2	-0.22	0.005	-0.57	0.008	down
Creld2	0.58	4.66e-08	0.54	0.008	up
Nfil3	0.40	0.002	0.57	0.008	up
Xbp1	0.41	3.78e-05	0.58	0.008	up
Calr	0.45	1.01e-05	0.53	0.009	up
Dusp11	0.23	0.007	0.59	0.009	up
Hspa1a	0.53	0.001	0.68	0.009	up
Pdia6	0.66	5.99e-09	0.59	0.009	up
Opalin	-0.94	7.06e-06	-0.81	0.009	down
Hsp90b1	0.46	9.40e-07	0.53	0.01	up
Hexim1	0.34	0.0001	0.51	0.01	up
Hsph1	0.60	1.91e-07	0.54	0.01	up
Plip	-0.43	1.01e-05	-0.52	0.01	down
Eny2	-0.19	0.02	-0.51	0.01	down
Homer1	0.52	4.64e-08	0.94	0.01	up
Armet	0.58	8.18e-07	0.54	0.01	up
Dnajb1	0.59	5.12e-05	0.44	0.02	up
Lrrk2	0.39	1.01e-05	0.50	0.02	up
Slc5a3	0.66	3.04e-07	0.59	0.02	up
4933437F05Rik	0.80	1.66e-07	0.51	0.02	up
Cbln4	0.24	0.005	0.51	0.02	up
EG665858 / EG665787	-0.28	0.04	-0.44	0.02	down
Arl4a	-0.14	0.02	-0.49	0.02	down
Synj2	0.28	0.0003	0.57	0.02	up
Bcl2	0.28	0.0005	0.42	0.02	up

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Gene Symbol	Sham SD/BL logFC	Sham SD/BL Adj. P value	ZT18/ZT12 logFC	ZT18/ZT12 Adj. P value	Direction
Pdia3	0.42	0.0007	0.41	0.02	up
Enc1	0.20	0.002	0.50	0.03	up
Zbtb40	0.37	0.0002	0.56	0.03	up
Zbtb22	-0.30	4.22e-05	-0.43	0.03	down
Mfsd4	-0.33	3.19e-06	-0.50	0.03	down
Ppm2c	0.36	7.60e-07	0.41	0.03	up
Tipin	-0.51	0.0003	-0.41	0.04	down
Ier5	0.17	0.04	0.36	0.04	up
Dnaja4	0.28	0.0005	0.37	0.04	up
Dnajib11	0.43	0.0002	0.35	0.04	up
Pcsk1	0.38	8.75e-05	0.55	0.04	up
Gfod1	0.35	2.38e-05	0.36	0.04	up
Snf1lk2	0.26	0.001	0.42	0.04	up
Dnaja3	0.40	3.42e-06	0.39	0.04	up
Pfkfb3	0.33	0.0001	0.42	0.04	up
Hspa4l	0.25	0.001	0.40	0.04	up
Tubd1	0.33	0.002	0.47	0.04	up
BC004004	-0.25	4.64e-05	-0.37	0.04	down
Stip1	0.43	0.0002	0.37	0.04	up
Fkbp4	0.29	0.0002	0.33	0.04	up
Rbm11	-0.65	2.55e-07	-0.55	0.04	down
Otub2	0.44	0.0001	0.44	0.05	up
Mett10d	0.30	0.0005	0.36	0.05	up
Luzp1	0.20	0.01	0.33	0.05	up
Dusp4	0.59	1.43e-05	0.47	0.05	up
Trib2	0.30	0.0005	0.40	0.05	up
Tfrc	-0.59	4.66e-08	-0.34	0.05	down

Supplementary Table 5: List of probe sets affected by SD (see Supplementary Table 1) that are considered potential targets of the microRNAs affected by sleep deprivation (SD) in both sham and ADX animals. Target genes among the probe sets that were either decreased (down) or increased (up) by SD were extracted from the Miranda data base. P values obtained from enrichment calculation using Fisher's Exact test. Gene symbol in **bold** (Homer1 and ler5) have been analyzed by qPCR in the present study.

miRNA	Affymetrix ID	Gene symbol	Gene description	Accession	Direction (P value)
miR-29c	10579219	Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	NM_001024922	down (p = 0.02)
	10400157	Nova1	neuro-oncological ventral antigen 1	ENSMUST0000021438	
	10551736	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	NM_026731	
	10378857	Coro6	coronin, actin binding protein 6	NM_139128	
	10516529	Adc	arginine decarboxylase	NM_172875	
	10491486	Atp11b	ATPase, class VI, type 11B	NM_029570	
	10420372	Cryl1	crystallin, lambda 1	NM_030004	
	10543466	Gpr37	G protein-coupled receptor 37	NM_010338	
	10386636	Usp22	ubiquitin specific peptidase 22	NM_001004143	
	10485282	Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	NM_026944	
	10546760	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	BC083059	
	10564978	Blm	Bloom syndrome homolog (human)	NM_007550	
	10372342	Nav3	neuron navigator 3	NM_001081035	
	10522303	Guf1	GUF1 GTPase homolog (S. cerevisiae)	NM_172711	
	10393620	Cbx4	chromobox homolog 4 (Drosophila Pc class)	NM_007625	
	10487945	Prei4	preimplantation protein 4	NM_028802	
	10460468	Ctsf	cathepsin F	NM_019861	
	10434934	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	NM_175177	
	10351749	Wdr42a	WD repeat domain 42A	NM_153555	
	10441718	Park2	parkin	NM_016694	
	10429100	Lrrc6	leucine rich repeat containing 6 (testis)	NM_019457	
	10546349	Xpc	xeroderma pigmentosum, complementation group C	NM_009531	
	10484227	Sestd1	SEC14 and spectrin domains 1	NM_175465	
	10400155	Nova1	neuro-oncological ventral antigen 1	ENSMUST0000066043	
	10603087	Pir	pirin	NM_027153	
	10357888	Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	AK173053	
	10408870	Tbc1d7	TBC1 domain family, member 7	NM_025935	
	10549473	Caprin2	caprin family member 2	NM_181541	
	10578138	Dctn6	dynactin 6	NM_011722	
	10589889	Glb1	galactosidase, beta 1	NM_009752	
	10487040	Fbn1	fibrillin 1	NM_007993	
	10377380	1500010J02Rik	RIKEN cDNA 1500010J02 gene	NM_026889	
	10470283	Egfl7	EGF-like domain 7	NM_198724	
	10450533	Vars2	valyl-tRNA synthetase 2, mitochondrial (putative)	NM_175137	
	10598723	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	NM_010028	
	10526897	Unc84a	unc-84 homolog A (C. elegans)	NM_024451	
	10589494	Cspg5	chondroitin sulfate proteoglycan 5	NM_013884	
	10434436	EG328644	predicted gene, EG328644	BC125016	
	10572679	Glt25d1	glycosyltransferase 25 domain containing 1	NM_146211	
	10512739	Xpa	xeroderma pigmentosum, complementation group A	NM_011728	
10556208	D930014E17Rik	RIKEN cDNA D930014E17 gene	NM_020616		
10395719	Npas3	neuronal PAS domain protein 3	NM_013780		
10458046	D0H4S114	DNA segment, human D4S114	NM_053078		

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miRNA	Affymetrix ID	Gene symbol	Gene description	Accession	Direction (P value)
	10594353	Map2k5	mitogen-activated protein kinase kinase 5	NM_011840	
	10505747	Rraga	Ras-related GTP binding A	NM_178376	
miR-151-5p	10361250	Camk1g	calcium/calmodulin-dependent protein kinase I gamma	NM_144817	up (p = 0.03)
	10480035	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphate 3	NM_133232	
	10399725	Sox11	SRY-box containing gene 11	NM_009234	
	10562576	Plekhf1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	NM_024413	
	10438478	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	NM_013790	
	10491780	Hspa4l	heat shock protein 4 like	NM_011020	
	10449452	Fkbp5	FK506 binding protein 5	NM_010220	
	10350733	Rgs16	regulator of G-protein signaling 16	NM_011267	
	10497417	Crh	corticotropin releasing hormone	NM_205769	
	10521331	A930005I04Rik	RIKEN cDNA A930005I04 gene	BC116928	
	10394690	E2f6	E2F transcription factor 6	NM_033270	
	10505213	E130308A19Rik	RIKEN cDNA E130308A19 gene	NM_153158	
	10416541	Enox1	ecto-NOX disulfide-thiol exchanger 1	NM_172813	
	10356628	Hdac4	histone deacetylase 4	NM_207225	
	10582008	2310061C15Rik	RIKEN cDNA 2310061C15 gene	NM_026844	
	10606969	Rbm41	RNA binding motif protein 41	NM_153586	
	10397912	9030205A07Rik	RIKEN cDNA 9030205A07 Gene	AB257853	
	10516064	Mfsd2	major facilitator superfamily domain containing 2	NM_029662	
	10536541	St7	Suppression of tumorigenicity 7	NM_022332	
	10539606	Cct7	chaperonin containing Tcp1, subunit 7 (eta)	NM_007638	
	10561247	Shkbp1	Sh3kbp1 binding protein 1	NM_138676	
	10366938	Stac3	SH3 and cysteine rich domain 3	NM_177707	
	10347427	Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	NM_175031	
	10445688	Ccnd3	cyclin D3	NM_001081636	
	10420516	Cdadc1	cytidine and dCMP deaminase domain containing 1	NM_027986	
	10346562	Cflar	CASP8 and FADD-like apoptosis regulator	NM_207653	
10430770	Tob2	transducer of ERBB2, 2	NM_020507		
10460312	Cdk2ap2	CDK2-associated protein 2	NM_026373		
10590821	9230110C19Rik	RIKEN cDNA 9230110C19 gene	BC115525		
miR-212	10394735	Pdia6	protein disulfide isomerase associated 6	NM_027959	up (p = 0.06)
	10406626	Homer1	homer homolog 1 (Drosophila)	NM_147176	
	10504218	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	NM_019874	
	10464905	Npas4	neuronal PAS domain protein 4	NM_153553	
	10361250	Camk1g	calcium/calmodulin-dependent protein kinase I gamma	NM_144817	
	10526553	Vgf	VGF nerve growth factor inducible	NM_001039385	
	10547386	Adipor2	adiponectin receptor 2	NM_197985	
	10496872	Eltf1	EGF, latrophilin seven transmembrane domain containing 1	NM_133222	
	10464819	Rbm14	RNA binding motif protein 14	NM_019869	
	10398147	Papola	poly (A) polymerase alpha	NM_011112	
	10419691	Mettl3	methyltransferase-like 3	NM_019721	
	10562576	Plekhf1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	NM_024413	
	10450369	Hspa1a	heat shock protein 1A	NM_010479	
	10353803	Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	NM_198899	
	10409278	Nfil3	nuclear factor, interleukin 3, regulated	NM_017373	
	10527332	Nptx2	neuronal pentraxin 2	NM_016789	

miRNA	Affymetrix ID	Gene symbol	Gene description	Accession	Direction (P value)
	10600034	Gm1141	gene model 1141, (NCBI)	ENSMUST0000101495	
	10505213	E130308A19Rik	RIKEN cDNA E130308A19 gene	NM_153158	
	10462752	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, <i>S. cerevisiae</i>)	NM_001080706	
	10462333	Cdc3711	cell division cycle 37 homolog (<i>S. cerevisiae</i>)-like 1	NM_025950	
	10453887	Cables1	Cdk5 and Abl enzyme substrate 1	NM_022021	
	10583834	9530077C05Rik	RIKEN cDNA 9530077C05 gene	BC054761	
	10458340	Hbegf	heparin-binding EGF-like growth factor	NM_010415	
	10565250	Mesdc1	mesoderm development candidate 1	NM_030705	
	10424909	Hsf1	heat shock factor 1	NM_008296	
	10358978	ler5	immediate early response 5	NM_010500	
	10400357	Baz1a	bromodomain adjacent to zinc finger domain 1A	NM_013815	
	10511510	Ints8	integrator complex subunit 8	NM_178112	
	10350753	Glul	glutamate-ammonia ligase (glutamine synthetase)	NM_008131	
	10439016	4930444G20Rik	RIKEN cDNA 4930444G20 gene	NM_053264	
	10469867	Pnpla7	patatin-like phospholipase domain containing 7	NM_146251	

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Supplementary Table 6: Sequences of primers and probes used for qPCR.

Gene Symbol	Direction	Sequence 5' to 3'	Accession #
<i>mNpas2</i>	fwd	GGTCATCGGATTCTTGCAGAA	NM_008719
	rev	TCCAGTCCTGCTGGATGTCA	
	probe	CACAATGAAGTCTCAGCACAAACAGAAATC	
<i>mPer1</i>	fwd	ACCAGCGTGTGATGATGACATAC	NM_011065
	rev	CTCTCCCGGTCTTGCTTCAG	
	probe	CCGTCCAGGGATGCAGCCTCT	
<i>mPer2</i>	fwd	ATGCTCGCCATCCACA AGA	NM_011066
	rev	GCGGAATCGAATGGGAGAAT	
	probe	ATCCTACAGG CCGGTGGACAGCC	
<i>mPer3</i>	fwd	CGCACACTGCTCCAACTCA	NM_011067
	rev	TTTC GCTGGTGCACATTCAT	
	probe	ACAACTGGACCCAAAGAGCCTCGCAG	
<i>mDbp</i>	fwd	CGTGGAGGTGCTTAATGACCTTT	NM_016974
	rev	CATGGCCTGGAATGCTTG A	
	probe	AACCTGATCCCGCTGATCTCGCC	
<i>mRev-Erbα</i>	fwd	CCAGCAGTGTGCTTCAAGA	NM_145434
	rev	GCAAGCATCCGTTGCTTCTC	
	probe	AGAGATGCTGTGCGTTTTGGGCG	
<i>mHomer1a</i>	fwd	GCATTGCCA TTTCCACATAGG	NM_011982
	rev	ATGAACTTCCATATTTATCCACCTTACTT	
	probe	ACACATTC AATTCAGCAATCATGA	
<i>mSgk1</i>	fwd	ACGGTGGACTGGTGGTGTCT	NM_011361
	rev	GCCGTGTTCCGGCTATAAAA	
	probe	TATGAGATGCTCTACGGCCTGCCCC	
<i>mPdk4</i>	fwd	TCACCACATGCTCTTCGAACTC	NM_013743
	rev	GGGTCAAGGAAGGACGGTTT	
	probe	TCAAGAATGCCATGAGGGCCACG	
<i>mXdh</i>	fwd	CAAGTCCGTGGCGTCCAT	NM_011723
	rev	GCCATGAGCACAGGGTTGA	
	probe	CATCATCACCGCGAGCCCAT	
<i>mMertk</i>	fwd	CGTGTTAATGAAAACCGGAAAG	NM_008587
	rev	GGGCTCACAGCTGAAGACT	
	probe	CTGTCTAACCGTACCTGGTCTGACAGAGACA	
<i>mIer5</i>	fwd	GAAGCGAAGGCAGGATGGA	NM_010500
	rev	ATCTTGCCCAGGGAGATGCT	
	probe	TTCAAGCTGGAGGCTCACCGCATC	
<i>mPpp1r1a</i>	fwd	GGCAACGGAAGAAGATGACAA	NM_021391
	rev	GCCCTAGGTGATGTTCAACCA	
	probe	CACCCACCATGAAAGAGCTCCAGACG	
<i>mGusB</i>	fwd	ACGGGATTGTGGTCATCGA	NM_010368
	rev	TGACTCGTTGCCAAAACCTCTGA	
	probe	AGTGTCCCGGTGTGGGCATTG TG	
<i>mTbp</i>	fwd	TTGACCTAAAGACCATTGCACT TC	NM_013684
	rev	TTCTCATGATGACTGCAGCAAA	
	probe	TGCAAGAAATG CTGAATATAATCCCAAGCG	
<i>mRsp9</i>	fwd	GACCAGGAGCTAAAGTTGATTGGA	NM_029767
	rev	TCTTGGCCAG GGTAACCTTGA	
	probe	AAACCTCACGTTTGTTCGGAGTCCATACT	