

1 Article

2 Differential gene expression in brain and liver tissue 3 of Wistar rats after rapid eye movement sleep 4 deprivation

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14 **Short title:** REM sleep deprivation of rats for 9 days affects the brain and liver differently.

15 Highlights of the study

- 16 ➤ Gene expression profile of brain and liver tissues of rats was analyzed using microarray
17 technique following 9 days of REM Sleep deprivation.
- 18 ➤ Many of the genes involved in essential physiological processes, such as protein synthesis and
19 neuronal metabolism are affected differently in the brain and liver tissue of rats after 9-day
20 REM sleep deprivation.

21 **Abstract:** Sleep is essential for the survival of most living beings. Numerous researchers have
22 identified a series of genes that are thought to regulate “sleep-state” or the “deprived state”. As
23 sleep has significant effect on physiology, we believe that lack of sleep or particularly REM sleep
24 for a prolonged period would have a profound impact on various body tissues. Therefore, using
25 microarray method, we sought to determine which genes and processes are affected in the brain
26 and liver of rats following 9 days of REM sleep deprivation. Our findings showed that REM sleep
27 deprivation affected a total of 652 genes in the brain and 426 genes in the liver. Only 23 genes were
28 affected commonly, 10 oppositely and 13 similarly across brain and liver tissue. Our results suggest
29 that 9-day REM sleep deprivation differentially affects genes and processes in the brain and liver of
30 rats.

31 **Keywords:** Microarray analysis; Rapid eye movement sleep deprivation; Differential Gene
32 expression in brain and liver tissue.
33

34 1. Introduction

35 Sleep is a universal phenomenon but still we lack fundamental knowledge of its overall
36 functions and purpose. However, most comparative sleep data exist for terrestrial vertebrates, with
37 much less known about sleep in invertebrates [1]. Though, recently the scientific community has
38 sought to characteristic sleep in non-mammalian species like the fruit fly (*Drosophila*
39 *melanogaster*) [2–4], the zebrafish (*Danio rerio*) [5–7], the nematode (*Caenorhabditis elegans*) [8], and bees
40 (*Apis mellifera*, and *Bombus terrestris*) [9–12]. Prolonged sleep deprivation is fatal in many animals
41 studied so far except pigeons and several studies have sought to address how sleep promotes
42 survival in rodents and primates [13–16]. Despite the lack of general knowledge regarding the

functions of sleep, loss of sleep has been shown to drastically alter physiology of many animals studied thus far [17–19]. The degree of physiological changes that sleep loss brings about and the fatality often varies depending upon the nature and duration of sleep deprivation [20,21]. Many theories have been proposed to explain the evolutionary significance and functions of sleep, which includes “null” and “synaptic plasticity” theories [22,23]. Recent advancements in sleep research has shed light on two major functions of sleep-reducing synaptic potentiation and waste clearance mediated by glymphatic system [24–26]. Thus, sleep seems to have specific, overarching functions for all species that depend on it [19]. While a single characterization cannot be ascribed to sleep, numerous studies links its loss to detrimental effects on metabolism, behavior, immunity, cellular functions and hormonal regulations across species [27–30]. Thus, we may suggest that sleep is generally necessary, and most living beings cannot be deprived of it for a long time. There are some mechanisms that are associated with behavioral plasticity which are dependent on sociality or physiological state in regard to sleep regulation [31,32]. Also, in *Drosophila*, not all stages of sleep are necessary for basic survival but questions relating to the critical functions of sleep, plasticity, and its overall importance are still being explored [31].

REM sleep is an essential part of sleep and is present only in avians and mammals, with the exception of reptiles, in which REM sleep has only been recently discovered [33]. Unearthed thus far, the functional aspects of REM sleep includes mainly memory consolidation, brain maturation, muscle re-aeration, special memory acquisition, and maintenance of general physiological mechanisms of the body [34–40]. In the brain, REM sleep is involved in the reorganization of hippocampal excitability, pruning and maintenance of new synapses during development, and learning & memory consolidation [41–43]. Some recent studies also suggest that lack of REM sleep may cause cell death of somatic cells and neurons [44–46]. Outside of the brain, deprivation of the REM sleep was found to be associated with acute phase response in the liver, increased synthesis of pro-inflammatory cytokines such as IL1 β , IL-6, and IL-12, and an increase in liver enzymes, alanine transaminase and aspartic transaminase [47]. In addition, REM sleep deprivation induces the production of reactive oxygen species (ROS), caused inflammation [48] and increase in nitric oxide (NO) in hepatocytes, along with an increase in sensitivity to oxidative stress by the hepatocytes [49]. REM loss also affected the weight and content of nucleic acid in liver [50]. REM loss was also found further associated with oxidative stress and liver circadian clock gene expression [51]. Elevated increase in metabolic rate and UCP1 gene expression is reported in response to chronic REM sleep loss in brown adipose tissue of rats [52]. Recently, REM sleep loss is found associated with blood-brain barrier function regulation and metabolic changes [53,54].

On genomic level, the reduction of gene expression related to energy metabolism (e.g. glucose type I transporter Glut1), growth (e.g. Bdnf), vesicle fusion and many other metabolic processes has been found affected by sleep [55,56]. Another study detected a decrease in GluR1-containing AMPA receptor (AMPA) levels during sleep, as well as a decrease in AMPAR, CamKII and GSK3 β phosphorylation [57]. The Synaptic Homeostasis Hypothesis (SHY), which postulates that wakefulness and sleep are linked to a net increase and decrease in synaptic strength, is supported by these findings [58,59]. In rodents, synaptic plasticity-related expression levels of immediate early genes (IEG), such as *Egr1*, *Arc* and *Fos*, were found to decrease from wakefulness to sleep [56,60–68]. Some of the genes related to synaptic plasticity theory e.g., *Arc*, *Bdnf*, *Creb1*, *Egr1*, *Fos*, *Nr4a1*, *Camk4*, *Ppp2ca*, and *Ppp2r2d* were studied in detail for short wave sleep and REM sleep [69]. It has been proposed that some of these genes, such as *Arc* and *Egr1*, play a key role in long term potentiation (LTP) [60,61,63–65,67,70–73]. It is suspected that other genes are also important for LTD, such as *Ppp2ca* and *Ppp2r2d*, which code for subunits of *PP2A* [74]. While, REM sleep deprivation in the rat dorsal hippocampus has been shown to decrease LTP, synaptic transmission, protein levels of the glutamate receptor, and activation of ERK / MAPK [75].

In the present study, we compared the effect of prolonged REM sleep loss in the brain and liver in order to compare and contrast the effects that occur simultaneously on these vital organs, as previous studies had indicated that REM sleep may have drastic effects on the liver [45,47,49]. To address this, we used a microarray technique to compare gene expression and identify the processes affected in the brain and liver of a given subject after REM sleep deprivation for 9 days. Microarray

is a valuable tool for measuring the dynamics of gene expression in a biological system and can be used to measure the differences in gene expression profile of different tissues under the same physiological conditions [19,76,77]. Most sleep studies that involved microarray analysis have been performed in brain, although recently, research has indicated that other organs may also play a crucial role [55,78–83]. We first hypothesized that prolonged REM sleep loss will differentially affect genes and associated processes in the brain and liver. Secondly, we hypothesized that REM sleep loss would affect functions related to synaptic potentiation and maintenance in the brain, and metabolism and immune response to infection related mechanisms, in the liver.

Previous studies involving analysis of microarray returned many genes which were associated with the GO term, potentiation of synaptic plasticity, which largely supports the ‘synaptic homeostasis theory’ [55,84]. In the cerebral cortex of the mouse and, to a lesser degree, hypothalamus, genes encoding proteins of various biosynthetic pathways for heme, protein, and lipid are upregulated throughout sleep [81]. Throughout sleep, a significant number of genes encoding the structural constituents of the ribosomes, translation-regulation activity, and formation of transfer RNA (tRNA) and ribosome biogenesis are also upregulated. Genes whose expression gradually increases during sleep include those that encode for several cholesterol-synthesis pathway enzymes, proteins involved in the uptake of cholesterol, the transport of transcription factors, and chaperones that regulated the transcription of genes associated with cholesterol [81]. Prolonged wakefulness results in the fruit fly results in the downregulation of several genes involved in protein production [83]. Sleep deprivation in mice causes a decrease in the expression of genes in the cerebral cortex and hypothalamus, which encode proteins that are involved in key pathways of carbohydrate metabolism, energy production, tricarboxylic acid (TCA) anabolism, and various metabolic pathways (lipid, aldehyde, amine synthesis) [81]. Further, microarrays have shown that there are transcript level variations in many genes involved in the regulation of reactive oxygen species (ROS), including heme oxygenase, superoxide dismutase, and catalase, in patients with obstructive sleep apnea [85]. The dopamine receptor-signaling pathway regulating sleep, learning, and its plasticity are well known [86,87]. Sleep disorders and sleep deprivation have been correlated with dopaminergic, cholinergic, and GABAergic regulation of synaptic transmission, each of which were terms that were significantly enriched for genes that were downregulated in our study [56,88–91]. A recent microarray analysis involving mice shows that *Hspa5* gene expression increases not only in the brain but also in the liver as sleep deprivation increases [82]. Overall, currently, however, there is little knowledge available about how sleep including REM, its loss and the prolonged wakefulness affects expression of genes in peripheral tissues, an area that is open for future research. Our current study fits nicely here to answer many REM sleep loss related questions comparing microarray dataset between brain and liver and provide unique dataset for future research.

2. Material and Methods

Male Wistar rats, weighing between 220-260 grams, were used for this study. Animals were housed with 12:12hrs L: D cycle (7:00 am lights on) and provided with food and water *ad libitum*. All experiments were carried out in compliance with the Institutional Animal Ethics Committee of the University.

2.1. REM sleep deprivation procedure

Rats were REM sleep-deprived for nine consecutive days by using the flower pot method [92,93]. Subjects were kept on a relatively small, raised platform (6.5 cm in diameter) and surrounded by water. While, for the sham control (large platform control, LPC) animals are kept on a larger platform (12.5 cm in diameter) under similar conditions of experimental group. REM sleep-deprived animals could sit, crouch, and have a NREM-related sleep on this platform. However, due to muscle atonia during REM sleep, they are unable to have REM sleep on the small platform. Upon entering REM sleep, subjects fell into water in order to disrupt the entirety of its cycle. Throughout our previous studies, there were no differences between the cage control (animals

146 kept in cages) and LPC control group of rats, and thus only the LPC control group is referred to as
147 the “control” group [47,49]. Rats were sacrificed between 10 a.m. and 12 p.m. on day 9 and the total
148 brain and liver were harvested and flash-frozen in liquid nitrogen for further analysis.

149 2.2. RNA extraction and quality analysis

150 Total RNA was isolated from the entire brain and liver samples using standard protocol. Rats
151 were anesthetized with isoflurane, and brain and liver samples were immediately dissected and
152 frozen in liquid nitrogen. We isolated total RNA from the whole brain and liver of each animal using
153 Trizol methods (Gibco-BRL, Gaithersburg, MD, USA), as directed by the manufacturer. The
154 concentration of total RNA was measured using Nanodrop and quality analyzed using Bioanalyzer.

155 2.3. Microarray: labeling, hybridization, and data analysis

156 An equal amount of total RNA from the brain and liver were collected and sent to Ocimum
157 Biosolutions (USA) genomics facility for microarray analysis. Affymetrix Rat Gene 1.0 ST Arrays
158 containing more than 7000 annotated sequences and 18,000 expressed sequence tags (ESTs) were
159 used. The Affymetrix Gene Chip Expression Technical Manual (Affymetrix Inc., Santa Clara, CA,
160 USA) was used for marking, hybridization, and expression analysis of microarrays, according to
161 previous methods [79]. The data analysis was performed using Affymetrix Expression Console and
162 Programming Language-R [94,95].

163 2.4. Gene Ontology analysis

164 Functional annotations of differentially expressed genes were obtained from the Gene Ontology
165 Consortium database, based on their respective biological process, molecular function and cellular
166 component [96]. Overrepresentation analysis, using a single-tailed Fisher exact probability test,
167 based on the hypergeometric distribution, was used and significant GO terms were stored ($p < 0.05$).

168 2.5. Pathway analysis

169 Pathway analysis of microarray data was performed using the Kyoto Encyclopedia of Genes
170 and Genomes (KEGG) software. Several biochemical pathways are identified by physiological
171 processes documented in the KEGG databank. Since rat species-specific functional gene annotations
172 are still few for several biological processes, general pathways, pathways of other organisms, and
173 species-specific pathways were combined for a comprehensive analysis. We used the KEGG map
174 pathway to visualize the maximal impact of REM sleep loss on highly up-regulated genes involved
175 in protein translation processes.

176 2.6. Validation of array expression with Real-Time quantitative qPCR

177 Following analysis of microarray, a group of genes were selected for validation by qPCR, based
178 on their degree of change in expression. We tested for correlation between the effects of the
179 microarray and qPCR, and statistical significance was calculated (Fig. 1). The microarray data used
180 for the correlation was input as Log2 ratio of the weighted average of each gene per composite array
181 for all subjects. For qPCR, we used the mean Log2 ratio value stated by qPCR of each subject. Six
182 transcripts were selected for validation of microarray analysis using RT-PCR (**Supplementary**
183 **Table, ST-1**). Controls were used to rule out the effect of any confounding variables. We tested the
184 respective mRNA levels with RT-PCR. Samples obtained from liver and brain tissue were frozen and
185 stored separately at -80°C before mRNA was quantified. Total RNA was isolated using Trizol
186 methods and re-transcribed using the ABI reverse transcription kit (Applied Biosystems, Catalog
187 number: 4368814). TaqMan gene expression Master Mix (Applied Biosystems, Catalog Number:
188 4369016) and probes (Applied Biosystems, **Supplementary Table, ST-1**) used for quantitative
189 analysis of mRNA. Each cDNA sample was analyzed in triplicate. The RT-PCR reactions for all focal
190 genes and Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) were measured from the same
191 cDNA sample and loaded onto the same 96-well analysis plate. We quantified the gene levels using

2 $\Delta\Delta C_t$ methods and GAPDH was used as a reference, control gene for expression level
normalization. Expression validation experiments were performed on the basis of five rats per
group.

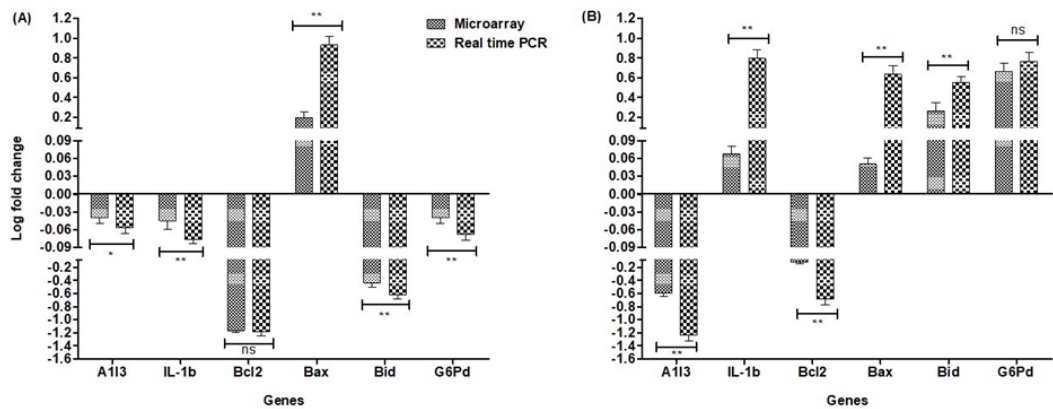


Figure 1. Relative expression of six candidate genes from the brain and liver tissue using real-time PCR and Microarray. (A) the comparative expression of genes in the brain; (B) the comparative expression of genes in the liver. Relative gene expressions were normalized by comparison with the expression of the Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene, while results were analyzed using the $2^{-\Delta\Delta C_t}$ method. For each gene, all RT-qPCRs used five biological replicates, with three technological replicates per experiment. The non-parametric Mann-Whitney U test was used to compare the pairwise expression of the microarray and the RT-PCR expression for the respective genes. We evaluated the normality of the data using the Kolmogorov-Smirnov normality test. Error bars indicate a \pm SE value.

2.7. Statistics

The results of qRT-PCR are presented as a mean of \pm SE. We used the Kolmogorov – Smirnov normality test to estimate the normality of the data. The Mann-Whitney U test was used to compare the pairwise expression of the microarray and RT-PCR expression for the respective genes used for liver and brain validation. The array experiments were analyzed, maintaining a $p < 0.5$ significance level. The KEGG bioinformatics map and diagrams were built based on an analysis of semantic similarity of terms, using Wang's method. Visualization of connectivity in network plots were designed in R using cluster Profiler package [97,98]. All statistical analyzes considered $p < 0.05$ to be significant and were performed and plotted using Sigma 8.0 and 12.0, Graph Pad 5.1 and Origin 6.0 software.

3. Results

3.1. General results

In the current analysis, we used the Affymetrix Rat Gene 1.0 ST Array and data analysis was performed using Affymetrix Expression Console and R-software. A total of 311 up-regulated genes (Supplementary Table, ST-2A) and 341 down-regulated genes (Supplementary Table, ST-2B) have been found in the brain. In contrast, 209 up-regulated genes (Supplementary Table, ST-2C) and 217 genes were down-regulated (Supplementary Table ST-2D) in the liver (Fig. 2).

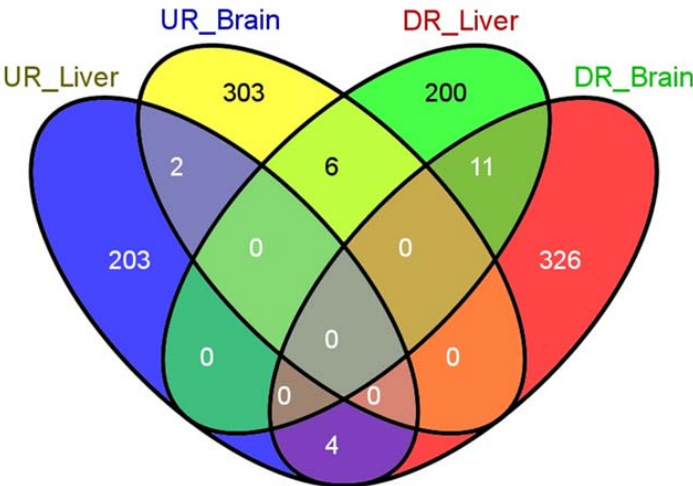


Figure 2. Venn diagram of the differentially expressed genes in the liver and brain after a rapid eye movement of sleep deprivation for 9 days in the rat. The Venn diagram shows overlapping genes of the UR_Liver: up-regulated liver; UR_Brain: up-regulated brain; DR_Liver: down-regulated liver; DR_Brain: down-regulated brain. Number in separate shaded panels reflects the genes typically affected in both tissues, in a similar or opposite direction.

Out of this pool, we found a set of genes that were commonly affected, either in the same or opposite direction, between the brain and the liver. For example, 4 of the 11 genes identified (Supplementary Table, ST-3A; namely *WEE1 G2 Checkpoint Kinase (Wee1)*, *Solute Carrier Family 2 Member 12 (Slc2a12)*, *Harakiri*, *BCL2 Interacting Protein (Hrk)*, and *Family With Sequence Similarity 110 Member B (Fam 110b)*) were negatively affected in both the brain and liver tissues (Fig. 2). Similarly, only 3 of the 6 genes identified (Supplementary Table, ST-3B; namely *Hemoglobin Subunit Alpha 1 (Hba-a1)* and *Major urinary protein 5 (Mup5)*) were up-regulated in the brain and down-regulated in the liver (Fig. 2). In addition, we identified 3 genes (Supplementary Table, ST-3C; namely *Histocompatibility 2, class II DR alpha (RT1-Da)*, *Zinc Finger And BTB Domain Containing 6 (Zbtb6)*, and *Transmembrane protein 106B (Tmem 106a)*) out of a total of 4 genes that were up-regulated in the liver and down-regulated in the brain (Fig. 2). In order to deepen our analysis, we moved forward with gene ontology and KEGG pathway analysis.

3.2. Gene Ontology analysis

Functional categories of genes that vary in their regulation between brain and liver upon REM sleep deprivation have been categorized. All processes and components were separated according to three main groups, namely biological processes, molecular functions, and cellular components (Fig. 3-5). In addition, we classified each group into two subcategories based on their direction of change (upregulation and downregulation), e.g. biological processes (Fig.3, A-D), molecular functions (Fig. 4, A-D) and cellular components (Fig. 5, A-D).

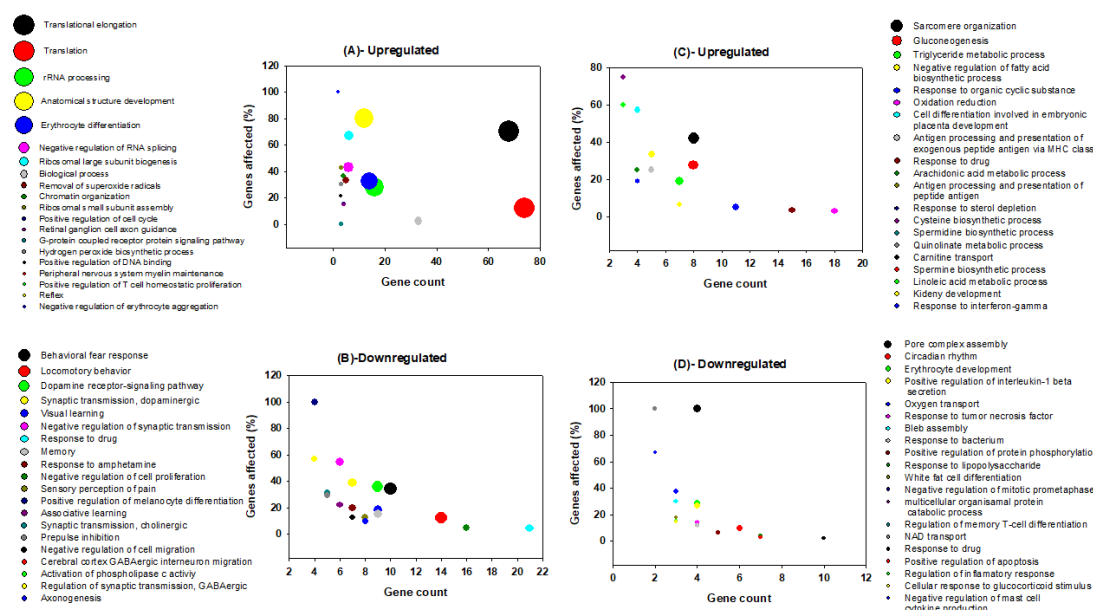


Figure 3. Graphical representation of GO terms from biological processes for genes which are up-regulated in the brain (A), down-regulated in the brain (B), up-regulated in the liver (C) and down-regulated in the liver (D) following rapid eye movements sleep deprivation in rats. The x-axis shows gene count, and the y-axis shows the percentage of genes affected for respective node. The bubble size represents the log transformed p -value [$Y = -0.5 \cdot \log(Y)$] of the respective biological processes. A bigger bubble size indicates a more significantly affected a given process, and thus, a lower p -value. The top 20 terms are displayed for each category.

Among the 208 significant GO terms of biological processes for genes which are upregulated in the brain, the top five are translational elongation, translation, rRNA processing, anatomical structure development and erythrocyte differentiation (Fig. 3A). Among the 77 significant GO terms of molecular functions for genes which are upregulated in the brain, the top five are structural components of ribosomes, protein binding, rRNA binding, translation regulator activity, and mRNA (Fig. 4A). Among the 57 significant GO terms of cellular components for genes which are upregulated in the brain, the top five include ribosomes, cytosol, intracellular anatomical structure, small ribosomal subunits, and nucleolus (Fig. 5A). REM sleep loss negatively affected 544 biological processes in the brain, of which the top five were behavioral fear response, locomotory behavior, dopamine receptor signaling pathway, dopaminergic synaptic transmission, and visual learning (Fig. 3B). A total of 140 significant molecular function terms were returned for genes which were negatively affected in the brain and the top five were protein binding, serotonin receptor activity, serotonin binding, drug binding and G-protein coupled receptor activity (Fig. 4B). A total of 57 cellular component terms were returned for genes which are negatively affected in the brain, of which the top five were plasma membrane, axon, membrane, dendrite, and extracellular space (Fig. 5B).

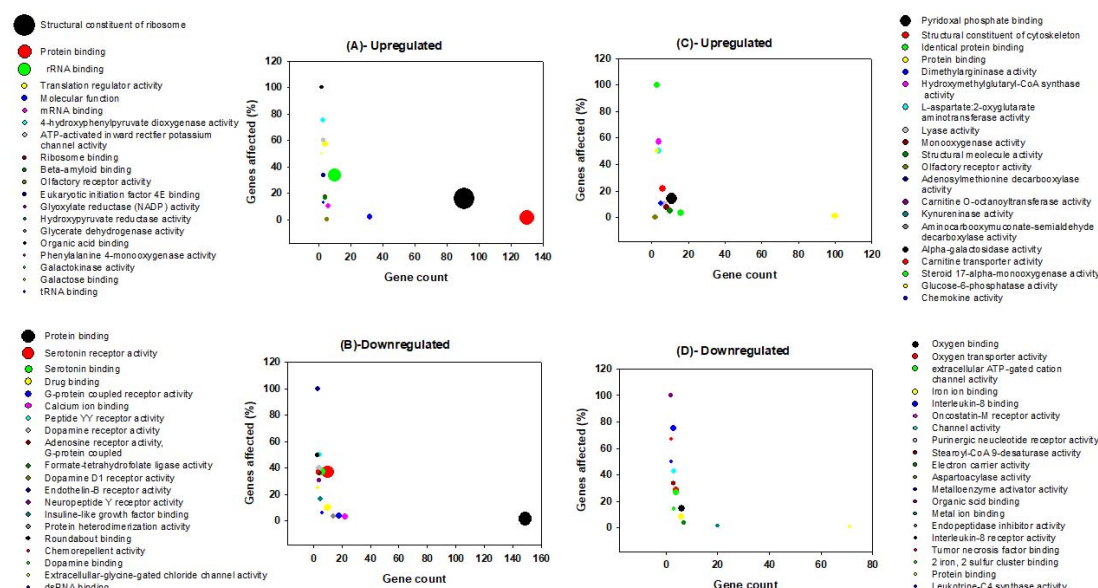


Figure 4. Graphical representation of molecular function terms for genes which are up-regulated in the brain (A), down-regulated in the brain (B), up-regulated in the liver (C) and down-regulated in the liver (D) following rapid eye movements sleep deprivation in rats. The x -axis shows gene count and the y -axis shows the percentage of genes affected. The bubble size represents the log transformed p -value [$Y=-0.5*\log(Y)$] of the respective molecular function. A bigger bubble size indicates a more significantly affected a given process, and thus, a lower p -value. The top 20 terms are displayed for each category.

The top five of 355 significant biological processes terms for genes which were positively affected in the liver are Sarcomere organization, Gluconeogenesis, triglyceride metabolic process, negative regulation of fatty acid biosynthetic process, and response to an organic cyclic substance (Fig. 3C). The top five of 150 significant molecular function terms for genes which were positively affected in the liver are pyridoxal phosphate binding, structural constituents of the cytoskeleton, identical protein binding, protein binding, and dimethyl arginase activity (Fig. 4C). The top five of 64 significant cellular component terms for genes which were positively affected in the liver are endoplasmic reticulum, plasma membrane, membrane, lysosome, and cytosol (Fig. 5C). Pore complex assembly, circadian rhythm, erythrocyte development, positive regulation of interleukin-1 beta secretion, and oxygen transport were the top five of 219 significant biological processes terms (Fig. 3D) for genes which were downregulated in the liver. Oxygen binding, oxygen transport activity, extracellular ATP-gated cation channel activity, Iron-ion binding, and Interleukin-8 binding were the top five of 86 significant molecular function terms for genes which were downregulated in the liver (Fig. 4D). Hemoglobin complex, extracellular space, soluble fraction, extracellular region, and mast cell granules were the top five of 27 significant cellular component terms for genes which were downregulated in the liver (Fig. 5D).

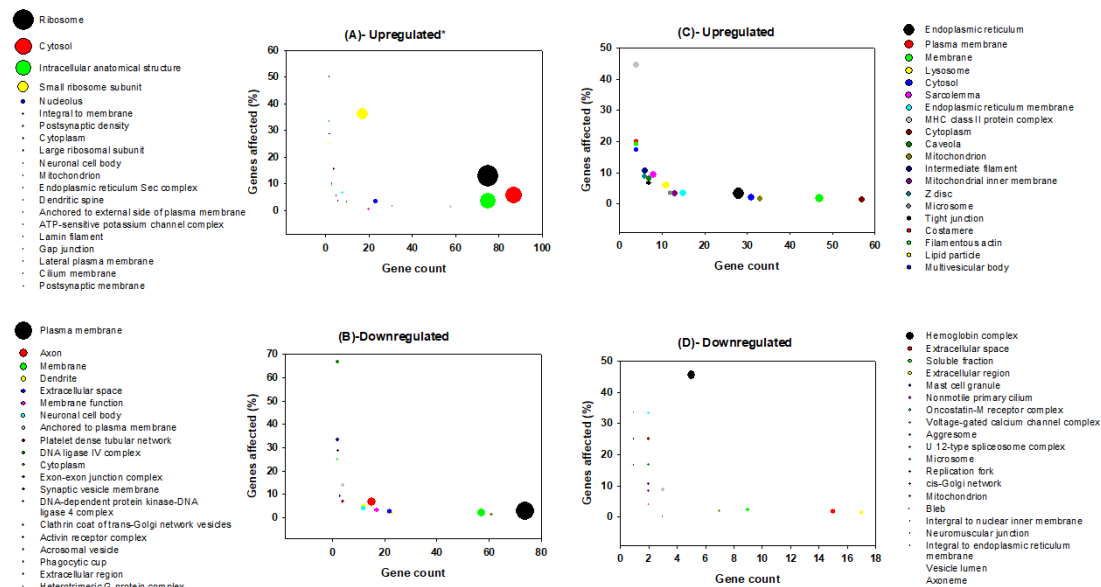


Figure 5. Graphical representation of cellular component terms for genes which are up-regulated in the brain (A), down-regulated in the brain (B), up-regulated in the liver (C) and down-regulated in the liver (D), following rapid eye movements sleep deprivation in rats. The x-axis shows gene count and the y-axis shows the percentage of genes affected. The bubble size represents the log transformed p -value [$Y=-0.5*\log(Y)$] of the respective cellular component. To fit the bubble size, the p -value in 5A* was normalized with formula [$Y=-0.5*\log(Y)/2$]. A bigger bubble size indicates a more significantly affected a given process, and thus, a lower p -value. The top 20 terms are displayed for each category.

3.3. Pathway analysis

KEGG analysis was used to evaluate the pathways affected by REM sleep loss in the brain and liver, and terms were plotted based on significance level ($p<0.05$), database count, and the number of genes affected by each pathway (node count). Shown are up- and down-regulated pathways in the brain (Fig. 6), up-regulated pathways in the liver (Fig. 7A), and down-regulated pathways (Fig. 7B). Pathways that were significantly upregulated in the brain included only ribosomes and olfactory transduction, while 11 were downregulated – of which the top five were neuroactive ligand-receptor interaction, axon guidance, calcium signaling pathway, olfactory transduction, and GAP junction (Fig. 6). The top five of 36 significantly upregulated liver pathways were glyceraldehyde metabolism, alanine and aspartate metabolism, cysteine metabolism, cell adhesion molecules, and glycine-serin & threonine metabolism (Fig. 7A), while just circadian rhythm, arachidonic acid metabolism, nitrogen metabolism, and retinol metabolism were downregulated (Fig. 7B).

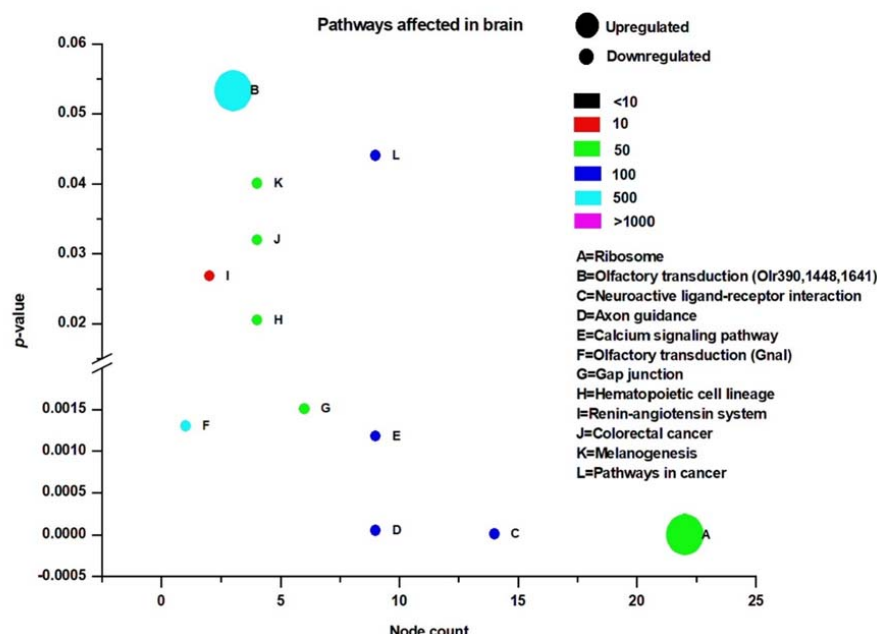


Figure 6. KEGG pathways affected by rapid eye movement sleep deprivation in rats in the brain. The x-axis depicts the number of nodes affected and the y-axis shows the p-value ($p < 0.05$). Color coding indicates the total number of database nodes evaluated. The size of the circle indicates the direction of change.

We used a KEGG pathway maps (Supplementary Figures, SF 1-4) to visualize the components, proteins, and genes that were highly associated with the involved processes. Displayed are the subunits of ribosomes (Supplementary Figure, SF-1) and neuroactive legend-receptor interaction pathways (Supplementary Figure, SF-2), which were negatively and positive affected pathways, respectively, in the brain. Additionally, the cancer pathway (Supplementary Figure, SF-3) and glycerophospholipid metabolism pathway (Supplementary Figure, SF-4), which were negatively and positively affected, respectively, due to REM sleep loss.

4. Discussion

We sought to characterize the effects of prolonged REM sleep deprivation using gene expression data from the brain and liver of rats. In order to confirm our findings and validate our analyses, six differentially expressed genes were analysed using RT-PCR (Fig.1). We found that our study corroborates with previous microarray findings of sleep deprivation relating to effects on genes such as *Egr1*, *Fos*, *Ptgs2*, several genes of Slc family, *Hba-a1* and *Hbb* [82,99–101]. Indeed, each of these six genes were found to be associated with sleep loss previously. Out of the hundreds of genes found to be significantly affected in the brain and liver, only a few genes were common between the tissues examined and their associated direction of change. Four genes, *Wee1*, *slc2a12*, *Hrk*, and *Fam110b* (Fig. 2, Supplementary Table, ST-3A), were commonly downregulated in the tissues examined but none were commonly upregulated. Three genes, *Hba-a1*, *Hba-a2* & *Mup5*, were up-regulated in the brain and down-regulated in the liver and associates with GO terms drug transport, oxidoreductase activity, heme binding, fatty acid biosynthesis processes, and catalytic activity (Fig. 2, Supplementary Table, ST-3B). Genes that were found to be up-regulated in the liver, and at the same time, down-regulated in the brain (*RT1Da*, *Zbtb6*, and *Tmem 106b*) are associated with the GO term stimulus response (Fig. 2, Supplementary Table, ST-3C).

Several of the aforementioned genes which were commonly associated between brain and liver tissue, and any combination of direction of change, were found in previous literature regarding sleep and REM. Several genes of solute carrier (Slc) family (**Supplementary Table, ST-4**) were up- and down-regulated in the brain and liver, respectively, except *slc2a12* which was downregulated in both the brain and liver. Previously, genes of the *slc* family were reported to be associated with glucose homeostasis and *slc17a8* is down-regulated in Tinaja cave fish in response to sleep deprivation [102]. *Slc38a5a* is upregulated in response to sleep deprivation when glucose levels drops and circulating amino acid levels increases [103]. Recently, *Hrk* gene was found to be

upregulated in mice after sleep deprivation, which is opposite to that of our findings and may be a result of differential expression between organisms or sleep-loss in general, as compared to only REM deprivation [104]. GO term analysis of molecular/biological functions associated with *Hrk* returned the terms protein tyrosine kinase activity, carbohydrate transmembrane transport activity, apoptosis regulation, and Bleb assembly (**Supplementary Table, ST-3A**). Previous studies and recent pre-prints support that REM sleep deprivation results in the apoptotic death of neuronal and hepatocytic cells [44–46]. Induction of *Hba-a1* gene in brain may cause cerebral hypoxia-like condition in the brain after REM loss as a result of cerebral hypoxemia and obstructive sleep apnea, and reduce hemoglobin denaturation [105,106]. A recent study on sleep restriction showed that there is an increase in free fatty acids in healthy men, which led us to speculate that REM sleep deprivation can affect genes such as *Mup5*, which our findings demonstrated an association with the term fatty acid biosynthetic processes and was differentially expressed as a result of REM sleep deprivation [58]. Similarly, *Zbtb6* is a homologous gene that codes for the BTB domain of zinc finger protein in mammals and *Tmem 106b* returned several GO terms, which include protein binding, dendrite morphogenesis, and lysosomal transport [107,108]. A recent study showed that *Tmem 106b* is associated with dementia, which is caused by faulty regulation of microRNAs [109]. Overall, our study provides a list of genes affected across different tissue of body and further commonly affected in same or different directions which would be interesting to explore in future.

Many of the GO terms in our findings indicated the presence of various phenomena associated the synapse, and more specifically, synaptic potentiation (**Fig 3-5**). Previous analyses demonstrated that several genes, *Arc*, *Bdnf*, *Camk4*, *Creb1*, *Egr1*, *Fos*, *Nr4a1*, *Ppp2ca*, and *Ppp2r2d* are associated with the GO term, potentiation of synaptic plasticity, which largely supports the ‘synaptic homeostasis theory’ [55,58]. Indeed, we found *Fos* and *Egr1* is significantly downregulated in our study in both brain and liver. In addition, several other genes (list not shown) of our study that were non-significantly upregulated/downregulated in the liver/brain, respectively are associated with GO terms related to synaptic plasticity, like positive regulation of long-term neuronal synaptic plasticity, regulation of neuronal synaptic plasticity, synaptic vesicle endocytosis, and neuromuscular synaptic transmission. Previously sleep loss has shown to be involved in the upregulation of genes associated with synaptic plasticity [110–112], however, many of its associated GO terms (**Supplementary Table, ST-5**) were a result of genes which were downregulated in the brain of REM sleep loss rats in our study. The regulation of synaptic plasticity during sleep and learning is essential [113] and loss of sleep was found to be associated with negative impact on glial signaling pathway important for synaptic plasticity [25,114–116].

REM sleep deprivation is found associated with modification of expression of long-term potentiation in visual cortex of immature rats [117] and we report upregulation of structural constituents of ribosomes, translation regulation activity, while dopamine receptor-signaling pathway, dopaminergic, cholinergic, GABAergic regulation of synaptic transmission, serotonin binding, and receptor activity were downregulated in brain (**Fig. 3B & 4B**). The dopamine receptor-signaling pathway regulating sleep, learning, and its plasticity are well known [84,85]. Sleep disorders and sleep deprivation have been correlated with dopaminergic, cholinergic, and GABAergic regulation of synaptic transmission, each of which were terms that were significantly enriched for genes that were downregulated in our study [86–90]. These observations support our hypothesis that REM sleep loss negatively affect the gens and processes related to synaptic homeostasis in brain.

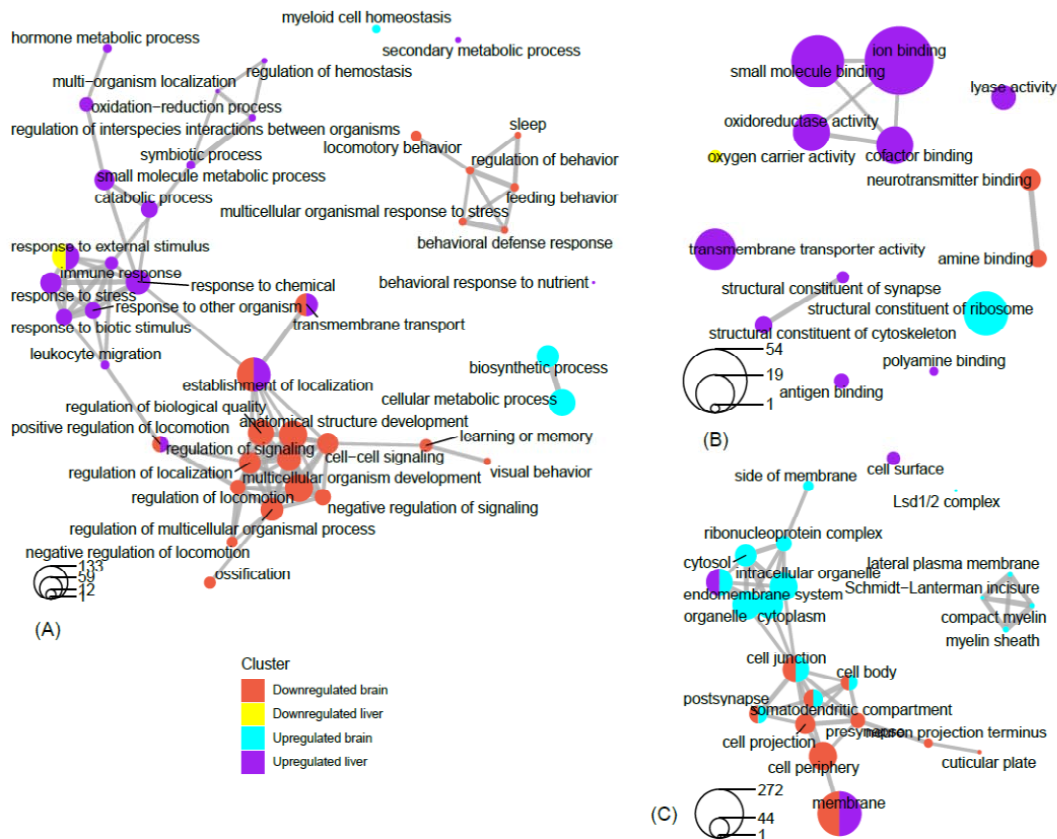
Processes and pathway in the liver following REM sleep deprivation are largely associated with metabolism and the immune system. Many metabolic process and cellular metabolic processes such as gluconeogenesis, triglyceride metabolic process, negative regulation of fatty acid biosynthetic process, oxidation reduction, and arachidonic acid metabolic process were upregulated in liver in response to REM loss. Whole body energy expenditure decreases by 15-35 percent, With the lowest expenditure during slow-wave sleep and marginally higher during REM sleep [118] and sleep restriction involves reduced muscle glucose uptake, elevated blood glucose production, and pancreatic β -cell dysfunction [119,120]. A increasing body of evidence indicates that Obstructive Sleep Apnea Syndrome is associated with a variety of metabolic alterations, such as dyslipidemia,

insulin resistance, glucose intolerance [121]. REM sleep impairs glucose metabolism that is involved in intermittent hypoxemia [122]. An upregulation of gluconeogenesis may serve as a mechanism to compensate for hypoxemia due to prolonged REM loss. The GO terms related to homeostatic processes like cholesterol homeostasis, nitric oxide homeostasis, fatty acid homeostasis, retina homeostasis, cytosolic calcium ion homeostasis are associated with genes which were upregulated in the liver, while T cell homeostasis and other processes associated with the immune system were downregulated (**Supplementary Table, ST-6**). The immune functions of sleep and associated diseases have been studied [123,124], as well as and evidence that the immune system is compromised from lack of sleep. [125]. The body of previous evidence and our results support our hypothesis, that while REM sleep loss is associated with synaptic potentiation and maintenance, its affects in the liver are more so related to metabolism and immune response to infections.

REM sleep loss negatively affects several genes linked to neuroactive ligand-receptor interaction pathways in brain, primarily gamma-Aminobutyric acid, Human Thrombin receptor, and associated receptor signaling dopamine (**Supplementary Figure, SF-2**). A recent review of sleep and protein-dependent synaptic plasticity, indicated that sleep deprivation impairs many of the related biological and physiological processes [126]. We have found that many of the pathways in the liver which have been upregulated are linked to metabolism, immunity, and depression (**Fig. 7A**). On the other hand, only a few downregulated pathways in the liver have been established, which include nitrogen metabolism and circadian rhythm (**Fig. 7B**). The findings further support our secondary hypothesis that REM sleep loss affects the processes and pathways related to synaptic potentiation and learning and memory (**Fig 8A**) and processes related to homeostasis and immunity in liver (**Fig. 8 A-C**).

Network analysis of filtered GO terms allowed for visualization of major themes and the connectivity of processes across brain and liver tissue in rats deprived of REM (**Fig. 8**). Several biological processes, like positive regulation of locomotion, establishment of localization, and transmembrane transport were terms that were significantly enriched for genes that were both downregulated in brain and upregulated in liver. Interestingly, response to external stimuli genes were found as both positively and negatively affected in the liver, indicating the up- and downregulation of separate sets of genes associated with this term (**Fig. 8A**). There was no connectivity between terms in the molecular function category, however, terms associated with metabolism and transport, like oxidoreductase activity, small molecule binding, iron binding and cofactor binding, were each upregulated in liver (**Fig. 8B**). Networking of terms in the cellular component category returned GO terms, cell junction, cell body, post synapse, and somatodendritic compartment, that were up- and downregulated in the in the brain and liver, respectively (**Fig. 8C**). To summarize a major theme, some processes which were mainly upregulated in liver were also downregulated in the brain as a result of REM sleep loss. One possible explanation for this is that REM sleep loss influences processes linked to fear response of the brain and locomotive activity related to the peripheral circadian clock, hemoglobin level, and transport of oxygen throughout the liver. The evidence suggests that the genes and processes involved are highly contrasted between the brain and liver, however, some processes may be connected across major organs in response to REM sleep loss and should be investigated in the future.

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Figure 8: Network view of GO term association. Network plots of the top filtered GO terms, depicting the degree of connectivity within and between terms of enriched genes which are upregulated in the brain, upregulated in the liver, downregulated in the brain, and downregulated in the liver. The circles-legend at the bottom of each left-hand corner indicates the number of genes that are enriched for a given term. Connecting lines indicate a significant degree of semantic similarity between terms. Biological process (A), cellular component (B), and molecular function (C). GO terms were filtered (level = 3) to reduce redundancy and capture major categorical themes prior to visualization of connectivity in network plots, which were designed in R using cluster Profiler package. Plots of filtered GO terms contained the top 20 significant categories, respectively, per subject cluster.

We further explored the common processes related to general interest like oxidative-stress, cancer, and cell-death. Processes related to reactive oxygen species metabolic and oxidative stress e.g., positive regulation of oxygen and reactive oxygen species metabolic process, response to oxidative stress were positively affected while, cellular response to reactive oxygen species, oxygen and reactive oxygen species metabolic processes negatively got affected in brain. Previous studies have shown that there are transcript level variations in many genes involved in the regulation of reactive oxygen species (ROS), including heme oxygenase, superoxide dismutase, and catalase, in patients with obstructive sleep apnea [127]. Similarly, REM sleep is recently found associated with acute phase response and ROS stress in liver [47,49]. REM sleep loss also affected several genes such as *prostaglandin-endoperoxide synthase (Ptgs2)*, *B-cell lymphoma 2 (Bcl-2)*, *Proto-Oncogene, Tyrosine Kinase receptor (Kit)*, *KRAS Proto-Oncogene (K-Ras)* and *Fos Proto-Oncogene (Fos)* which are marked in cancer pathways (Supplementary Figure, SF-3). A number of recent studies have shown that sleep dysfunction/loss and cancer processes are very related [128–134]. However, some emerging evidence also suggests that sleep loss/insomnia prior to the onset of cancer is independently associated with cancer risk [129,133,135,136]. *Ptgs2*, an enzyme, plays a key role in various pathological processes by catalyzing conversion of arachidonic acid to prostaglandins [137].

Studies have shown that overexpression of *Ptgs2* is associated with angiogenesis, metastases, and immunosuppression [75,76]. *Pgst2* is also found to be associated with the chemoresistance of some malignant tumors, including liver, pancreatic, lung, esophageal, and gastric cancers [77–79]. Inhibition of *Ptgs2* effectively increased the sensitivity of tumors to drugs [138]. Similarly, *Bcl-2*, *Kit*, *K-Ras*, and *Fos* genes have been found associated with cancer [139–142]. These genes play an important role in the sleep-wake cycle regulation and are shown to be correlated with sleep [44,45,143–145]. At the same time, glycerophospholipid metabolism pathway was found significantly upregulated in liver (Supplementary Figure, SF-4). These include the genes *Phospholipase*, *PLa2g*, *Phosphatidylcholine 2-Acylhydrolase 12A* *Pla2g12a*, *Glycerol-3-Phosphate Dehydrogenase 2*, *Gpd2*, *CDP-Diacylglycerol Synthase 2*, *Cds2*, and *Phospholipid Phosphatase 2*, *Plpp2*. The *PLa2g* associates with neurodegeneration and elevated mitochondrial lipid peroxidation and dysfunction [146–148]. The *PLa2g* is further found positively associated with sleep loss and psoriasis in humans [149,150]. Similarly, *Gpd2* gene is found associated with intellectual disability in humans [151] and positively affected due to circadian desynchrony in mouse [152]. The chronic sleep deprivation in rats affected the protein profile of *Gpd2* in hypothalamic astrocytes [101]. The functional aspect of other genes affected (e.g., *Pla2g12a*, *Cds2* and *Plpp2*) is lacking and needs further exploration. These findings further support the idea of REM sleep related to restorative functions against diseases and oxidative stress.

Many KEGG pathways were associated with genes that were either significantly up- or downregulated (Fig. 6 and Fig. 7A & 7B) in the brain or liver as a result of REM sleep loss. The KEGG pathway map (Supplementary Figures, SF 1-4) demonstrated that many of the genes for ribosomal proteins that are involved in protein synthesis processes were upregulated in the brain by REM sleep loss (Supplementary Figure, SF-1). Indeed, research has shown that long-term sleep loss has been found to control several genes in the brain that are linked to DNA binding/regulation of transcription, immunoglobulin synthesis, and stress response [56,91]. Contrary to the notion that *Homer-1a* is a key brain molecule in response to sleep loss in mice, no effect on gene expression of *Homer* gene was observed in our study, which suggests that its regulation is modulated during other stages of sleep or an organism-specific phenomenon [82]. The results underscore the complexity of sleep loss and its associated consequences, and requires sleep phase-, species-, and/or tissue-specific considerations rather than overarching, vague generalizations to deeply understand the phenomenon.

Additionally, REM sleep loss negatively affected several genes linked to neuroactive ligand-receptor interaction pathways in brain, primarily related to gamma-Aminobutyric acid, Human Thrombin receptor, and associated receptor signaling dopamine (Supplementary Figure, SF-2). A recent review of sleep and protein-dependent synaptic plasticity, indicated that sleep deprivation impairs many of the related biological and physiological processes [126]. We have found that many of the pathways in the liver which have been upregulated are linked to metabolism, immunity, and depression (Fig. 7A). On the other hand, only a few downregulated pathways in the liver have been established, which include nitrogen metabolism and circadian rhythm (Fig. 7B). The findings further support our secondary hypothesis that REM sleep loss affects the processes and pathways related to synaptic potentiation and learning and memory (Fig 8A) and processes related to homeostasis and immunity in liver (Fig. 8 A-C).

Findings across studies are inconsistent in regard to REM sleep deprivation, and locomotor behavior and pain tolerance in rodents. Several studies have shown that REM sleep loss induces locomotor activity [93,153,154], while others have shown decreased locomotor activity [155]. The lack of consistent explanation could be related to procedural changes in the methods of a given study, such as the degree of REM sleep loss. Few studies have used multiple pots compared to our classic single flower pot method for deprivation, and other studies have implemented less total time for deprivation (72-96 hrs.) compared to ours, which was ~216 hrs. Recent research supports that REM sleep deprivation can affect locomotor activity in rats in an inverted-U manner [156,157]. A widely accepted view in the scientific community is that sleep deprivation decreases pain tolerance and increases the transmission of pain in multiple chronic pain conditions [158–163]. There is a conflict between reports on the sensory perception of pain [164,165] which was negatively affected in

our study (Fig. 3B) and few studies indicated only total sleep deprivation raises the intensity of pain rather than REM sleep deprivation [166,167]. Nonetheless, selective REM sleep deprivation is correlated with enhanced placebo analgesia effects [168]. Similarly, consistency exists between REM sleep loss and its association with the perception of pain [170]. Perhaps sleep in general and short-term REM sleep deprivation lower the pain threshold, while long-term sleep deprivation increases the pain threshold. REM sleep deprivation and pain is significantly correlated with environmental conditions (e.g. dry or wet conditions), with pain sensitivity enhanced in dry test conditions but no different in wet conditions. [171]. This suggests that further work is needed to understand deeply the relationship between experience of pain and lack of sleep. Furthermore, a recent microarray analysis shows that *Hspa5* gene expression increases not only in the brain but also in the liver as sleep deprivation increases [82]. Our analysis did not return any genes which were commonly upregulated in both the brain and liver, however, this may simply be due to differences between species and many of the studies related to *Hspa5* and sleep-wakefulness involved mice and drosophila [13,55,169]. Genes such as, *Wee1*, *Slc2a12*, *Hrk*, and *Fam110b* were commonly downregulated in both the brain and liver. Currently, however, there is consensus about the relationship between expression of genes associated with locomotor behavior and pain tolerance, an area that is open for future research.

Our approach to GO term and KEGG pathway analysis is quite relevant in the current era of genomics and sequencing, but it also involves discrepancies in gene function across organisms, distributed biases and biases linked to positive and negative annotations (more information in 56–58). Like GO term analysis, KEGG analysis also has its limitations, apart from reducing the complexity of the data and helping to increase the explanatory power. One of the key disadvantages of KEGG is the independent consideration of pathways, even though crosses and overlaps occur in the natural system [177–180]. Therefore, the findings of our current study involving REM sleep deprivation affecting brain and liver should be taken as case study. The present study also provides as data set for future studies to compare the effect of RMS sleep loss across organs. We have only few microarray studies to understand effect of molecular signatures of diseases, effect of sleep deprivation, and disorders and looking forward to our study as one [127,181–186]. We further need more research related to total sleep or REM sleep loss to determine stage and tissue-specific effects on body in order to understand particular effects and to evaluate the influence of sleep loss and in effects of sleep related disorders.

5. Conclusion

Microarray analysis of brain and liver tissue in rats found that many of the physiological processes and the genes involved in the pathways are regulated differently in the two organs body as a consequence of REM sleep loss, which also supported our hypothesis that REM sleep is crucial for proper metabolism and immune function in the liver synaptic potentiation in the brain. Our findings underscore the idea that the brain have shown to be more receptive to processes such as synaptic potentiation, learning and memory, oxidative stress, and circadian rhythms in response to REM sleep loss. On the other hand, the function of the liver is more so related to processes like protein synthesis, stress balance, and detoxification. The study provides a fundamental platform for visualizing the effects of REM sleep loss across the brain and liver and future studies should address the underlying dynamics of REM sleep deprivation throughout the body.

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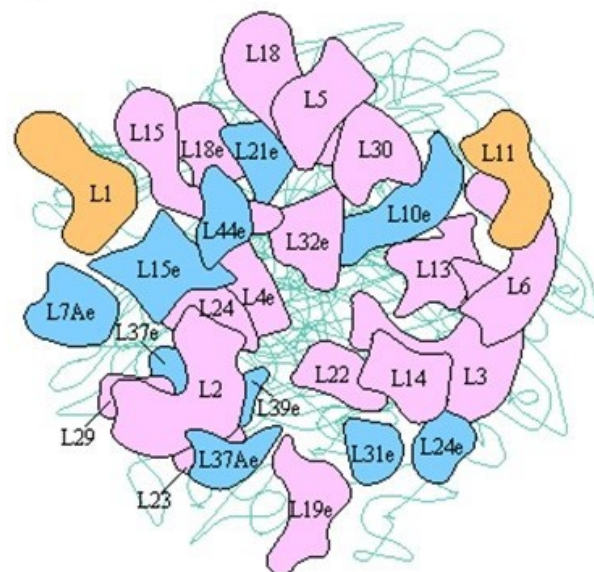
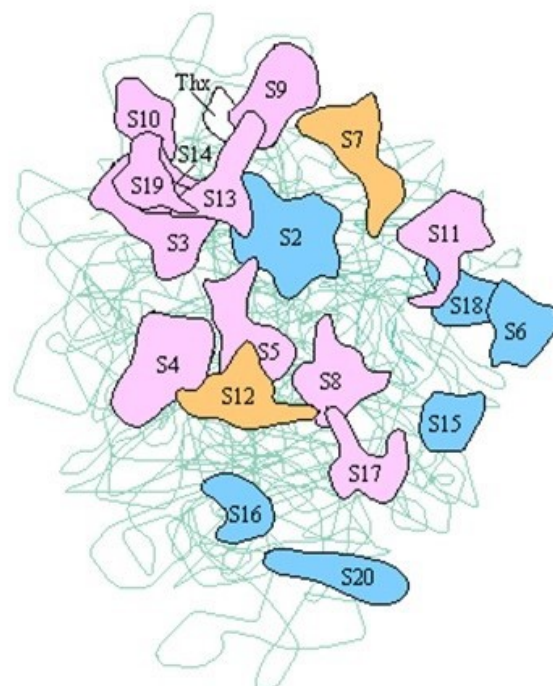
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RIBOSOME

Large subunit (*Haloarcula marismortui*)Small subunit (*Thermus aquaticus*)

Ribosomal RNAs

Bacteria / Archaea	23S	5S		16S
Eukaryotes	25S	5S	5.8S	18S

Ribosomal proteins

EF-Tu

S10 L3 L4 L23 L2 S19 L22 S3 RP-L16 L29
S20e L3e L4e L23Ae L8e S15e L17e S3e L35e

L7/L12 stalk

S17 L14 L24 L5 S14 S8 L6 L18 S5 L30 L15 SecY
S11e L23e L26e S4e L11e S29e S15Ae L9e L32e L19e L5e S2e L7e L27Ae

IF1 RpoA
L34e L14e L36 S13 S11 S4 L17 L13 S9
S18e S14e S9e L18e L13Ae S16e

EF-Tu,G RpoC,B
S7 S12 L7A L7/L12 L12 L10 L1 L11
S5e S23e L30e L7Ae LP1,LP2 LP0 L10Ae L12e

EF-Ts IF2 IF3 RF1
S2 S15 S35 L35 L20 L34 L31 L32 L9 S18 S6
SAe S13e

L28 L33 L21 L27 FtsY,Ffh S16 L19 S1 S20 S21 L25

L10e L13e L15e L21e L24e L31e L35Ae L37e L37Ae L39e L40e L41e L44e

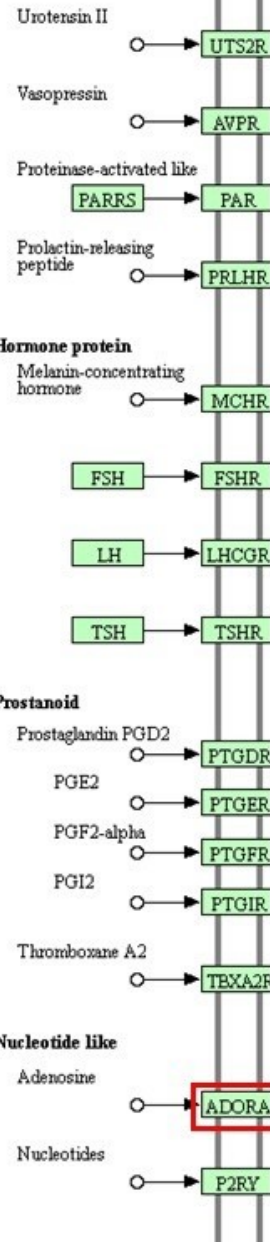
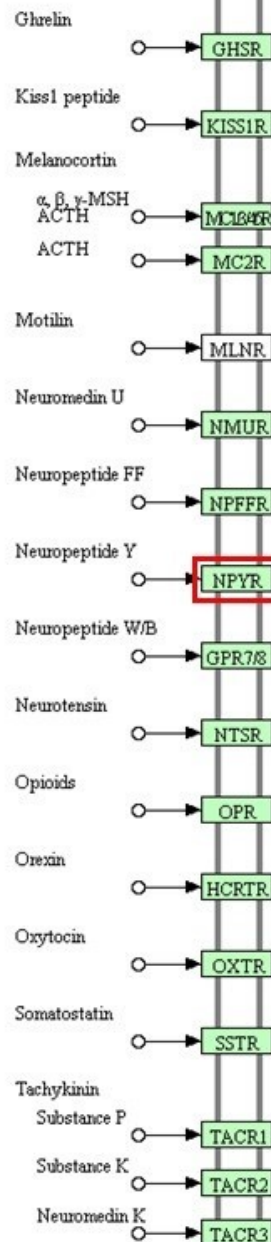
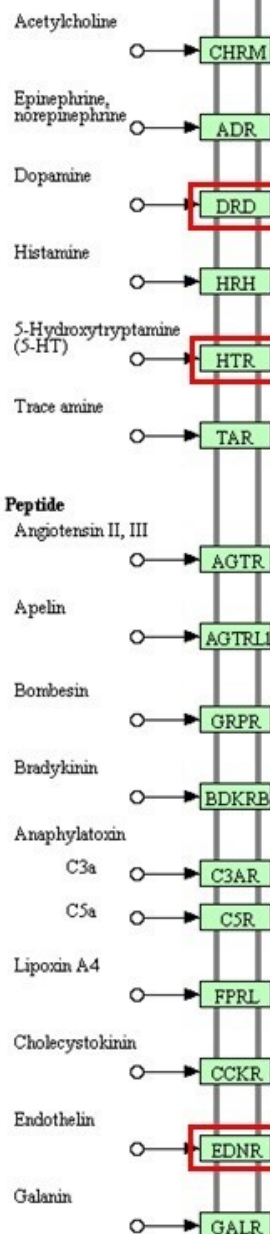
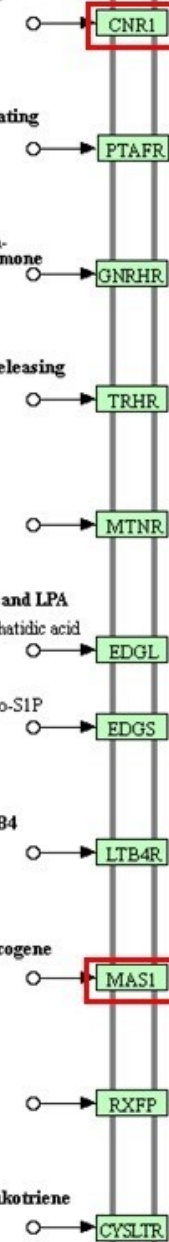
S3Ae S6e S8e S17e S19e S24e S25e S26e S27e S27Ae S28e S30e LX

L6e L18Ae L22e L27e L28e L29e L36e L38e

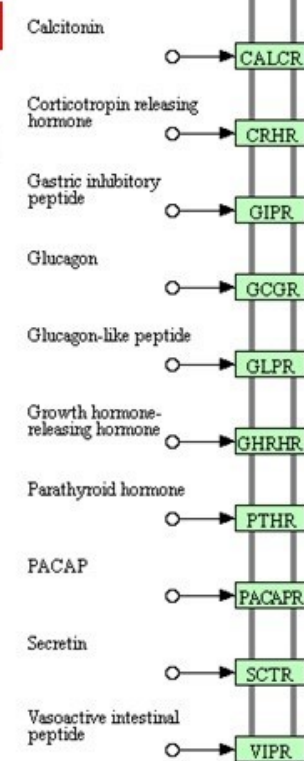
S7e S10e S12e S21e

NEUROACTIVE LIGAND-RECEPTOR INTERACTION

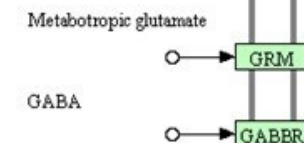
GPCRs

Class A Rhodopsin like
AmineCannabinoid
Anandamide

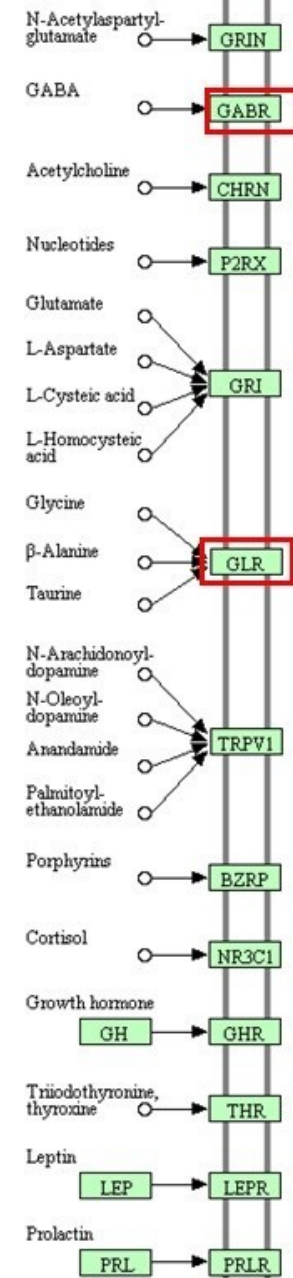
Class B Secretin like



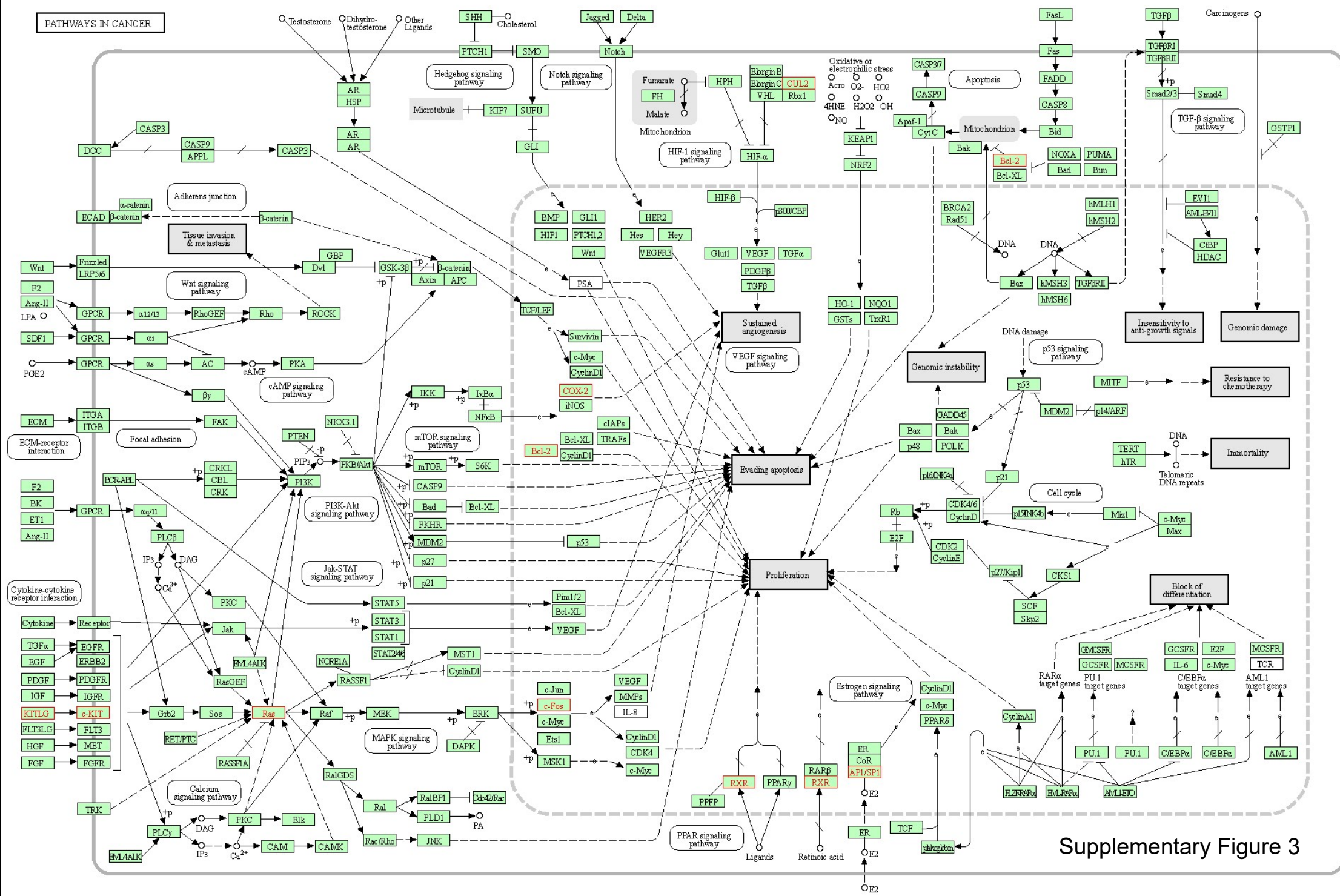
Class C Metabotropic glutamate / pheromone



Channels /other receptors

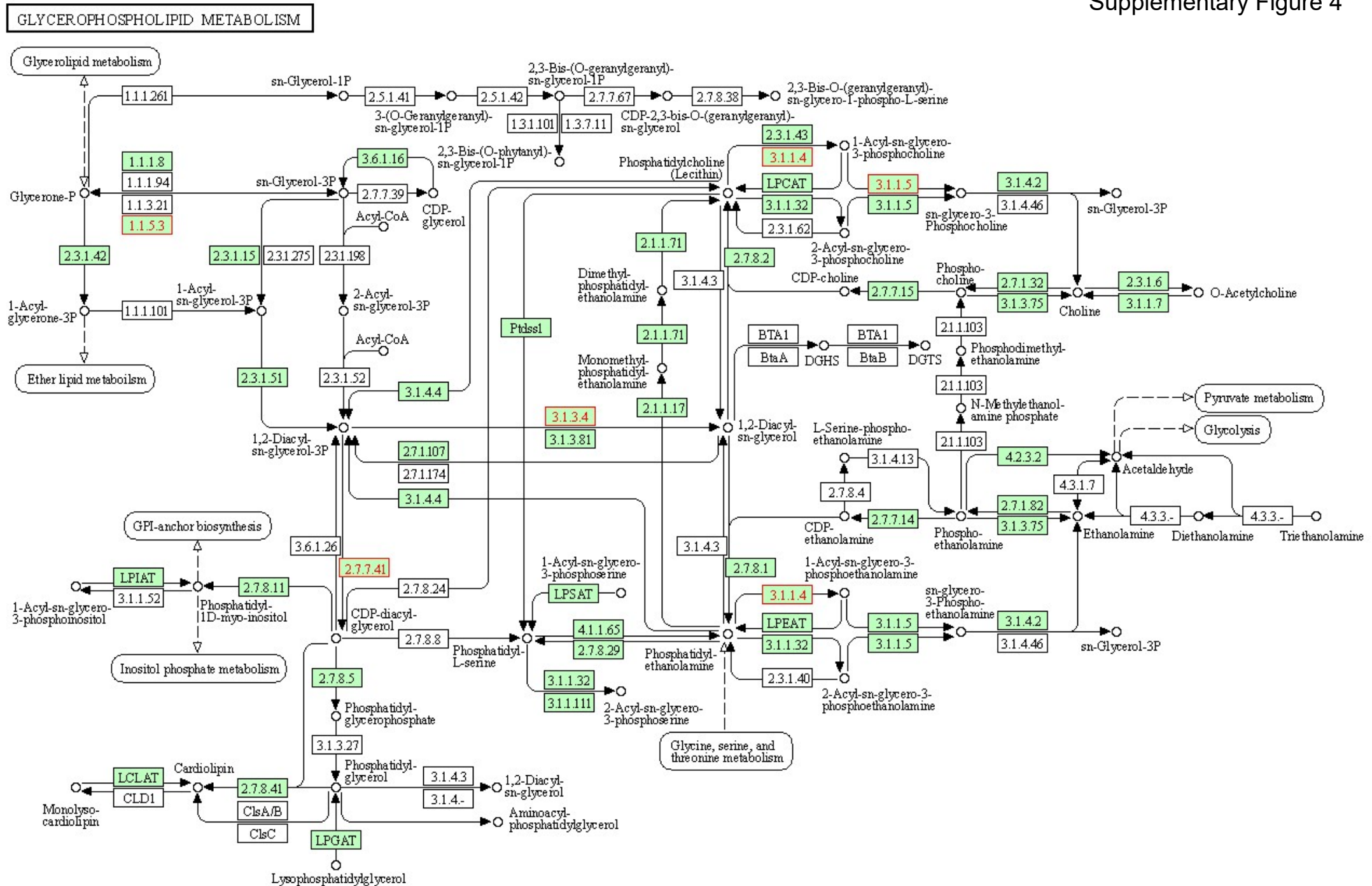


PATHWAYS IN CANCER



Supplementary Figure 3

Supplementary Figure 4



Supplementary materials:

Supplementary table (ST1): List of real time PCR gene primers used in microarray validation experiments.

S. N	Primer/probe	Primer/probe sequence ID's
1	Alpha 1 inhibitor 3	Rn00440636-m1
2	Interleukin-1b	Rn00580432_m1
3	TP53	Rn00755717_m1
4	Bcl2	Rn99999125_m1
5	Bax	Rn02532082_g1
6	Bid	Rn01459517_m1
7	G6pD	Rn01529640_g1
8	GAPDH	Rn01749022_g1
9	Master mix	Cat. 4304437

Supplementary table (ST2A): List of genes upregulated in brain

Probe Set ID	Control Brain	Sleep Deprived Brain	Log Fold Change	Fold Change	Entrez ID	Gene Symbol	Accession
10701797	5.09	5.98	0.89	1.85	680891	Sf3b5	NM_001126092
10701825	4.66	5.69	1.03	2.05	361453	Deadc1	NM_001115028
10702286	6.52	7.54	1.01	2.02	65139	Rps12	NM_031709
10702306	2.93	3.79	0.86	1.81	252856	Tcf21	NM_001032397
10702361	3.80	4.81	1.01	2.01	155430	Hey2	NM_130417
10702592	7.46	8.37	0.90	1.87	683872	LOC683872	ENSRNOT00000031807
10704411	6.75	7.69	0.94	1.92	29287	Rps19	NM_001037346
10704452	4.48	5.53	1.05	2.08	361514	Meis3	NM_001108472
10705414	6.97	8.33	1.35	2.55	361528	Ttc9b	NM_001108478
10705511	9.06	10.12	1.06	2.08	140655	Rps16	ENSRNOT00000026576
10705753	5.28	6.17	0.89	1.85	114004	Ppp1r14a	NM_130403
10706571	5.53	6.71	1.18	2.27	292876	Josd2	NM_001106256
10710771	7.00	7.97	0.97	1.96	117053	Rps15a	NM_053982
10713538	5.99	6.89	0.90	1.87	24913	Pla2g16	NM_017060
10716085	6.70	7.84	1.13	2.19	65139	Rps12	NM_031709
10716373	3.40	4.45	1.05	2.07	25702	Pnlp	NM_013161

10717434	7.73	8.83	1.16	2.15	287417	Rpl26	NM_001105788
10722005	4.04	5.20	1.16	2.23	83535	Kcnj11	NM_031358
10722084	7.07	8.13	1.05	2.08	365243	Sergef	ENSRNOT00000015352
10723233	7.22	8.45	1.23	2.34	29286	Rps17	NM_017152
10725078	3.48	4.50	1.02	2.02	499249	Plekha7	NM_001144861
10726477	3.85	4.94	1.09	2.13	309095	Nkx6-2	NM_001107558
10728312	6.40	7.34	0.94	1.92	293702	Fkbp2	NM_001134429
10731729	8.40	9.28	0.88	1.84	363248	Rpl37a	NM_001100994
10732439	4.86	6.28	1.41	2.66	685451	Gng13	NM_001135918
10733888	4.80	5.92	1.12	2.17	287336	Olr1448	NM_001000019
10734817	7.35	8.39	1.05	2.07	287417	Rpl26	NM_001105788
10736053	9.03	9.98	0.94	1.92	81770	Rpl37	NM_031106
10736232	8.78	9.71	0.93	1.90	360572	Rpl23a	NM_001108283
10737445	9.98	10.97	0.99	1.98	688136	LOC688136	XM_001081257
10738657	5.82	6.80	0.98	1.98	303577	Acbd4	NM_001012013
10739395	9.56	10.47	0.91	1.88	689284	Rpl38	NM_001077592
10739994	2.84	3.86	1.02	2.03	303735	Rnf213	ENSRNOT00000004904
10741529	4.91	5.93	1.02	2.03	287151	Metrn	NM_001009962
10741756	7.65	9.22	1.57	2.98	25632	Hba-a2	NM_013096
10741778	7.39	8.85	1.45	2.74	25632	Hba-a2	NM_013096
10745595	2.70	3.65	0.95	1.94	303378	Slnf8	NM_001013970
10746952	7.41	8.31	0.90	1.87	57809	Rpl35a	NM_021264
10749058	6.94	7.91	0.96	1.95	294282	Rps18	NM_213557
10749061	4.93	5.87	0.93	1.91	287835	Galk1	NM_001008282
10751767	4.53	5.54	1.02	2.03	27139	Rps26	NM_013224
10752146	6.99	7.86	0.87	1.82	117053	Rps15a	NM_053982
10753005	7.85	8.88	1.03	2.04	24786	Sod1	NM_017050
10756054	5.11	6.41	1.30	2.46	65131	Cldn5	NM_031701
10756455	4.06	4.97	0.91	1.88	140635	Flt3	NM_001100822
10756546	9.69	10.57	0.88	1.84	690441	Atp5j2	ENSRNOT00000033537
10758457	4.37	5.35	0.98	1.97	29531	Hpd	NM_017233
10758777	2.96	4.04	1.08	2.12	192281	Oas1a	NM_138913
10760018	7.59	8.47	0.87	1.83	57809	Rpl35a	NM_021264
10761299	6.29	7.22	0.93	1.90	498173	Auts2	ENSRNOT00000044800
10762537	6.27	7.29	1.02	2.03	83620	Cit	NM_001029911
10766797	3.83	4.74	0.90	1.87	364081	Irf6	NM_001108859
10767371	8.85	9.86	1.01	2.01	27139	Rps26	NM_013224
10770117	4.99	5.99	1.01	2.01	289264	Grem2	NM_001105974
10771040	5.24	6.17	0.93	1.90	689919	LOC689919	ENSRNOT00000061643
10771592	3.88	4.77	0.89	1.85	289501	Ankrd56	ENSRNOT00000002995
10772655	7.26	8.49	1.23	2.35	124323	Rps23	NM_078617
10772901	9.84	10.70	0.86	1.82	29507	Cox7a2	NM_022503
10772982	5.59	6.48	0.88	1.84	58927	Rpl36	NM_022504
10772984	5.59	6.48	0.88	1.84	58927	Rpl36	NM_022504
10774359	9.55	10.49	0.94	1.92	689284	Rpl38	NM_001077592
10774372	7.68	8.72	1.04	2.06	691531	Rps28	NM_001105730
10774894	8.32	9.57	1.25	2.37	124440	Rpl41	NM_139083

10776237	9.05	10.15	1.16	2.15	360572	Rpl23a	NM_001108283
10778058	4.63	5.48	0.85	1.81	681091	Ccdc157	ENSRNOT00000006911
10778918	6.18	7.05	0.87	1.82	29287	Rps19	NM_001037346
10780979	6.51	7.55	1.04	2.06	360572	Rpl23a	NM_001108283
10781984	5.99	6.95	0.97	1.96	306157	Gpc5	NM_001107285
10782041	5.80	7.10	1.31	2.48	306170	RGD1560050	ENSRNOT00000057567
10783353	6.26	7.12	0.86	1.82	29287	Rps19	NM_001037346
10783357	2.60	3.51	0.92	1.89	290050	Olr1641	NM_001000100
10784117	4.22	5.46	1.24	2.36	394266	Gjb2	NM_001004099
10784512	2.85	3.79	0.94	1.92	498534	RGD1565212	NM_001109103
10787085	2.59	3.71	1.12	2.17	25331	Mat1a	NM_012860
10788293	2.23	3.07	0.85	1.80	290757	F11	NM_001047848
10790471	4.76	5.81	1.05	2.07	64347	Sncg	NM_031688
10790525	9.55	10.49	0.94	1.92	689284	Rpl38	NM_001077592
10791497	2.81	3.84	1.03	2.04	29395	Hmgb2	NM_017187
10792163	5.13	5.98	0.85	1.80	116636	Eif4ebp1	NM_053857
10795546	6.25	7.15	0.90	1.86	29287	Rps19	NM_001037346
10796677	9.55	10.41	0.86	1.82	81770	Rpl37	NM_031106
10796991	5.32	6.27	0.95	1.93	290963	Npepo	NM_001012346
10797469	5.11	6.00	0.89	1.85	25461	Hrh2	NM_012965
10798499	7.02	8.00	0.98	1.98	64627	Hist1h4b	NM_022686
10800426	3.36	4.23	0.88	1.84	24856	Ttr	NM_012681
10801821	4.50	5.35	0.85	1.80	116685	Lmnbl	NM_053905
10802128	8.53	9.64	1.11	2.17	124323	Rps23	NM_078617
10803025	4.32	5.58	1.25	2.38	361354	Fbxo15	NM_001108436
10805996	4.79	5.89	1.10	2.14	64364	Pllp	NM_022533
10806210	2.61	3.69	1.07	2.10	29225	Es22	NM_031565
10807044	4.69	5.95	1.26	2.39	688429	Arhgap10	NM_001109501
10807514	6.79	7.90	1.12	2.17	65139	Rps12	NM_031709
10807542	2.52	3.77	1.25	2.38	83502	Cdh1	NM_031334
10808107	3.72	4.66	0.93	1.91	498954	RGD1563834	XR_085682
10809402	7.21	8.71	1.50	2.83	117038	Mt3	NM_053968
10810299	7.25	8.21	0.96	1.94	361385	Ndufb7	NM_001108442
10812416	8.60	9.62	1.02	2.03	124323	Rps23	NM_078617
10812899	9.01	10.01	1.00	1.99	360572	Rpl23a	NM_001108283
10813330	8.98	9.94	0.96	1.94	81770	Rpl37	NM_031106
10813951	5.20	6.16	0.95	1.94	619558	Fam134b	ENSRNOT00000014423
10814540	6.08	7.19	1.11	2.16	310269	RGD1307225	NM_001107663
10816675	2.94	3.80	0.85	1.81	24651	Pklr	NM_012624
10821695	7.01	7.94	0.93	1.91	117053	Rps15a	NM_053982
10822005	4.65	5.54	0.88	1.85	78961	Golph3	NM_023977
10822929	2.77	3.67	0.89	1.86	207120	Nudt6	NM_181363
10824689	5.30	6.19	0.88	1.84	295214	S100a1	NM_001007636
10825236	9.55	10.49	0.94	1.92	689284	Rpl38	NM_001077592
10825238	1.68	2.60	0.92	1.89	365885	Olr390	NM_001000558
10825768	2.68	3.69	1.00	2.00	310771	Chi3l4	XM_001069770
10828433	7.49	8.53	1.04	2.06	294282	Rps18	NM_213557
10828737	7.31	8.18	0.86	1.82	81729	Rpl10a	NM_031065
10830624	6.65	7.54	0.89	1.85	25145	Cd24	NM_012752
10832847	3.57	4.44	0.87	1.83	309902	Tet1	NM_001107643

10833564	4.24	5.36	1.13	2.19	499454	RGD1560095	ENSRNOT00000040584
10834310	7.11	8.00	0.89	1.85	296570	Edf1	NM_001106557
10839400	8.99	9.86	0.86	1.82	28298	Rpl32	NM_013226
10839443	3.88	4.95	1.07	2.11	65192	Slc27a2	NM_031736
10839876	6.77	7.92	1.15	2.23	65139	Rps12	NM_031709
10840783	3.65	4.60	0.95	1.93	311536	RGD1304644	BC099097
10841484	5.64	6.74	1.11	2.15	679572	Romo1	ENSRNOT00000026856
10842436	8.85	9.73	0.89	1.85	689284	Rpl38	NM_001077592
10842667	4.55	5.43	0.88	1.84	64307	Rpl24	NM_022515
10842805	8.48	9.72	1.24	2.37	81775	Rps21	NM_031111
10842971	5.31	6.30	0.99	1.99	362288	Rtel1	ENSRNOT00000055030
10844327	6.85	7.93	1.08	2.12	499780	RGD1561113	ENSRNOT00000034930
10844946	7.17	8.33	1.15	2.23	29286	Rps17	NM_017152
10851386	8.32	9.31	0.99	1.98	81765	Rpl13	NM_031101
10851650	3.10	5.10	2.00	4.01	296369	Tnnc2	NM_001037351
10853871	2.28	3.49	1.21	2.31	24255	Cftr	NM_031506
10854386	2.69	3.57	0.88	1.84	296968	RGD1308226	NM_001106589
10857231	3.78	4.87	1.09	2.12	685999	Uroc1	ENSRNOT00000038251
10861676	9.43	10.31	0.89	1.85	689284	Rpl38	NM_001077592
10863218	4.07	5.08	1.01	2.01	83730	Vamp8	NM_031827
10863664	5.00	5.91	0.91	1.88	312504	RGD1566130	NM_001107871
10863679	5.96	7.29	1.33	2.52	114020	Cml5	NM_080884
10864121	4.38	5.53	1.16	2.23	171571	Grip2	NM_138535
10864425	5.51	6.40	0.89	1.85	297481	Eif4e3	NM_001106612
10864769	9.59	10.54	0.95	1.93	28298	Rpl32	NM_013226
10865630	3.83	4.84	1.00	2.01	362438	Ncapd2	ENSRNOT00000025889
10866505	8.90	9.85	0.95	1.93	690830	LOC690830	XM_001075809
10868673	4.81	5.82	1.01	2.01	680021	Grhpr	NM_001113754
10870043	6.60	7.45	0.85	1.80	294282	Rps18	NM_213557
10871071	2.78	3.71	0.93	1.91	313507	Tal1	NM_001107958
10871169	7.97	8.92	0.95	1.93	366448	Uqcrh	NM_001009480
10872015	3.84	4.99	1.16	2.23	362597	Fam176b	BC167091
10872093	7.21	8.08	0.88	1.84	57809	Rpl35a	NM_021264
10872139	6.41	7.28	0.87	1.83	286923	Dlgap3	NM_173138
10873322	10.01	10.92	0.90	1.87	287005	Camk2n1	NM_173337
10874691	6.17	7.06	0.88	1.85	117053	Rps15a	NM_053982
10875089	4.87	5.73	0.85	1.81	362472	Cspp1	ENSRNOT00000008480
10876652	3.62	4.71	1.09	2.12	362515	Anks6	NM_001015028
10877372	2.63	4.04	1.41	2.65	298107	Mup5	AB039828
10878428	9.57	10.45	0.87	1.83	28298	Rpl32	NM_013226
10878910	10.00	11.11	1.11	2.16	27139	Rps26	NM_013224
10878954	8.19	9.04	0.85	1.80	65136	Rps8	NM_031706
10880710	3.96	5.00	1.04	2.06	313633	Ephb2	NM_001127319
10881596	4.05	4.98	0.93	1.90	313705	Ptchd2	NM_001107992
10882221	5.23	6.10	0.86	1.82	680723	Tmem88b	NM_001109426
10886036	5.18	6.03	0.86	1.81	116674	Jdp2	NM_053894

10891400	5.47	6.44	0.98	1.97	64629	Porfl	ENSRNOT00000005162
10891679	3.84	4.84	1.00	2.00	314386	Gpr68	NM_001108049
10892702	9.55	10.45	0.90	1.87	28298	Rpl32	NM_013226
10892937	5.93	6.90	0.97	1.95	29287	Rps19	NM_001037346
10894055	4.90	5.87	0.97	1.96	314612	Shc2	NM_001108065
10894681	3.46	4.72	1.25	2.39	24616	Pah	NM_012619
10894810	6.69	7.96	1.27	2.41	314721	Anks1b	ENSRNOT00000064242
10894812	9.54	10.68	1.13	2.19	314721	Anks1b	ENSRNOT00000064242
10894814	8.48	9.80	1.32	2.49	314721	Anks1b	ENSRNOT00000064242
10897450	4.97	5.85	0.88	1.84	300317	Kctd17	NM_001134529
10899465	4.89	6.07	1.18	2.26	25641	Igfbp6	NM_013104
10899824	8.93	9.93	1.00	2.00	124440	Rpl41	NM_139083
10899868	9.28	10.32	1.04	2.05	27139	Rps26	NM_013224
10900533	7.47	8.59	1.12	2.17	29285	Rps15	NM_017151
10900618	7.94	8.86	0.92	1.89	29328	Gpx4	NM_017165
10901178	8.62	9.60	0.98	1.97	691531	Rps28	NM_001105730
10902047	2.67	4.50	1.83	3.56	299757	Nts	NM_001102381
10903583	6.68	7.68	1.01	2.01	81763	Rpl5	NM_031099
10904227	5.88	6.86	0.98	1.98	29287	Rps19	NM_001037346
10905277	6.56	7.47	0.91	1.88	25269	Pvalb	NM_022499
10905558	6.83	7.82	0.99	1.98	287417	Rpl26	NM_001105788
10907297	3.76	4.65	0.89	1.85	300236	Smagp	NM_182817
10907324	4.08	4.95	0.87	1.83	683264	Galnt6	NM_001172063
10908347	4.44	5.68	1.24	2.36	25638	Pde4a	NM_013101
10909002	3.39	4.80	1.41	2.67	619560	Rup2	NM_001034950
10909009	2.12	3.94	1.83	3.55	619560	Rup2	AF368860
10909758	8.33	9.51	1.19	2.28	81775	Rps21	NM_031111
10909892	6.43	7.39	0.96	1.95	25420	Cryab	NM_012935
10910458	9.55	10.49	0.94	1.92	689284	Rpl38	NM_001077592
10914308	9.02	10.12	1.10	2.14	29236	Rpsa	NM_017138
10915345	5.30	6.22	0.93	1.90	313783	Olfm2	NM_001015017
10918055	3.75	4.67	0.91	1.88	315741	Paqr5	NM_001014092
10918776	7.03	7.90	0.87	1.82	681849	LOC681849	ENSRNOT00000067627
10920967	2.90	3.76	0.86	1.81	363165	Csrnp1	NM_001108786
10921036	3.59	5.10	1.50	2.83	363168	Lyzl4	ENSRNOT00000026173
10921274	7.90	8.82	0.92	1.89	316164	Satb1	NM_001012129
10922268	4.54	5.66	1.12	2.18	170843	Khdrbs2	NM_133318
10924217	9.88	10.80	0.91	1.89	363248	Rpl37a	NM_001108801
10926386	4.45	5.39	0.94	1.93	681367	LOC681367	XM_001061427
10926683	5.93	6.98	1.05	2.07	301265	Pla2g7	NM_001009353
10927281	6.87	7.73	0.86	1.81	29284	Rps14	NM_022672
10927372	3.86	4.98	1.12	2.17	367251	Ankrd39	NM_001135014
10930091	6.64	7.55	0.91	1.88	316643	Chchd2	NM_001015019
10930762	1.98	3.22	1.24	2.36	171521	Cyp2c13	NM_138514
10933957	9.74	10.61	0.87	1.82	28298	Rpl32	NM_013226
10934500	9.55	10.53	0.99	1.98	27139	Rps26	NM_013224
10937356	9.22	10.26	1.05	2.07	27139	Rps26	NM_013224

10938962	8.59	9.64	1.04	2.06	81775	Rps21	NM_031111
10940358	3.97	5.10	1.13	2.19	293862	Fam50a	NM_001170573

Supplementary table (ST-2B): List of genes downregulated in brain

Probe Set ID	Control Brain	Sleep Deprived Brain	Log Fold Change	Fold Change	Entrez ID	Gene Symbol	Accession
10702201	5.59	4.73	-0.86	0.55	361458	Akap7	NM_001001801
10702626	6.12	4.91	-1.21	0.43	361472	Mthfd11	NM_001108462
10702991	4.68	3.67	-1.02	0.49	25153	Mas1	NM_012757
10705825	5.51	4.65	-0.86	0.55	246264	Zfp382	NM_144749
10708616	7.21	6.08	-1.13	0.46	293112	Crebzf	NM_001106279
10709020	9.84	8.79	-1.05	0.48	685076	Pgm21l	NM_001109454
10709844	5.46	4.42	-1.04	0.49	308937	Wee1	NM_001012742
10715149	4.35	3.30	-1.05	0.48	294072	Tmem20	ENSRNOT00000044895
10715519	5.67	4.80	-0.87	0.55	293939	Erlin1	NM_001106353
10716026	6.12	5.05	-1.07	0.48	294043	Sorcs3	NM_001106367
10717053	3.43	2.38	-1.05	0.48	308717	Slc35d3	NM_001107522
10717069	6.29	5.25	-1.04	0.49	140929	Pde7b	NM_080894
10717325	4.44	3.51	-0.94	0.52	308028	Slc2a12	NM_001107451
10719134	4.63	3.58	-1.05	0.48	499083	Zscan18	ENSRNOT00000036880
10720126	3.49	2.62	-0.87	0.55	687333	LOC687333	ENSRNOT00000025586
10722218	4.11	3.23	-0.88	0.54	404658	Mrgprb4	ENSRNOT00000045792
10722532	5.36	4.09	-1.27	0.41	25302	Chrna7	NM_012832
10723351	4.35	3.48	-0.87	0.55	116996	Il16	NM_001105749
10724785	6.69	5.64	-1.05	0.48	361625	Nrip3	NM_001108498
10725778	5.06	4.18	-0.88	0.54	113900	Nupr1	NM_053611
10726999	4.57	3.28	-1.29	0.41	24483	Igf2	NM_031511
10727717	6.79	5.68	-1.11	0.46	266734	Npas4	NM_153626
10729314	9.46	8.61	-0.85	0.55	83585	Gda	NM_031776
10730206	7.14	6.28	-0.85	0.55	65047	Slit1	NM_022953
10734045	6.24	5.08	-1.16	0.45	287371	Lrrc48	NM_001013857
10734422	5.23	4.36	-0.88	0.54	117251	Dnah9	ENSRNOT00000005583
10739351	4.86	2.66	-2.20	0.22	29719	Kcnj16	NM_053314
10739984	4.91	4.02	-0.89	0.54	303735	Rnf213	ENSRNOT00000004904
10741907	6.97	6.01	-0.97	0.51	25498	Npm1	NM_012992
10743715	4.80	3.18	-1.62	0.32	497926	Shisa6	ENSRNOT00000057509
10744081	5.82	4.33	-1.49	0.36	360546	Efnb3	NM_001100980
10748498	5.07	3.95	-1.12	0.46	29481	Rgs9	NM_019224

10750551	7.40	6.53	-0.88	0.54	29202	Epha6	ENSRNOT00000 047310
10750928	7.54	6.59	-0.95	0.52	303963	Dzip3	ENSRNOT00000 002678
10751237	4.51	3.29	-1.22	0.43	498085	RGD15 63835	ENSRNOT00000 042756
10751700	7.89	7.00	-0.89	0.54	192361	Ppp1r2	NM_138823
10752576	5.49	4.49	-0.99	0.50	287925	Pkp2	NM_001100499
10752738	7.18	6.32	-0.87	0.55	29734	Hspa13	NM_019271
10753269	6.49	5.45	-1.03	0.49	25743	Kcnj6	NM_013192
10758020	7.30	6.33	-0.98	0.51	288620	Cct6a	NM_001033684
10762426	5.93	4.74	-1.20	0.44	117271	Hrk	NM_057130
10763421	3.92	2.91	-1.00	0.50	297865	Dsel	ENSRNOT00000 043890
10763933	7.54	6.32	-1.22	0.43	289020	Lrn2	NM_001177368
10764139	6.93	6.05	-0.88	0.54	304807	Rabif	NM_001007678
10764460	6.98	5.95	-1.04	0.49	304827	Kcnt2	NM_198762
10764551	5.85	4.97	-0.87	0.55	29527	Ptgs2	NM_017232
10764837	7.03	6.07	-0.97	0.51	304881	Tor1aip 2	NM_001165896
10765044	4.73	3.84	-0.88	0.54	289150	Cenpl	NM_001033061
10765413	5.21	4.24	-0.97	0.51	83574	Rxrg	NM_031765
10766953	5.16	4.03	-1.13	0.46	24224	Bcl2	NM_016993
10768269	6.55	5.35	-1.20	0.44	155012	Cfh	NM_130409
10768357	4.45	2.88	-1.57	0.34	289076	Rgs18	NM_001047084
10769177	5.66	4.34	-1.31	0.40	684623	LOC684 623	ENSRNOT00000 003659
10770161	5.12	4.08	-1.03	0.49	289270	Pld5	ENSRNOT00000 005332
10772534	8.47	7.28	-1.20	0.44	289606	Gabra2	NM_001135779
10774267	7.13	5.93	-1.20	0.44	689106	Vstm2a	ENSRNOT00000 006897
10774432	4.50	3.42	-1.09	0.47	690096	LOC690 096	ENSRNOT00000 012255
10775283	4.45	3.15	-1.31	0.40	360910	Abcg3l2	NM_001014133
10776437	5.81	4.92	-0.89	0.54	64030	Kit	NM_022264
10777011	6.24	5.09	-1.15	0.45	289657	Tbc1d19	NM_001106008
10777137	5.84	4.39	-1.45	0.37	360272	Slit2	NM_022632
10778179	5.00	3.71	-1.29	0.41	114107	Kremen 1	NM_053649
10781467	6.53	4.79	-1.73	0.30	29595	Htr2a	NM_017254
10781496	6.25	5.32	-0.94	0.52	306071	Lcp1	NM_001012044
10781745	6.67	5.81	-0.86	0.55	306055	Pcdh17	NM_001107279
10781787	9.58	8.69	-0.88	0.54	29150	Matr3	NM_019149
10782187	4.94	3.22	-1.72	0.30	498564	Itgbl1	NM_001017505
10782590	8.34	7.36	-0.98	0.51	66030	Synpr	NM_023974
10785724	8.09	7.04	-1.05	0.48	50672	Ednrb	NM_017333
10788542	3.41	2.12	-1.29	0.41	306511	RGD15 61928	ENSRNOT00000 042609

10788889	4.27	3.20	-1.07	0.48	306564	Htra4	NM_001107321
10791000	5.71	4.14	-1.56	0.34	290655	Crklf1	NM_001106074
10791250	5.42	3.71	-1.71	0.31	24539	Lpl	NM_012598
10791950	6.61	5.76	-0.85	0.55	364601	Efha2	ENSRNOT00000017025
10793429	4.53	3.42	-1.11	0.46	290952	RGD1563615	ENSRNOT00000046525
10793433	3.75	2.74	-1.01	0.50	290952	RGD1563615	ENSRNOT00000046525
10793446	4.99	3.56	-1.44	0.37	290952	RGD1563615	ENSRNOT00000046525
10794195	5.51	3.70	-1.81	0.28	24316	Drd1a	NM_012546
10796507	5.20	4.10	-1.10	0.47	291328	Slc39a12	NM_001106124
10796751	7.76	6.39	-1.37	0.39	24380	Gad2	NM_012563
10797648	6.68	5.41	-1.27	0.41	291015	Ogn	NM_001106103
10797657	3.29	2.36	-0.93	0.52	83717	Omd	NM_031817
10798119	4.41	3.26	-1.15	0.45	291084	Nqo2	NM_001004214
10798390	6.64	5.69	-0.94	0.52	306934	Fam65b	NM_001014009
10798479	3.67	2.59	-1.08	0.47	306966	Znf184	NM_001100573
10798856	6.86	5.93	-0.93	0.52	361258	Cul2	NM_001108417
10799733	7.92	6.65	-1.27	0.41	680404	C1ql3	NM_001109403
10800140	7.94	5.06	-2.88	0.14	291794	Snrpd1	NM_001106163
10801174	4.59	3.57	-1.02	0.49	291654	Pcdhb5	NM_001114602
10802391	5.47	3.56	-1.90	0.27	24611	Gnal	ENSRNOT00000025172
10803037	8.88	8.01	-0.87	0.55	307206	Neto1	NM_001107371
10803394	8.19	7.23	-0.96	0.51	65196	B4galt6	NM_031740
10803474	6.68	5.83	-0.85	0.55	307553	Nol4	NM_001107401
10804714	5.87	4.63	-1.24	0.42	307396	Pcyox11	NM_001134542
10805591	3.35	2.35	-1.00	0.50	498895	RGD1559751	ENSRNOT00000058177
10806492	6.78	5.85	-0.93	0.53	25479	Vps35	ENSRNOT00000024020
10806864	7.13	6.15	-0.98	0.51	364981	Scoc	NM_001013235
10807632	7.40	6.41	-0.99	0.50	80773	Cyb5b	NM_030586
10808603	6.78	5.78	-1.00	0.50	361433	Cpne7	NM_001108454
10810736	5.74	4.63	-1.11	0.46	24530	Lcat	NM_017024
10810964	4.23	3.14	-1.10	0.47	117059	Calb2	NM_053988
10812879	6.16	4.36	-1.80	0.29	24473	Htr1a	NM_012585
10813249	7.21	5.41	-1.81	0.29	310358	RGD1308448	NM_001107671
10813563	4.73	3.80	-0.93	0.52	294789	Ranbp31	ENSRNOT00000050942
10813817	4.59	3.27	-1.32	0.40	29163	Cdh9	NM_001168630
10813872	6.57	5.69	-0.88	0.54	310174	Cdh18	NM_001107656
10814396	5.37	3.50	-1.87	0.27	365748	Bhlhe22	NM_001108940
10815655	4.41	2.97	-1.44	0.37	66024	Npy2r	NM_023968
10815679	3.90	3.01	-0.88	0.54	24590	Mme	NM_012608

10817419	5.45	4.46	-0.98	0.51	29175	Ctsk	NM_031560
10820300	4.77	3.74	-1.03	0.49	309995	Xrcc4	NM_001006999
10820586	5.24	4.29	-0.95	0.52	25439	F2r	NM_012950
10820613	5.31	3.72	-1.59	0.33	29643	Sv2c	NM_031593
10820693	8.21	7.30	-0.90	0.53	294673	Hexb	NM_001011946
10822107	4.90	3.99	-0.91	0.53	310190	Fam105a	BC107649
10822386	7.64	6.64	-1.00	0.50	114906	Pkia	NM_053772
10823303	9.93	8.96	-0.97	0.51	81531	Pfn2	NM_030873
10823412	3.45	2.46	-0.99	0.50	192251	Gpr149	NM_138891
10823937	4.41	2.97	-1.44	0.37	66024	Npy2r	NM_023968
10824041	6.17	5.32	-0.85	0.55	60382	Arfp1	NM_021763
10824422	5.29	4.42	-0.87	0.55	310641	Trim46	NM_001107691
10825495	5.36	4.46	-0.89	0.54	310732	Slc22a15	NM_001107707
10825915	3.67	2.74	-0.93	0.52	24424	Gstm2	NM_177426
10826148	5.97	4.92	-1.05	0.48	295382	Ntng1	NM_001106465
10826261	7.18	5.74	-1.44	0.37	64443	Gpr88	NM_031696
10826392	8.58	7.35	-1.24	0.42	295401	Lppr4	NM_001001508
10827231	5.97	4.85	-1.12	0.46	83476	Cyr61	NM_031327
10828344	5.32	3.47	-1.85	0.28	294269	RT1-Da	NM_001008847
10832577	6.25	4.52	-1.73	0.30	25369	Adora2a	NM_053294
10836638	7.55	6.68	-0.87	0.55	311114	Klhl23	NM_001134504
10838039	7.57	6.37	-1.20	0.44	295934	Chst1	NM_001011955
10838255	3.59	2.70	-0.89	0.54	691083	LOC691083	NM_001144862
10838326	6.20	5.21	-0.99	0.50	25469	Kcna4	NM_012971
10839726	5.00	4.03	-0.97	0.51	64300	Mthfd1	NM_022508
10842677	4.91	4.01	-0.91	0.53	100328908	RGD1565819	NM_001171096
10844082	5.63	4.62	-1.01	0.50	311836	Ntng2	NM_001107825
10844275	4.36	3.20	-1.16	0.45	311861	Fibcd1	NM_001107829
10844801	6.59	5.72	-0.86	0.55	366029	Zbtb6	NM_001108953
10844949	5.19	4.15	-1.04	0.49	311926	Lrp1b	NM_001107843
10844960	6.15	5.29	-0.87	0.55	311926	Lrp1b	NM_001107843
10844962	5.43	4.30	-1.13	0.46	311926	Lrp1b	NM_001107843
10844968	4.90	3.89	-1.01	0.50	311926	Lrp1b	NM_001107843
10845416	5.96	4.84	-1.12	0.46	245921	Acvrlc	NM_139090
10845809	5.94	5.07	-0.87	0.55	497770	Scn3a	NM_013119
10846685	5.19	4.26	-0.94	0.52	29458	Neurod1	NM_019218
10847758	6.20	5.22	-0.99	0.51	366140	Fjx1	NM_001108955
10849857	4.89	3.79	-1.10	0.47	29190	Pdyn	NM_019374
10850543	8.11	7.00	-1.11	0.46	499903	Napb	ENSRNOT00000006329
10850929	7.15	6.27	-0.88	0.54	363469	Sms	NM_001033899
10852953	5.77	4.70	-1.06	0.48	499975	Fam126a	ENSRNOT00000014023
10853683	3.73	2.81	-0.92	0.53	24806	Tac1	NM_012666
10853842	8.47	7.59	-0.88	0.54	493810	Capza2	NM_001009180

10855549	6.05	3.66	-2.39	0.19	297096	Snx10	NM_001013085
10856472	8.08	7.16	-0.92	0.53	679668	LRRTM1	NM_001109374
10858165	7.87	6.97	-0.89	0.54	24772	Cxcl12	NM_001033883
10858707	3.03	1.99	-1.04	0.49	297594	Cdca3	NM_001007648
10859342	5.85	4.42	-1.42	0.37	50677	Ptpro	NM_017336
10860481	6.06	5.20	-0.86	0.55	29751	Sema3a	NM_017310
10860535	7.03	6.18	-0.85	0.56	688590	Rundc3b	NM_001047116
10860623	5.42	4.54	-0.89	0.54	85261	Mterf	NM_053499
10861038	6.66	5.72	-0.94	0.52	500032	Thsd7a	ENSRNOT00000052063
10861066	7.76	6.87	-0.88	0.54	312132	Tmem106b	NM_001004267
10862527	5.66	4.79	-0.87	0.55	155183	Skap2	NM_130413
10863615	7.24	6.38	-0.85	0.55	500233	Exoc6b	NM_001109246
10863688	3.64	2.68	-0.96	0.51	500237	Cml2	NM_001173449
10866576	9.42	8.49	-0.93	0.52	497798	RGD1561357	ENSRNOT00000010623
10866850	7.44	6.51	-0.93	0.53	24525	Kras	NM_031515
10867060	4.81	3.91	-0.90	0.54	500377	Tuba8	NM_001024339
10867497	7.68	6.66	-1.01	0.50	500400	Fam110b	BC091289
10867731	6.97	5.82	-1.15	0.45	83839	Calb1	NM_031984
10868186	7.18	6.16	-1.01	0.50	25248	Cnr1	NM_012784
10868289	8.60	7.66	-0.94	0.52	65028	Dnaja1	NM_022934
10869010	6.40	5.11	-1.29	0.41	313219	Zfp189	NM_001107930
10869094	5.75	4.90	-0.86	0.55	313211	Nipsnap3b	NM_001009422
10869253	7.81	6.88	-0.93	0.52	83626	Ugcg	NM_031795
10870733	5.04	4.15	-0.89	0.54	298385	Magoh	NM_001100536
10874193	7.78	6.83	-0.95	0.52	313729	Errfi1	NM_001014071
10875256	7.13	6.01	-1.12	0.46	312946	Tmem68	NM_001107903
10875300	6.07	4.18	-1.89	0.27	29237	Penk	NM_017139
10875532	6.43	5.55	-0.87	0.55	54705	Pdp1	NM_019372
10883801	7.18	5.38	-1.80	0.29	50871	Hpcal1	NM_017356
10884215	3.32	2.38	-0.94	0.52	85489	Twist1	NM_053530
10884309	8.50	7.34	-1.16	0.45	54248	Dgkb	NM_019304
10884811	6.93	5.74	-1.19	0.44	314164	Lrfr5	NM_001108024
10886031	5.13	4.18	-0.96	0.52	314322	Fos	NM_022197
10889575	6.65	5.37	-1.28	0.41	298944	Gpr22	NM_001106722
10890229	5.12	4.22	-0.90	0.54	85261	Mterf	NM_053499
10891402	4.94	3.37	-1.57	0.34	65162	Dio2	NM_031720
10893661	8.32	7.00	-1.32	0.40	58979	Gng7	NM_024138
10895152	6.37	5.29	-1.08	0.47	60427	Kitlg	NM_021843
10895241	3.96	2.79	-1.17	0.45	299756	Mgat4c	NM_001135814
10895499	4.22	2.85	-1.37	0.39	171048	Tspan8	NM_133526
10895508	5.30	4.14	-1.16	0.45	94202	Ptpr	NM_053594

10896541	9.05	8.18	-0.87	0.55	81526	Nov	NM_030868
10899552	5.39	4.30	-1.09	0.47	24790	Sp1	NM_012655
10899676	9.08	8.20	-0.88	0.54	29691	Pde1b	NM_022710
10901409	6.98	6.13	-0.85	0.55	314694	Chst11	NM_001108079
10902080	4.56	3.70	-0.86	0.55	299762	Tmtc2	XM_001080732
10902843	6.50	5.65	-0.85	0.56	171329	Usp15	NM_145184
10903501	6.45	5.15	-1.30	0.41	314941	Lrp12	NM_001134883
10903651	4.58	2.92	-1.66	0.32	314942	LOC314942	ENSRNOT00000057108
10903653	4.22	2.93	-1.29	0.41	314942	LOC314942	ENSRNOT00000057108
10908990	4.79	3.89	-0.90	0.54	315554	Pus3	NM_001108134
10909328	8.21	7.06	-1.15	0.45	245956	Scn3b	NM_139097
10909849	4.42	3.21	-1.21	0.43	24318	Drd2	NM_012547
10911380	4.44	3.55	-0.89	0.54	116676	Aldh1a2	NM_053896
10912054	4.04	2.94	-1.09	0.47	363111	Ripply2	ENSRNOT00000013285
10912614	3.65	2.32	-1.33	0.40	24546	Slco2a1	NM_022667
10912718	7.27	5.42	-1.85	0.28	367160	Cpne4	NM_001109003
10914935	7.80	6.49	-1.31	0.40	363015	RGD1310444	XM_002729871
10916379	4.01	2.91	-1.10	0.47	300608	RGD1311744	ENSRNOT00000066669
10916697	5.45	4.25	-1.20	0.44	315599	Nlr1	NM_001025010
10918955	4.55	3.60	-0.96	0.51	246776	Filip1	NM_145682
10918979	6.52	5.08	-1.44	0.37	25075	Htr1b	NM_022225
10919694	5.49	4.62	-0.87	0.55	300967	Tmem108	ENSRNOT00000014519
10921208	3.08	2.07	-1.01	0.50	85426	Slc5a7	NM_053521
10922895	4.52	2.96	-1.56	0.34	24785	Slc9a4	NM_173098
10922909	4.31	3.35	-0.96	0.51	24783	Slc9a2	NM_012653
10923338	5.36	4.05	-1.31	0.40	301416	Coq10b	NM_001009671
10923782	9.44	8.34	-1.10	0.47	286928	Abi2	NM_173143
10923866	6.30	5.35	-0.95	0.52	501153	Zdbf2	ENSRNOT00000016038
10926740	6.98	5.83	-1.15	0.45	316256	Tnfrsf21	NM_001108207
10927903	6.89	5.83	-1.07	0.48	363228	Tmeff2	NM_001108795
10928056	8.26	7.29	-0.97	0.51	316400	Pgap1	NM_201990
10928522	7.81	6.92	-0.89	0.54	316444	Mdh1b	ENSRNOT00000017207
10928837	6.77	5.43	-1.34	0.40	25285	Igfbp5	NM_012817
10929263	7.98	6.41	-1.57	0.34	24765	Scg2	NM_022669
10929482	8.47	6.87	-1.60	0.33	316573	Dner	BC086329
10929536	4.82	3.62	-1.21	0.43	316578	Slc16a14	NM_001108229
10931669	4.80	3.93	-0.87	0.55	288979	C1ql2	NM_001105949
10932066	7.51	6.54	-0.97	0.51	313445	Klhl13	ENSRNOT00000067114
10932646	7.61	6.75	-0.86	0.55	360785	Ap1s1	BC168682

10932795	7.72	6.72	-1.00	0.50	113976	Acs14	NM_053623
10933393	4.16	2.48	-1.68	0.31	24397	Gla2	NM_012568
10934270	4.56	3.59	-0.97	0.51	302421	Gdpd2	NM_001106944
10935038	4.09	3.17	-0.92	0.53	501624	Bex4	NM_001037554
10935418	3.16	1.96	-1.20	0.44	317589	Mst4	ENSRNOT00000010596
10935882	3.50	2.44	-1.07	0.48	293849	Zfp275	NM_001106343
10936360	6.95	5.55	-1.40	0.38	313436	Zcchc12	NM_001014065
10936742	5.07	4.21	-0.86	0.55	554353	Gpr34	NM_001024925
10937302	6.64	5.29	-1.35	0.39	25187	Htr2c	NM_012765
10937362	7.96	7.06	-0.91	0.53	29433	Pak3	NM_019210
10937479	7.81	6.90	-0.91	0.53	117043	RragB	NM_053972
10937660	6.97	6.03	-0.93	0.52	501550	Trappc2	NM_001024965
10937769	5.22	4.15	-1.07	0.48	302671	Ap1s2	NM_001127531
10938897	7.98	7.02	-0.96	0.51	246284	Atrx	NM_001105757
10939002	6.31	5.02	-1.29	0.41	363487	RGD1566265	NM_001134589
10939226	6.47	5.11	-1.35	0.39	317183	Pcdh19	NM_001169129
10939460	6.24	5.37	-0.88	0.54	367915	Rab9b	NM_001109018
10939764	4.76	3.07	-1.69	0.31	25236	Gpc3	NM_012774
10939837	7.92	6.97	-0.95	0.52	302864	Mmgt1	NM_001106970

Supplementary table (ST-2C): List of genes upregulated in liver

Probe Set ID	Control Liver	Sleep Deprived Liver	Log Fold Change	Fold Change	Gene Symbol	Accession
10704284	9.50	10.74	1.24	2.36	Slc27a5	NM_024143
10707151	5.06	6.32	1.25	2.39	Tmem86a	NM_001135016
10708665	4.24	5.34	1.10	2.15	Rab30	NM_001015012
10712657	8.66	9.95	1.28	2.44	Cpt1a	NM_031559
10713974	4.99	5.86	0.88	1.83	Slc15a3	NM_139341
10714323	5.37	7.66	2.29	4.91	Aldh1a1	NM_022407
10714413	6.98	7.94	0.96	1.94	Klf9	NM_057211
10715364	9.40	10.92	1.51	2.86	Got1	NM_012571
10715416	4.57	6.75	2.18	4.54	Loxl4	NM_001107592
10717459	4.93	6.34	1.40	2.65	Tppp	NM_001108461

10723728	6.21	7.14	0.93	1.91	Aqp11	NM_173105
10726604	4.07	5.01	0.94	1.91	RGD1311186	NM_001106310
10726824	8.05	9.02	0.98	1.97	Slc25a22	NM_001014027
10728466	5.16	6.89	1.73	3.32	UST4r	NM_134379
10730031	3.13	5.51	2.39	5.23	Cyp2c13	ENSRNOT00000015801
10730599	4.87	7.61	2.74	6.70	Cyp17a1	NM_012753
10732068	7.27	8.13	0.86	1.82	Dci	NM_017306
10736863	3.74	4.62	0.88	1.84	Ccl4	NM_053858
10738399	8.91	10.70	1.79	3.45	G6pc	NM_013098
10738477	3.88	5.02	1.14	2.21	Arl4d	NM_001107052
10738576	7.84	8.76	0.92	1.90	Grn	NM_017113
10742645	4.90	6.28	1.37	2.59	Slc22a5	NM_019269
10744233	2.97	4.05	1.08	2.12	Tmem102	ENSRNOT00000020578
10744245	2.86	3.80	0.95	1.93	Nlgn2	NM_053992
10744460	4.84	5.85	1.02	2.02	Cxcl16	NM_001017478
10745345	3.42	4.50	1.08	2.12	Evi2a	ENSRNOT00000039261
10746139	7.90	8.90	1.00	2.00	Scpep1	NM_133383
10747262	3.15	4.12	0.97	1.96	Krt19	NM_199498
10749612	9.75	10.69	0.94	1.92	Actg1	NM_001127449
10750524	6.77	8.04	1.27	2.41	Mx2	NM_134350
10751295	4.15	5.52	1.38	2.60	Pla1a	NM_138882
10751352	8.17	9.78	1.61	3.05	Krt8	NM_199370
10751896	3.49	5.92	2.43	5.39	Cldn1	NM_031699

10754058	3.31	4.21	0.90	1.87	Ccdc52	NM_001008285
10755088	3.49	4.39	0.90	1.86	Rtp4	NM_001108321
10757082	4.05	4.99	0.94	1.91	Zfand2a	NM_001008363
10757632	4.16	5.44	1.28	2.43	Ccl24	NM_001013045
10757962	9.23	10.74	1.52	2.86	Asl	NM_021577
10759018	6.45	7.39	0.94	1.92	Mlec	NM_001013983
10762324	7.63	9.17	1.54	2.90	Sds	NM_053962
10762740	4.06	5.27	1.21	2.31	Oasl	NM_001009681
10765090	10.14	11.25	1.12	2.17	Actg1	NM_001127449
10766923	5.66	7.02	1.36	2.57	Rnf152	NM_001106305
10767175	7.69	9.22	1.53	2.89	Insig2	NM_178091
10767290	6.12	7.58	1.46	2.75	Acmsd	NM_134372
10768998	3.90	4.80	0.90	1.87	Tor3a	NM_001009683
10769361	8.58	9.51	0.93	1.90	Fmo1	NM_012792
10769476	6.52	8.11	1.59	3.01	Atp1b1	NM_013113
10770710	3.53	4.74	1.21	2.31	Atf3	NM_012912
10771655	3.40	4.56	1.15	2.23	Cxcl10	NM_139089
10771660	4.50	6.57	2.06	4.17	Cxcl9	NM_145672
10771936	7.90	8.88	0.97	1.96	Ugt2a3	NM_001135869
10771998	6.48	7.47	0.99	1.99	RGD1559459	ENSRNOT00000065079
10772986	4.27	5.36	1.09	2.12	Ppargc1a	NM_031347
10773221	7.64	8.70	1.05	2.08	Slc2a9	ENSRNOT00000042200
10773773	8.07	8.92	0.86	1.81	Sec14l4	NM_001109090

10776954	5.68	6.55	0.86	1.82	Rell1	NM_001113776
10777918	7.04	7.88	0.85	1.80	Drg1	NM_001009685
10778620	4.72	6.18	1.46	2.75	Slc1a4	NM_198763
10779673	4.79	5.68	0.89	1.85	Lgals3	NM_031832
10781321	3.79	5.63	1.84	3.58	Tnfrsf10b	NM_001108873
10789857	5.38	6.28	0.90	1.87	Il17rb	NM_001107290
10790670	4.61	5.71	1.10	2.14	Klf2	NM_001007684
10791233	7.28	8.30	1.02	2.02	Atp6v1b2	NM_057213
10791552	3.60	5.41	1.82	3.52	Gpm6a	NM_178105
10794829	4.47	5.39	0.92	1.90	Tubb2a	NM_001109119
10796016	5.55	6.43	0.87	1.83	RGD1564865	NM_001164396
10796018	6.82	8.02	1.21	2.31	RGD1564865	NM_001164396
10796440	5.01	6.00	0.99	1.99	Pter	NM_022224
10796445	6.41	7.40	0.98	1.98	Vim	NM_031140
10797811	3.18	4.07	0.89	1.85	Cd83	NM_001108410
10800991	6.04	7.19	1.15	2.22	Pura	ENSRNOT00000025756
10802013	7.54	8.94	1.40	2.63	Cd74	NM_013069
10803653	9.91	10.90	0.99	1.99	Actg1	NM_001127449
10805731	4.58	5.43	0.86	1.81	Tk2	NM_001106166
10807464	5.89	6.92	1.02	2.03	Pla2g15	NM_001004277
10813214	9.80	10.77	0.97	1.96	Hmgcs1	NM_017268
10813628	2.51	3.97	1.47	2.76	Prlr	NM_012630
10813992	7.13	8.16	1.04	2.05	LOC683212	XR_086164

10815281	5.43	6.49	1.05	2.08	Ccrn4l	NM_138526
10815503	10.49	11.53	1.04	2.05	Tm4sf4	NM_053785
10817686	7.70	8.81	1.11	2.16	Fmo5	NM_144739
10818090	7.53	8.51	0.98	1.97	Slc16a1	NM_012716
10819024	5.60	6.51	0.90	1.87	Pla2g12a	NM_001108565
10819402	2.52	4.70	2.18	4.54	Adh6	NM_001012084
10819523	4.21	5.18	0.97	1.96	Gbp2	NM_133624
10819644	7.37	8.24	0.87	1.83	Ddah1	NM_022297
10819905	5.36	6.45	1.08	2.12	Ptger3	NM_012704
10820494	11.83	12.95	1.12	2.17	Bhmt	NM_030850
10821851	2.77	4.11	1.34	2.53	Il7r	NM_001106418
10825244	5.76	6.88	1.13	2.18	Chd1l	NM_001107704
10826691	6.12	7.06	0.94	1.92	Ap1ar	ENSRNOT00000055607
10827517	9.91	11.24	1.33	2.51	Cth	NM_017074
10828154	5.24	6.18	0.94	1.92	Hspa1b	NM_212504
10828344	7.29	8.92	1.63	3.10	RT1-Da	NM_001008847
10828351	4.88	6.01	1.14	2.20	RT1-Ba	NM_001008831
10829244	4.28	5.26	0.98	1.97	Pwp2	NM_001168653
10829346	3.57	4.46	0.89	1.85	Lrrc3	NM_145679
10830630	5.37	6.62	1.25	2.38	Rtn4ip1	NM_001107644
10831308	2.88	3.92	1.03	2.05	Slc44a4	NM_212541
10831567	5.17	6.46	1.29	2.45	RT1-Bb	NM_001004084
10831747	5.06	6.22	1.15	2.22	Wdr46	NM_212491

10832563	6.63	7.51	0.88	1.84	Gstt3	NM_001137643
10833617	6.33	7.55	1.22	2.33	RGD1561777	ENSRNOT00000035047
10833659	6.48	7.40	0.93	1.90	Amd1	NM_031011
10835703	3.86	5.00	1.14	2.20	RGD1564854	NM_001109341
10836019	9.10	10.25	1.15	2.21	Kynu	NM_053902
10836277	4.67	5.57	0.90	1.87	Gpd2	NM_012736
10837537	9.82	10.79	0.97	1.95	Actg1	NM_001127449
10838729	3.75	4.70	0.95	1.94	Rpusd2	NM_001135845
10839771	6.92	7.80	0.88	1.84	Slc20a1	NM_031148
10840085	6.82	7.71	0.90	1.86	Cds2	NM_053643
10841240	3.71	5.20	1.49	2.82	LOC690521	ENSRNOT00000042148
10844183	4.61	6.41	1.79	3.47	Crat	NM_001004085
10844801	5.23	6.17	0.94	1.92	Zbtb6	NM_001108953
10846604	4.28	5.20	0.91	1.88	LOC311134	ENSRNOT00000037015
10846781	3.94	4.86	0.93	1.90	Tfpi	NM_001177321
10849275	7.28	9.30	2.02	4.05	Slc28a2	NM_031664
10849279	6.12	7.06	0.94	1.92	Slc28a2	NM_031664
10850631	7.22	8.24	1.02	2.03	RGD1308874	NM_001034003
10850775	4.57	5.43	0.87	1.82	Trib3	NM_144755
10853229	4.81	5.94	1.13	2.18	Gnail	NM_013145
10853300	5.46	6.66	1.21	2.31	Abcb1a	NM_133401
10853816	4.05	4.98	0.92	1.89	Cav1	NM_031556
10854548	11.18	12.13	0.95	1.93	Akr1d1	NM_138884

10855449	5.42	6.88	1.46	2.75	Gpnmb	NM_133298
10857314	4.72	5.89	1.17	2.24	Slc6a6	NM_017206
10858374	9.06	9.97	0.91	1.88	Slc6a13	NM_133623
10860076	4.59	5.44	0.86	1.81	Nos3	NM_021838
10860548	5.73	6.91	1.18	2.26	Crot	NM_031987
10861066	7.30	8.23	0.93	1.90	Tmem106b	NM_001004267
10861986	9.65	10.58	0.93	1.90	Insig1	NM_022392
10867329	2.75	4.05	1.30	2.46	Mybl1	NM_001106632
10870773	4.88	5.91	1.03	2.04	RGD1305274	NM_001106674
10873688	4.42	5.35	0.93	1.91	Arhgef19	NM_001108692
10875119	2.84	3.73	0.89	1.86	RGD1561849	NM_001109260
10877907	6.87	8.03	1.16	2.23	Adfp	NM_001007144
10878157	6.82	8.22	1.40	2.64	Cyp2j4	NM_023025
10878780	9.69	11.14	1.45	2.72	Cyp4a2	NM_001044770
10878787	9.61	10.94	1.33	2.52	Cyp4a3	NM_175760
10878938	4.91	6.33	1.41	2.66	Plk3	NM_022187
10879380	5.99	6.88	0.89	1.86	Ppcs	NM_001039010
10879516	8.47	9.96	1.48	2.80	Mfsd2	NM_001106683
10885851	5.03	6.36	1.33	2.52	Acot2	NM_138907
10886786	8.86	10.17	1.31	2.48	Hdmcp	NM_001001509
10887622	5.02	5.93	0.92	1.89	Crip	NM_001134933
10888196	5.82	6.74	0.92	1.90	Abcg5	NM_053754
10889728	4.60	5.53	0.92	1.90	Arl4a	NM_019186

10890206	6.12	7.25	1.13	2.18	Rpl10l	ENSRNOT000000 47597
10893035	3.38	4.24	0.86	1.82	Timeless	NM_031340
10894100	6.59	7.60	1.01	2.01	Ppap2c	NM_139252
10894167	5.04	6.03	0.99	1.99	Cyp4f39	ENSRNOT000000 07548
10897304	4.22	5.14	0.92	1.89	Gpr172b	NM_001109670
10897360	7.99	8.93	0.95	1.93	Gpt	NM_031039
10899713	9.07	10.03	0.96	1.95	Hsd17b6	NM_173305
10899764	3.43	4.46	1.03	2.04	Slc39a5	NM_001108728
10900905	2.69	3.56	0.87	1.83	Olr1088	ENSRNOT000000 12907
10901910	7.09	7.97	0.89	1.85	Amdhd1	ENSRNOT000000 07331
10907524	8.28	9.87	1.59	3.01	Krt8	NM_199370
10908108	3.81	4.75	0.93	1.91	RGD1309410	NM_001134584
10909072	4.68	5.53	0.86	1.81	Esam	NM_001004245
10911145	2.94	5.64	2.70	6.51	Car12	NM_001080756
10911287	5.88	7.02	1.14	2.20	Anxa2	NM_019905
10913487	6.80	7.68	0.89	1.85	Shisa5	NM_001006989
10914411	7.53	9.59	2.06	4.16	Cyp8b1	NM_031241
10915018	3.66	4.66	1.00	2.00	Panx1	NM_199397
10917727	4.59	5.47	0.87	1.83	Neil1	NM_001025754
10918288	4.81	5.70	0.89	1.85	Plekho2	ENSRNOT000000 42633
10918364	4.58	5.71	1.12	2.18	LOC691658	ENSRNOT000000 57704
10918848	5.85	7.04	1.20	2.29	Slc17a5	NM_001009713
10919712	6.15	7.43	1.28	2.43	Ccr1l	ENSRNOT000000 15265

10921687	8.77	10.55	1.78	3.44	Gnmt	NM_017084
10922151	2.57	3.84	1.28	2.42	Gsta5	NM_001009920
10924223	3.91	5.73	1.82	3.52	Igfbp2	NM_013122
10928902	3.98	4.96	0.97	1.97	Tmbim1	NM_001007713
10930738	6.37	7.39	1.02	2.03	Oit3	NM_001001507
10931017	3.49	4.51	1.02	2.02	Sema6b	NM_053471
10933366	5.47	7.36	1.88	3.69	Rab9a	NM_053458
10933809	7.28	8.61	1.32	2.50	Tmem47	NM_001109317
10935177	7.17	8.06	0.89	1.85	Cldn2	NM_001106846
10937254	7.41	8.28	0.87	1.83	Pls3	NM_031084
10937570	7.11	7.96	0.85	1.80	LOC685431	XR_086366
10939310	6.42	7.45	1.03	2.04	Gla	NM_001108820

Supplementary table (ST-2D): List of genes downregulated in liver

Probe Set ID	Control Liver	Sleep Deprived Liver	Log Fold Change	Fold Change	Entrez ID	Gene Symbol	Accession
10703272	4.73	3.83	-0.90	0.53	365122	RGD1561706	ENSRNOT00000059957
10705230	8.49	6.01	-2.48	0.18	361523	Cyp2b2	ENSRNOT00000028196
10708687	4.26	3.21	-1.05	0.48	499205	Fam181b	BC158703
10709844	4.60	3.54	-1.06	0.48	308937	Wee1	NM_001012742
10710647	5.18	4.30	-0.88	0.54	25023	Prkcb	NM_012713
10714254	4.64	3.51	-1.12	0.46	499330	LOC499330	NM_001024292
10717325	4.59	3.51	-1.08	0.47	308028	Slc2a12	NM_001107451
10720555	7.09	6.18	-0.91	0.53	688574	LOC688574	ENSRNOT00000043132
10721880	3.44	2.53	-0.91	0.53	308586	Sec1	NM_001135584

10724311	7.95	6.97	-0.98	0.51	24440	Hbb	NM_033234
10724319	7.21	6.06	-1.14	0.45	361619	MGC72973	NM_198776
10730310	9.14	7.44	-1.70	0.31	309375	Marveld1	NM_001107590
10730349	10.89	8.35	-2.54	0.17	246074	Scd1	NM_139192
10730830	5.16	4.15	-1.01	0.50	308760	Rccd1	ENSRNOT00000029471
10732652	9.55	8.54	-1.00	0.50	114856	Dusp1	NM_053769
10736875	10.19	8.75	-1.44	0.37	360228	LOC360228	NM_001003706
10741268	6.07	5.22	-0.85	0.55	302983	Mapk8ip3	NM_001100673
10741756	11.56	10.70	-0.85	0.55	25632	Hba-a2	NM_013096
10741778	11.16	10.29	-0.87	0.55	25632	Hba-a2	NM_013096
10742402	5.82	4.55	-1.27	0.41	114097	Ltc4s	NM_053639
10744766	5.02	4.08	-0.94	0.52	79251	Aspa	NM_024399
10745224	6.04	4.17	-1.87	0.27	65202	Slc13a2	NM_031746
10746209	6.84	5.70	-1.15	0.45	363667	Hlf	ENSRNOT00000055664
10749372	6.19	4.81	-1.38	0.38	89829	Socs3	NM_053565
10751931	7.55	6.03	-1.53	0.35	303836	Bcl6	NM_001107084
10753214	10.17	9.12	-1.06	0.48	266766	Rcan1	NM_153724
10756075	3.63	2.77	-0.87	0.55	501794	Vom2r60	ENSRNOT00000041244
10757442	4.32	3.43	-0.89	0.54	288585	Rab15	NM_001011902
10759604	3.15	2.29	-0.86	0.55	498128	RGD1565374	NM_001134602
10760877	5.71	4.55	-1.16	0.45	288545	RGD1305455	NM_001024969
10761992	6.78	5.54	-1.25	0.42	29665	P2rx7	NM_019256
10762426	3.88	3.00	-0.88	0.54	117271	Hrk	NM_057130
10766835	8.30	7.35	-0.96	0.51	289392	Plxna2	NM_001105988
10767518	6.91	6.05	-0.87	0.55	363984	Ikbke	NM_001108854
10767539	6.35	5.27	-1.07	0.47	360840	Srgap2	NM_001134958
10768412	8.79	7.57	-1.22	0.43	289104	Prg4	NM_001105962
10772212	5.73	4.85	-0.88	0.54	364136	Aasdh	ENSRNOT00000002907
10775243	4.50	3.61	-0.89	0.54	363337	LOC363337	BC082068

10775260	4.56	3.26	-1.30	0.41	363337	LOC363337	BC082068
10775647	4.08	3.01	-1.07	0.48	289486	Fras1	ENSRNOT00000002814
10775731	4.31	3.28	-1.03	0.49	498335	Cxcl13	NM_001017496
10775900	8.58	6.83	-1.75	0.30	81503	Cxcl1	NM_030845
10776873	4.61	3.62	-0.99	0.50	305350	RGD1565119	ENSRNOT00000048106
10779093	6.24	5.36	-0.89	0.54	408223	Usp54	NM_001008863
10781273	5.02	3.13	-1.89	0.27	81801	Stc1	NM_031123
10781525	5.51	4.30	-1.20	0.43	113936	Cpb2	BC107447
10784980	7.32	6.11	-1.20	0.43	282843	Sorbs3	NM_001005762
10789442	9.65	8.50	-1.16	0.45	58935	Gas6	NM_057100
10789869	6.13	5.10	-1.03	0.49	29716	Cacna1d	NM_017298
10796831	4.16	3.28	-0.88	0.54	291345	RGD1561231	ENSRNOT00000047232
10797527	7.79	6.44	-1.35	0.39	291005	Gadd45g	NM_001077640
10797929	6.23	5.08	-1.15	0.45	306860	Gcnt2	NM_001001511
10798438	6.98	6.07	-0.91	0.53	24828	Hist1h2aa	ENSRNOT00000050526
10798943	5.58	4.61	-0.97	0.51	113938	Snurf	NM_130738
10798964	8.08	7.09	-0.99	0.50	85419	Lyst	NM_053518
10799888	5.28	4.15	-1.12	0.46	291367	RGD1564552	ENSRNOT00000050803
10800024	4.75	3.61	-1.13	0.46	291345	RGD1561231	ENSRNOT00000047232
10800919	6.57	5.45	-1.13	0.46	24330	Egr1	NM_012551
10801260	4.11	2.90	-1.21	0.43	680470	Pcdhgb6	ENSRNOT00000060466
10803194	5.52	4.65	-0.87	0.55	680014	Esco1	NM_001126299
10803692	7.16	5.96	-1.20	0.44	338475	Nrep	NM_178096
10804127	4.46	3.49	-0.97	0.51	25317	Fgf1	NM_012846
10804281	4.97	3.78	-1.19	0.44	24833	Spink3	NM_012674
10806191	4.74	3.79	-0.95	0.52	679726	LOC679726	ENSRNOT00000040473
10812734	5.61	4.76	-0.85	0.55	502503	Serf1	ENSRNOT00000024291
10813949	5.29	4.13	-1.16	0.45	619558	Fam134b	ENSRNOT00000014423
10814184	3.82	2.68	-1.14	0.45	310218	Car1	NM_001107660

10817142	4.31	3.43	-0.87	0.55	310586	RGD156 6121	ENSRNOT000000 35763
10817222	7.94	7.05	-0.89	0.54	499668	Lingo4	NM_001109189
10821698	5.01	4.10	-0.91	0.53	310132	Osmr	NM_001005384
10822242	11.78	10.22	-1.56	0.34	54232	Car3	NM_019292
10826216	6.60	5.68	-0.92	0.53	691538	Rnpc3	NM_001100810
10826723	8.96	7.91	-1.05	0.48	64017	Enpep	NM_022251
10826967	4.12	3.00	-1.11	0.46	365948	Bank1	XM_345295
10830223	9.15	8.29	-0.85	0.55	80841	Fabp7	NM_030832
10830270	5.06	3.41	-1.64	0.32	499453	RGD156 5550	ENSRNOT000000 44322
10830279	7.05	5.99	-1.07	0.48	499454	RGD156 0095	ENSRNOT000000 40584
10830854	7.92	6.70	-1.22	0.43	29168	Ubd	NM_053299
10832487	4.55	3.21	-1.34	0.39	690315	Derl3	NM_001109577
10832772	7.40	5.83	-1.58	0.34	309722	Rhobtb1	NM_001107622
10834335	3.76	2.76	-1.00	0.50	414138	Lcn6	NM_001001519
10834670	4.76	3.70	-1.07	0.48	311827	Adamtsl2	ENSRNOT000000 36995
10838443	2.88	1.99	-0.88	0.54	405231	Olr786	NM_001000916
10844331	10.33	5.05	-5.28	0.03	170496	Lcn2	NM_130741
10846652	5.59	4.71	-0.88	0.54	311137	Zfp385b	NM_001107736
10847957	6.36	4.55	-1.80	0.29	499847	Prrg4	NM_001109203
10857130	7.91	7.06	-0.86	0.55	29254	Mgll	NM_138502
10858408	6.78	4.64	-2.14	0.23	24153	A2m	NM_012488
10859671	4.66	3.81	-0.85	0.56	362464	LOC362 464	ENSRNOT000000 55473
10860314	3.51	2.59	-0.92	0.53	286924	Gnat3	NM_173139
10861793	7.82	6.60	-1.21	0.43	503568	Slc13a4	NM_001012621
10863608	3.90	2.79	-1.11	0.46	312495	Cyp26b1	NM_181087
10863686	6.71	5.01	-1.70	0.31	64570	Nat8	NM_022635
10867497	4.65	3.55	-1.10	0.47	500400	Fam110b	BC091289
10867667	7.52	6.51	-1.01	0.50	117048	Cdh17	NM_053977
10869476	11.86	10.50	-1.36	0.39	24614	Orm1	NM_053288
10875567	5.33	4.35	-0.98	0.51	297903	Fam92a1	ENSRNOT000000 22249
10877372	7.29	5.84	-1.45	0.37	298107	Mup5	AB039828
10877755	8.66	7.71	-0.96	0.51	29227	Nfib	NM_031566
10881861	7.79	6.39	-1.40	0.38	78962	Per3	NM_023978
10887486	5.85	4.98	-0.86	0.55	362790	RGD130 8350	ENSRNOT000000 18225

10887492	5.87	4.70	-1.17	0.44	362790	RGD130 8350	ENSRNOT000000 18225
10887939	4.89	4.03	-0.85	0.55	313838	Cdc42ep 3	NM_001048044
10890547	10.65	9.16	-1.48	0.36	299131	Dhrs7	NM_001013098
10894414	3.61	2.70	-0.91	0.53	300308	LOC300 308	NM_001013952
10894525	5.94	5.07	-0.87	0.55	299691	Cry1	NM_198750
10895888	6.80	5.91	-0.89	0.54	362894	R3hdm2	NM_001130557
10895915	7.67	5.34	-2.33	0.20	362895	Stac3	NM_001130558
10903573	6.94	4.77	-2.17	0.22	500865	Golsyn	ENSRNOT000000 05584
10905312	5.60	4.17	-1.43	0.37	171044	Sstr3	NM_133522
10906296	5.24	4.31	-0.92	0.53	500917	Odf3b	ENSRNOT000000 55805
10909105	3.63	2.35	-1.28	0.41	406021	Olr1197	NM_001001120
10912076	4.87	3.87	-1.00	0.50	502642	RGD156 3348	NM_001114939
10912908	7.43	6.46	-0.97	0.51	83681	Cish	NM_031804
10913043	4.46	3.54	-0.92	0.53	300999	Mst1r	NM_001106855
10917518	7.06	6.08	-0.98	0.51	315676	Dmxl2	ENSRNOT000000 66197
10917617	6.35	4.53	-1.82	0.28	690919	Nrg4	ENSRNOT000000 20332
10919010	4.85	3.93	-0.93	0.53	113990	Hmgn3	NM_001007020
10919262	5.53	4.56	-0.96	0.51	300888	Tmed3	NM_001004249
10920002	5.62	4.63	-0.99	0.50	315992	Dock3	NM_001108184
10920498	4.91	3.95	-0.96	0.51	316014	Nbeal2	ENSRNOT000000 56130
10921141	7.34	6.47	-0.87	0.55	301085	Fyco1	NM_001106870
10922260	4.20	3.31	-0.89	0.54	316304	Lgsn	NM_181383
10922499	4.42	3.28	-1.14	0.45	679806	Fer115	ENSRNOT000000 59806
10923432	10.86	9.46	-1.39	0.38	493909	Aox3	NM_001008527
10923474	7.39	6.11	-1.28	0.41	316424	Aox4	ENSRNOT000000 33068
10923476	11.44	10.02	-1.43	0.37	316424	Aox4	ENSRNOT000000 33068
10924245	3.36	2.31	-1.04	0.49	29385	Il8rb	NM_017183
10926651	7.75	6.32	-1.43	0.37	316249	Enpp5	NM_001012744
10926851	6.05	4.57	-1.48	0.36	301287	Pkhd1	ENSRNOT000000 60760
10928191	4.39	3.33	-1.06	0.48	501145	Satb2	NM_001109306
10928452	7.58	6.68	-0.91	0.53	363239	Raph1	NM_001108798

10929842	6.68	5.75	-0.93	0.53	63840	Per2	NM_031678
10930766	9.51	7.07	-2.44	0.18	25011	Cyp2c12	NM_031572
10932037	4.24	3.25	-0.99	0.50	313434	RGD156 6363	ENSRNOT000000 39809
10932139	5.06	4.04	-1.02	0.49	317170	Slc9a7	NM_001108242
10933772	3.74	2.81	-0.93	0.52	192267	Obp1f	NM_138903
10938524	6.71	5.08	-1.63	0.32	312102	Vsig4	NM_001025004

Supplementary table (ST3): List of common genes affected in brain and liver

(A) Common genes "down-regulated" in the brain and liver:

Gene Symbol	Accession No.	GO term molecular/biological functions
Wee1	NM_001012742	Protein tyrosine kinase activity
Slc2a12	NM_001107451	Carbohydrate transmembrane transporter activity
Hrk	NM_057130	Apoptosis regulation, Bleb assembly
Fam110b	NM_001024341.1	Tumor progression

(B) Common genes "up-regulated" in the brain and "down-regulated" in the liver:

Gene Symbol	Accession	GO term molecular/biological functions
Hba-a1	NM_013096	Heme binding, Oxidoreductase activity, Drug transport
Hba-a1	NM_013096	Heme binding, Oxidoreductase activity, Drug transport
Mup5	NM_203325.1	Fatty acid biosynthetic process, Catalytic activity

(C) Common genes "up-regulated" in the liver and "down-regulated" in the brain:

Gene Symbol	Accession	GO term molecular/biological functions
RT1-Da	NM_001008847	Response to stimulus
Zbtb6	NM_001108953	Transcriptional regulation
Tmem106b	NM_001004267	Dendrite morphogenesis, Required for dendrite branching

Supplementary Table 4 (ST-4): Log fold change of gene expression after REM sleep loss compared to control. Values in positive numbers shows upregulation while negative values show downregulation.

Genes	Brain	Liver	Accession number
Slc1a4		1.46	NM_198763
Slc2a9		1.05	ENSRNOT00000042200
Slc2a12	-0.94	-1.08	NM_001107451
Slc5a7	-1.01		NM_053521
Slc6a6		1.17	NM_017206
Slc6a13		0.91	NM_133623
Slc9a4	-1.56		NM_173098
Slc9a2	-0.96		NM_012653
Slc15a3		0.88	NM_139341
Slc16a1		0.98	NM_012716
Slc16a14	-1.21		NM_001108229
Slc17a5		1.20	NM_001009713
Slc20a1		0.88	NM_031148
Slc22a5		1.37	NM_019269
Slc22a15	-0.89		NM_001107707
Slc25a22		0.98	NM_001014027
Slc27a2	1.07		NM_031736
Slc27a5		1.24	NM_024143
Slc28a2		2.02	NM_031664
Slc35d3		-1.05	NM_001107522
Slc39a5		1.03	NM_001108728
Slc39a12	-1.10		NM_001106124
Slc44a4		1.03	NM_212541

Supplementary Table 5 (ST-5): List of GO terms related to synaptic plasticity

GO terms	Brain	RGD ID
Positive regulation of synaptic plasticity	DR ($p=0.03$)	GO:0031915
Positive regulation of long-term synaptic plasticity	UR ($p=0.002$)	GO:0048170
Regulation of long-term neuronal synaptic plasticity	DR ($p=2.87E-005$)	GO:0048169
Synaptic transmission	DR ($p= 0.001$)	
Synaptic transmission, dopaminergic	DR ($p= 2.64E-009$)	GO:0001963
Regulation of synaptic transmission, dopaminergic	DR ($p= 0.0009$)	GO:0032225
Negative regulation of synaptic transmission	DR ($p= 0.004$)	GO:0050805
Negative regulation of synaptic transmission, glutamatergic	DR ($p=7.77E-009$)	GO:0051967
Positive regulation of synaptic transmission, glutamatergic	DR ($p=9.93E-006$)	GO:0051968
Synaptic transmission, cholinergic	DR ($p= 1.33E-006$)	GO:0007271
Regulation of synaptic transmission, GABAergic	DR ($p=2.47E-006$)	GO:0032228
Positive regulation of synaptic transmission, GABAergic	DR ($p=0.0002$)	GO:0032230
Positive regulation of synaptic transmission, glutamatergic	DR ($p=9.93E-006$)	GO:0051968
Negative regulation of synaptic transmission, glutamatergic	DR ($p=7.77E-009$)	GO:0051967
Long term synaptic depression	DR ($p=0.006$)	GO:0060292
Long-term synaptic potentiation	DR ($p=0.009$)	GO:0060291
Neuromuscular synaptic transmission	DR ($p=0.03$)	GO:0007274
Negative regulation of synaptic transmission, dopaminergic	DR ($p= 0.04$)	GO:0032227
Establishment of synaptic specificity at neuromuscular junction	DR ($p=0.04$)	GO:0007529

Supplementary Table 6 (ST-6): List of GO terms related to immune system

GO terms	Brain	Liver	RGD ID
Immune response		UR ($p=0.0002$)	GO:0006955

Immunoglobulin mediated immune response		UR ($p=0.009$)	GO:0016064
Negative regulation of type 2 immune response		DR ($p=0.001$)	GO:0002829
Regulation of immune system process		DR ($p=0.01$)	GO:0002682
Type 2 immune response		DR ($p=0.01$)	GO:0042092
Positive regulation of T cell mediated immune response to tumor cell	UR ($p=0.0006$)		GO:0002842
Immune system development	DR ($p=0.001$)		GO:0002520
T cell activation involved in immune response	DR ($p=0.002$)		GO:0002286