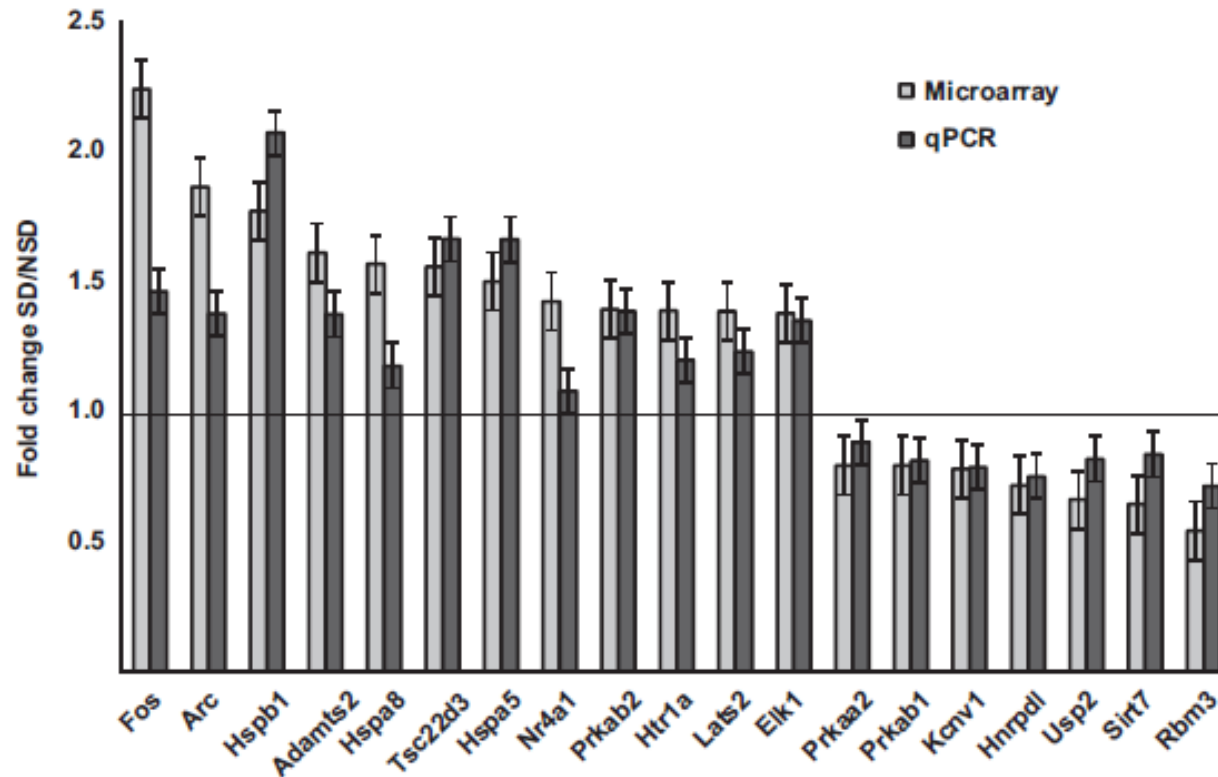


**Supplementary Table 1:** Genes detected as differentially regulated in sleep deprivation microarray (multiple testing corrected P value <0.05) tested by qPCR. All comparisons between sleep-deprived (SD) and non-sleep-deprived (NSD) samples measured by qPCR are significant at P< 0.05 using 1-tailed t-tests, except Nr4a1. For each gene, qPCR expression is represented as the fold change (FC) in SD mice relative to NSD mice, normalized to the average expression of the housekeeping genes Actg, Hprt, and Tuba4a (Used with permission)

Gene Name	Probe-set ID	Microarray FC	qPCR FC	qPCR P Value	SD, n	NSD, n	Forward Primer	Reverse Primer
<i>Fos</i>	1423100_at	2.24	1.46	2E-03	9	9	CCGACTCCTTCTCCAGCA	TGTCACCGTGGGGATAAAGT
<i>Arc</i>	1418687_at	1.87	1.38	8E-03	8	9	AGCAGCAGACCTGACATCCT	GGTGTCAATTCTCCTGGCTCT
<i>Hspb1</i>	1425964_x_at	1.77	2.07	1E-04	10	9	CACAGTGAAGACCAAGGAAGG	GGTGAAGCACCGAGAGATGT
<i>Adamts2</i>	1455720_at	1.61	1.38	3E-02	8	9	GAACCACAGGCTCTGGACAC	AACTGGACCACCGAGTCATC
<i>Hspa8</i>	1431182_at	1.57	1.18	2E-03	9	8	CGGAAGAGCTGATGGTAAAGA	CACCTTCTGCTGCTTCTCT
<i>Tsc22d3</i>	1420772_a_at	1.56	1.67	1E-06	19	19	TTCTCTGCTTGGAGGGGATT	GCTCACGAATCTGCTCCTTT
<i>Hspa5</i>	1416064_a_at	1.50	1.66	1E-05	10	9	GGAGACTGCTGAGGCGTATT	TGGGCATCATTGAAGTAAGC
<i>Nr4a1</i>	1416505_at	1.43	1.08	1E-01	9	9	AAAATCCCTGGCTTCATTGAG	TTTAGATCGGTATGCCAGGCG
<i>Prkab2</i>	1435874_at	1.39	1.39	3E-04	10	10	GGGAAAGGAGCACAAAGATC	CTGCTGCCAGGGTACAAAC
<i>Htr1a</i>	1450219_at	1.39	1.20	5E-02	9	9	CTGTTTATCGCCCTGGATGT	ATGAGCCAAGTGAGCGAGAT
<i>Lats2</i>	1419678_at	1.39	1.23	3E-02	14	13	ACCAAATTACATCGCTCCGG	TCGTCTCCCAGTTGATCACCT
<i>Elk1</i>	1421897_at	1.38	1.35	2E-03	15	15	TCAAGTTGGTGGATGCAGAG	GCAACCTCTGGGTAGGACAC
<i>Prkaa2</i>	1434766_at	0.79	0.88	5E-02	10	10	GGAATCCCGAAGCCAGAGCAA	CGATGCTTTTGAAGTCCAGA
<i>Prkab1</i>	1424119_at	0.79	0.81	3E-02	10	10	CATCCTCCCGCCACACCTGC	GAGCACCATCACTCCATC
<i>Kcnv1</i>	1439333_at	0.78	0.79	8E-03	8	9	GTCTGGTCCAGGTCTTGAGG	CACCATGCACAAGGAACACT
<i>Hnrpdl</i>	1449039_a_at	0.72	0.75	3E-03	13	14	AAGAACCAGCAGGATGACGGT	TGCAGTCTACCACTTCCCCAA
<i>Usp2</i>	1417168_a_at	0.66	0.82	7E-03	8	9	AAAGAGTGCCAGGGTCTG	TCTCTCAGCTCTCGGGTGT
<i>Sirt7</i>	1457279_at	0.65	0.84	3E-02	10	10	GAGCCTACCCTACCCACA	GTGGAGCCCATCACAGTTC
<i>Rbm3</i>	1429169_at	0.54	0.72	2E-02	14	13	AGGACTTGCTTCTGCCATGT	ATAGGCCCAAAGCTGCTGAA

ION REGULATES TRANSLATION IN MOUSE HIPPOCAMPUS



**Supplementary Fig.1.** Quantitative RT-PCR validation of genes upregulated or downregulated by sleep deprivation in the hippocampus. Quantitative RT-PCR (dark gray) was used to validate the expression level of genes identified by microarray analysis (light gray) as being changed in the hippocampus by sleep deprivation. For each gene, expression is represented as the fold change in SD mice relative to NSD mice, normalized to the average expression of housekeeping genes *Actg*, *Hprt*, and *Tuba4a*. The fold change values from the microarray for SD/NSD are shown for each gene for comparison. All SD/NSD qPCR comparisons are significant at  $P < 0.05$ , except *Nr4a1* induction (see Table 1). Bars indicate  $\pm$  SE. (Used with permission)