

## Supplementary Data

Gene	Description	log2FC	P-value	FDR
<i>Fam107a</i>	family with sequence similarity 107 member A	1.08	4.05E-08	0.0002
<i>Hmgcs2</i>	3-hydroxy-3-methylglutaryl-CoA synthase 2	1.20	2.13E-07	0.001
<i>Tst</i>	thiosulfate sulfurtransferase	-1.27	8.52E-07	0.001
<i>Pad12</i>	peptidyl arginine deiminase 2	-1.10	1.44E-06	0.001
<i>Phyhd1</i>	phytanoyl-CoA dioxygenase domain containing 1	2.01	1.10E-06	0.001
<i>Fbln5</i>	fibulin 5	1.51	1.70E-06	0.002
<i>Mfsd2a</i>	major facilitator superfamily domain containing 2A	1.42	3.08E-06	0.002
<i>Acss3</i>	acyl-CoA synthetase short chain family member 3	1.74	2.81E-06	0.002
<i>Wfikkn2</i>	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	2.73	2.43E-06	0.002
<i>C030029H02Rik</i>	RIKEN cDNA C030029H02 gene	-1.23	4.13E-06	0.002
<i>Col5a3</i>	collagen type V alpha 3 chain	1.14	4.44E-06	0.002
<i>Itgad</i>	integrin subunit alpha D	2.94	4.65E-06	0.002
<i>Ugt8a</i>	UDP galactosyltransferase 8A	-1.03	5.52E-06	0.002
<i>Gbp3</i>	guanylate binding protein 3	-1.15	8.27E-06	0.002
<i>Pnpla7</i>	patatin like phospholipase domain containing 7	1.23	7.78E-06	0.002
<i>Slc38a5</i>	solute carrier family 38 member 5	-2.02	9.71E-06	0.003
<i>Cdh19</i>	cadherin 19	1.19	9.81E-06	0.003
<i>Alpl</i>	alkaline phosphatase, biomineralization associated	-1.44	1.03E-05	0.003
<i>Serp1nb1a</i>	uncharacterized LOC105262837	-1.10	1.02E-05	0.003
<i>Arhgef37</i>	Rho guanine nucleotide exchange factor 37	1.63	1.14E-05	0.003
<i>A730020M07Rik</i>	RIKEN cDNA A730020M07 gene	1.84	1.16E-05	0.003
<i>Pkd2l1</i>	polycystin 2 like 1, transient receptor potential cation channel	-1.11	1.74E-05	0.003
<i>Rab7b</i>	RAB7B, member RAS oncogene family	-1.16	1.82E-05	0.004
<i>Pla2g3</i>	phospholipase A2 group III	2.87	2.41E-05	0.004
<i>Hr</i>	HR lysine demethylase and nuclear receptor corepressor	1.84	2.87E-05	0.004
<i>Aif1</i>	allograft inflammatory factor 1	-1.26	3.42E-05	0.005
<i>Npy</i>	neuropeptide Y	1.39	3.43E-05	0.005
<i>Stab2</i>	stabilin 2	1.79	4.20E-05	0.006
<i>Angptl2</i>	angiopoietin like 2	-1.26	6.21E-05	0.007
<i>5330429C05Rik</i>	RIKEN cDNA 5330429C05 gene	3.09	1.15E-04	0.011
<i>Uhrf1</i>	ubiquitin like with PHD and ring finger domains 1	-1.52	1.22E-04	0.012
<i>Fam83d</i>	family with sequence similarity 83 member D	1.44	1.31E-04	0.012
<i>Ctla2a</i>	cytotoxic T lymphocyte-associated protein 2 alpha	1.57	1.30E-04	0.012
<i>Gabbr2</i>	gamma-aminobutyric acid type A receptor subunit rho2	1.90	1.50E-04	0.013
<i>Hsf3</i>	heat shock transcription factor 3	3.21	1.84E-04	0.014
<i>Agtr1a</i>	angiotensin II receptor, type 1a	1.12	2.16E-04	0.016
<i>Rnase1</i>	ribonuclease A family member 1, pancreatic	-1.23	3.01E-04	0.019
<i>Pcdh12</i>	protocadherin 12	-1.80	3.05E-04	0.019
<i>Aplnr</i>	apelin receptor	-1.57	3.91E-04	0.021
<i>Lrrc29</i>	leucine rich repeat containing 29	1.03	3.86E-04	0.021

<i>Sds</i>	serine dehydratase	1.63	4.00E-04	0.022
<i>Fmo2</i>	flavin containing dimethylaniline monooxygenase 2	1.49	4.15E-04	0.022
<i>Cd163</i>	CD163 molecule	1.10	4.24E-04	0.023
<i>Tmem82</i>	transmembrane protein 82	2.18	4.23E-04	0.023
<i>Gipc3</i>	GIPC PDZ domain containing family member 3	-1.10	4.49E-04	0.023
<i>Dnah14</i>	dynein axonemal heavy chain 14	1.21	4.64E-04	0.023
<i>Map3k6</i>	mitogen-activated protein kinase kinase kinase 6	2.01	4.63E-04	0.023
<i>Cd300lf</i>	CD300 molecule like family member f	2.07	5.76E-04	0.026
<i>Epx</i>	eosinophil peroxidase	-1.41	5.80E-04	0.026
<i>Lipg</i>	lipase G, endothelial type	-1.26	5.80E-04	0.026
<i>Cd180</i>	CD180 molecule	-1.05	7.96E-04	0.032
<i>Pglyrp1</i>	peptidoglycan recognition protein 1	1.08	8.66E-04	0.034
<i>Gm15201</i>	predicted gene 15201	1.11	9.11E-04	0.034
<i>Rtbdn</i>	retbindin	1.17	1.02E-03	0.038
<i>Slc18a1</i>	solute carrier family 18 member A1	1.37	1.03E-03	0.038
<i>Myh1</i>	myosin heavy chain 1	1.54	1.05E-03	0.038
<i>Slc43a3</i>	solute carrier family 43 member 3	1.33	1.09E-03	0.039
<i>Anxa8</i>	annexin A8	1.01	1.16E-03	0.040
<i>Gkn3</i>	gastrokine 3	-1.69	1.21E-03	0.041
<i>Fut9</i>	fucosyltransferase 9	1.10	1.26E-03	0.042
<i>A230009B12Rik</i>	RIKEN cDNA A230009B12 gene	-1.33	1.29E-03	0.043
<i>Neurod6</i>	neuronal differentiation 6	1.04	1.34E-03	0.043
<i>Srarp</i>	steroid receptor associated and regulated protein	-1.02	1.38E-03	0.044
<i>Gm29508</i>	predicted gene 29508	-1.09	1.48E-03	0.045
<i>Ankrd63</i>	ankyrin repeat domain 63	-1.61	1.62E-03	0.048
<i>Klrg2</i>	killer cell lectin like receptor G2	1.88	1.67E-03	0.049
<i>Fyb2</i>	FYN binding protein 2	1.83	1.73E-03	0.050
<i>Sgk3</i>	serum/glucocorticoid regulated kinase family member 3	1.41	1.83E-03	0.052
<i>Fkbp5</i>	FKBP prolyl isomerase 5	1.20	1.86E-03	0.052
<i>Agrp</i>	agouti related neuropeptide	1.24	1.98E-03	0.054

**Supplementary Table S1. Differentially Expressed Genes in Hypothalamus only (FDR  $\leq$  0.05 and  $\text{abs}(\log_2\text{FC}) > 1.0$ ).** 70 differentially expressed genes of the hypothalamus with an absolute  $\log_2$  fold change larger than 1.0 and an FDR less than 0.05 except for 11 genes that are commonly significantly expressed in the hypothalamus and hippocampus are shown. Abbreviations:  $\text{abs}(\log_2\text{FC})$ , absolute  $\log_2$  fold change; FDR, false discovery rate.

Gene	Description	log2FC	P-value	FDR
<i>Rtp1</i>	Receptor Transporter Protein 1	2.26	5.14.E-06	0.006
<i>Etmpp1</i>	Ethanolamine-Phosphate Phospho-Lyase	1.48	1.35.E-05	0.011
<i>Lcn2</i>	Lipocalin 2	2.93	1.24.E-05	0.011
<i>Ada</i>	Adenosine Deaminase	1.54	2.78.E-05	0.014
<i>COX3</i>	Mitochondrially Encoded Cytochrome C Oxidase III	2.22	3.02.E-05	0.014
<i>Atp2c2</i>	ATPase Secretory Pathway Ca <sup>2+</sup> Transporting 2	1.22	3.36.E-05	0.015
<i>Plekhf1</i>	Pleckstrin Homology And FYVE Domain Containing 1	1.05	3.64.E-05	0.016
<i>Gbp5</i>	Guanylate Binding Protein 5	-1.31	9.36.E-05	0.026
<i>Tmem52</i>	Transmembrane Protein 52	1.33	2.22.E-04	0.041
<i>H2bc6</i>	H2B Clustered Histone 6	-1.05	4.17.E-04	0.050

**Supplementary Table S2. Differentially Expressed Genes in Hippocampus only (FDR ≤ 0.05 and abs(log2FC) > 1.0).** 10 differentially expressed genes of the hippocampus with an absolute log2 fold change larger than 1.0 and an FDR less than 0.05 except for 10 genes that are commonly significantly expressed in hypothalamus and hippocampus are shown. Abbreviations: abs(log2FC), absolute log2 fold change; FDR, false discovery rate.

Gene Name	log2FC of Hypothalamus	FDR of Hypothalamus	log2FC of Hippocampus	FDR of Hippocampus
<i>Tnc</i>	-1.07	0.003	-1.12	0.011
<i>Angptl4</i>	1.30	0.004	1.32	0.005
<i>Tekt4</i>	1.33	0.016	1.27	0.030
<i>Xdh</i>	1.88	0.031	1.15	0.043
<i>Kirrel2</i>	1.88	0.007	1.02	0.002
<i>Cdkn1a</i>	2.34	0.006	1.65	0.008
<i>Sult1a1</i>	2.40	0.000	1.47	0.001
<i>Hif3a</i>	2.66	0.004	1.75	0.001
<i>Otoa</i>	3.02	0.002	2.52	0.043
<i>Lao1</i>	3.53	0.002	2.44	0.053
<i>Plin4</i>	4.37	0.002	3.21	0.011

**Supplementary Table S3. Differentially Expressed Genes in both Hypothalamus and Hippocampus (FDR ≤ 0.05 and abs(log2FC) > 1.0).** 11 common differentially expressed genes in both the hypothalamus and hippocampus with an absolute log2 fold change larger than 1.0 and an FDR less than 0.05 are shown. Abbreviations: abs(log2FC), absolute log2 fold change; FDR, false discovery rate.