

Table S1. Downregulated genes in the hippocampus between CON and CIEO groups.

Gene symbol	Gene name	Fold change (vs. CON)	P-value
<i>Asb4</i>	Ankyrin repeat and SOCS box-containing 4	-1.63 ± 0.32	0.0030
<i>Col25a1</i>	Collagen, type XXV, alpha 1	-1.38 ± 0.17	0.0177
<i>Dcc</i>	Deleted in colorectal carcinoma	-1.58 ± 0.22	0.0492
<i>Depp1</i>	DEPP1 autophagy regulator	-1.60 ± 0.48	0.0171
<i>Egr2</i>	Early growth response 2	-2.09 ± 0.23	0.0075
<i>Egr4</i>	Early growth response 4	-1.58 ± 0.50	0.0082
<i>Fos</i>	FBJ osteosarcoma oncogene	-1.53 ± 0.36	0.0255
<i>Gbp4</i>	Guanylate binding protein 4	-1.77 ± 0.54	0.0232
<i>Gm4971</i>	Smad nuclear interacting protein 1 pseudogene	-1.56 ± 0.32	0.0069
<i>Gsdma2</i>	Gasdermin A2	-1.43 ± 0.16	0.0344
<i>Hsf5</i>	Heat shock transcription factor family member 5	-1.40 ± 0.13	0.0243
<i>Insc</i>	INSC spindle orientation adaptor protein	-1.47 ± 0.34	0.0154
<i>Itgal</i>	integrin alpha 1	-1.42 ± 0.13	0.0378
<i>Nckap5</i>	NCK-associated protein 5	-1.52 ± 0.47	0.0076
<i>Rbm3</i>	RNA binding motif (RNP1, RRM) protein 3	-1.46 ± 0.26	0.0440
<i>Ssh1</i>	Slingshot protein phosphatase 1	-1.42 ± 0.13	0.0093
<i>Stag3</i>	Stromal antigen 3	-1.49 ± 0.39	0.0019

Table S2. Upregulated genes in the hippocampus between CON and CIEO groups.

Gene symbol	Gene name	Fold change (vs. CON)	P-value
<i>A930015D03Rik</i>	RIKEN cDNA A930015D03 gene	1.65 ± 0.32	0.0207
<i>Cytl1</i>	Cytokine-like 1	1.89 ± 0.28	0.0007
<i>Elmo1</i>	Engulfment and cell motility 1	2.34 ± 0.63	0.0040
<i>Galnt15</i>	Polypeptide N-acetylgalactosaminyltransferase 15	1.59 ± 0.20	0.0000
<i>Hif3a</i>	Hypoxia inducible factor 3, alpha subunit	1.71 ± 0.15	0.0058
<i>I830077J02Rik</i>	RIKEN cDNA I830077J02 gene	1.73 ± 0.08	0.0030
<i>Plin4</i>	Perilipin 4	2.96 ± 0.29	0.0108
<i>Rxfp1</i>	Relaxin/insulin-like family peptide receptor 1	1.76 ± 0.13	0.0359
<i>Sult1a1</i>	Sulfotransferase family 1A, phenol-preferring, member 1	1.62 ± 0.13	0.0011
<i>Tmem52</i>	Transmembrane protein 52	1.81 ± 0.17	0.0479
<i>Trim41</i>	Tripartite motif-containing 41	1.70 ± 0.31	0.0191
<i>Tshz2</i>	Teashirt zinc finger family member 2	1.59 ± 0.26	0.0050
<i>Uvssa</i>	UV stimulated scaffold protein A	1.65 ± 0.29	0.0413
<i>Vwa3a</i>	Von Willebrand factor A domain containing 3A	1.66 ± 0.38	0.0017
<i>Zfp868</i>	Zinc finger protein 868	1.74 ± 0.27	0.0030

Table S3. GO Biological Process enrichment of DEGs.

GO Biological Process	Related genes
regulation of cellular protein metabolic process (GO:0032268)	<i>Rbm3, Ssh1</i>
protein modification by small protein conjugation (GO:0032446)	<i>Egr2, Hif3a, Trim41, Uvssa</i>
negative regulation of collateral sprouting (GO:0048671)	<i>Dcc</i>
Schwann cell differentiation (GO:0014037)	<i>Egr2</i>
regulation of neuron death (GO:1901214)	<i>Dcc, Fos</i>
protein ubiquitination (GO:0016567)	<i>Asb4, Hif3a, Trim41, Uvssa</i>
ethanol catabolic process (GO:0006068)	<i>Sult1a1</i>
amine metabolic process (GO:0009308)	<i>Sult1a1</i>
regulation of collateral sprouting (GO:0048670)	<i>Dcc</i>
cellular response to muramyl dipeptide (GO:0071225)	<i>Trim41</i>
cellular response to oxygen-containing compound (GO:1901701)	<i>Fos, Ssh1, Trim41</i>
positive regulation of vasculogenesis (GO:2001214)	<i>Asb4</i>
primary alcohol catabolic process (GO:0034310)	<i>Sult1a1</i>
apical protein localization (GO:0045176)	<i>Insc</i>
skeletal muscle cell differentiation (GO:0035914)	<i>Egr2</i>
positive regulation of myelination (GO:0031643)	<i>Egr2</i>
supramolecular fiber organization (GO:0097435)	<i>Col25a1, Elmo1, Nckap5</i>
response to muramyl dipeptide (GO:0032495)	<i>Trim41</i>
defense response to protozoan (GO:0042832)	<i>Gbp4</i>
regulation of vasculogenesis (GO:2001212)	<i>Asb4</i>

Table S4. WikiPathway enrichment of DEGs.

WikiPathway	Related genes
Signaling of Hepatocyte Growth Factor Receptor WP313	<i>Itgal, Fos</i>
Chromosomal and microsatellite instability in colorectal cancer WP4216	<i>Dcc, Fos</i>
Arylamine metabolism WP694	<i>Sult1a1</i>
Neuroinflammation WP4919	<i>Fos</i>
Serotonin and anxiety-related events WP3944	<i>Fos</i>
Transcriptional cascade regulating adipogenesis WP4211	<i>Egr2</i>
Brain-derived neurotrophic factor (BDNF) signaling pathway WP2380	<i>Egr2, Fos</i>
Regulation of Actin Cytoskeleton WP51	<i>Itgal, Ssh1</i>
Hepatitis B infection WP4666	<i>Egr2, Fos</i>
MAPK pathway in congenital thyroid cancer WP4928	<i>Fos</i>
Myometrial relaxation and contraction pathways WP289	<i>Fos, Rxfp1</i>
NOTCH1 regulation of endothelial cell calcification WP3413	<i>Itgal</i>
Serotonin and anxiety WP3947	<i>Fos</i>
Sulfation Biotransformation Reaction WP692	<i>Sult1a1</i>
Estrogen metabolism WP697	<i>Sult1a1</i>
Galanin receptor pathway WP4970	<i>Sult1a1</i>
Tamoxifen metabolism WP691	<i>Fos</i>
miRNA targets in ECM and membrane receptors WP2911	<i>Itgal</i>
Estrogen signaling pathway WP712	<i>Fos</i>
Photodynamic therapy-induced NFE2L2 (NRF2) survival signaling WP3612	<i>Fos</i>