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Supplementary Materials

Depletion of microglia with PLX3397 attenuates MK-801-induced hyperactivity associated with regulating inflammation-related genes in the brain

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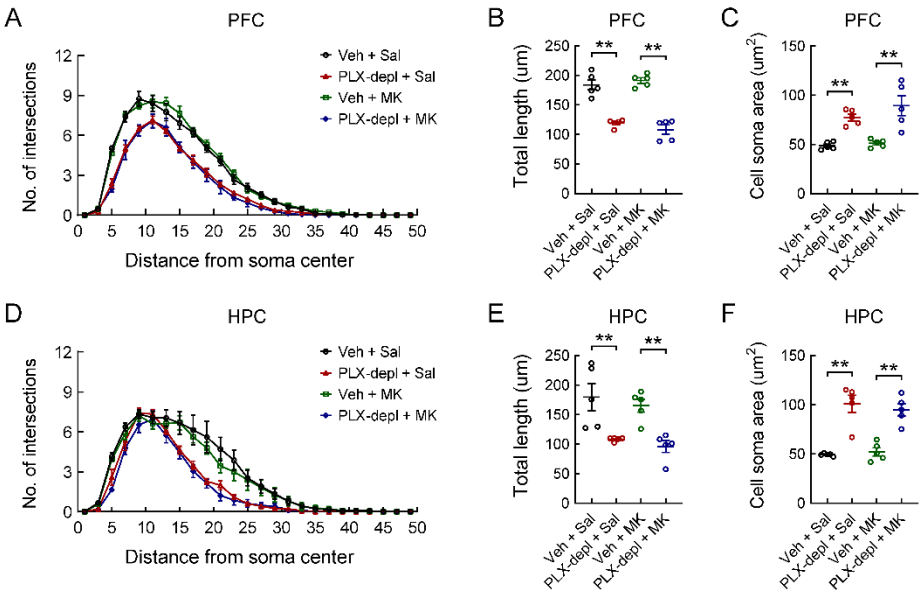
Supplementary Materials and Methods

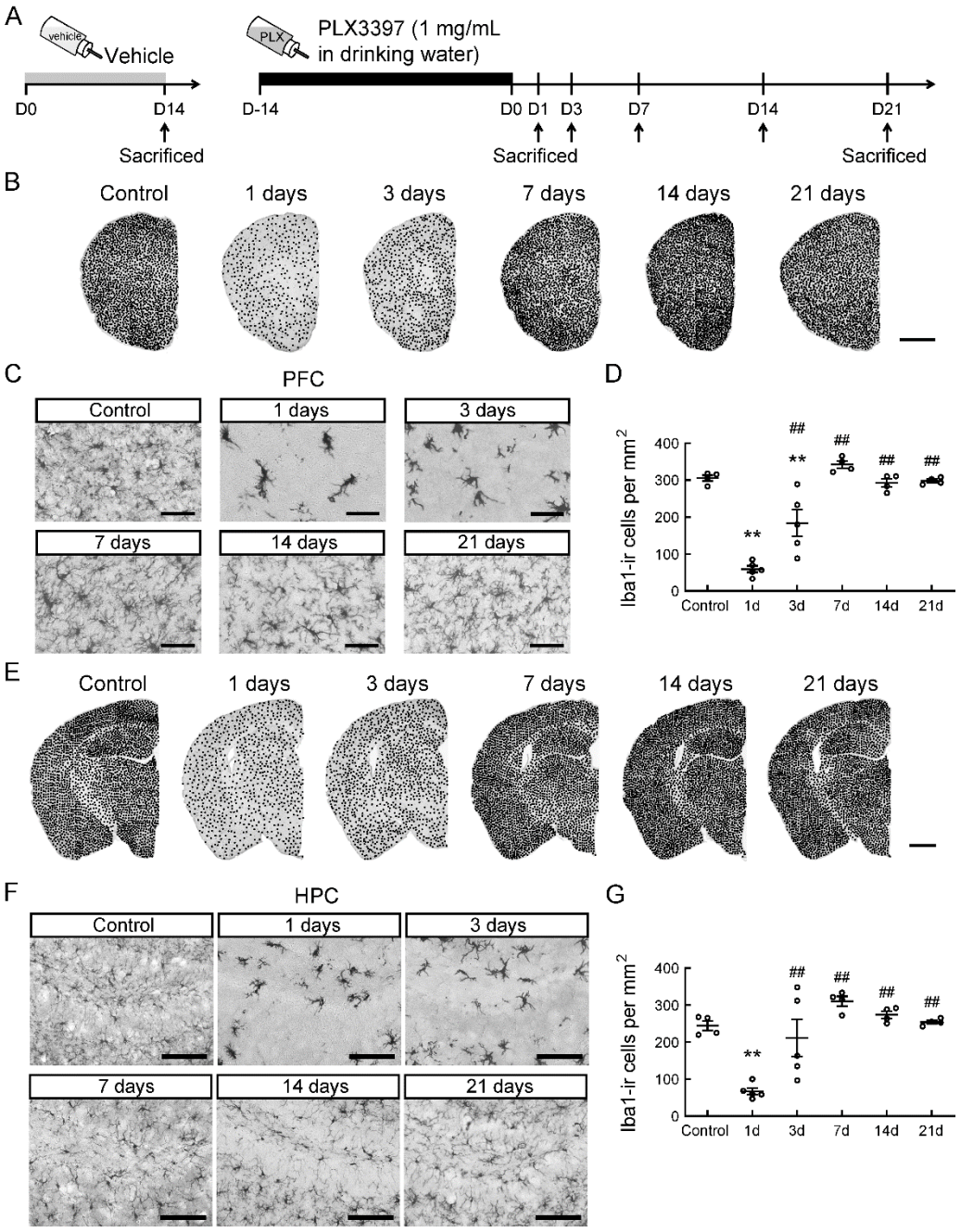
Image processing

All photographs were stored at a size of 1 920×1 080 pixels (219 pixels equals 25 μm). To exclude adjacent microglia or nonspecific immunoreactivity, we sketched the traces and cell bodies manually to obtain skeletonized microglial cell images. This step was conducted using Adobe Illustrator software and a Wacom Intuos CTL-4100 tablet. The skeletonized microglial cell images were then used to quantitatively investigate the branch density and distance from the soma center of the cells using Sholl analysis (Binley et al., 2014). The skeletonized images were also used to calculate microglial density, microglial soma area, total length of microglial processes, and maximum length of microglial processes. To investigate these parameters, we split the skeletonized images into two layers for each cell, one for the traced branches and one for the longest branch. Additionally, a small dot was placed into the trace layer to mark the cell soma center for Sholl analysis. The cell soma sketch was filled with pure black and collected in a single new layer. We then exported these layers from Adobe Illustrator to separate files in JPG format.



Supplementary Figure S1 Microglial morphology after single injection of MK-801 or saline with PLX3397 or vehicle pretreatment, respectively

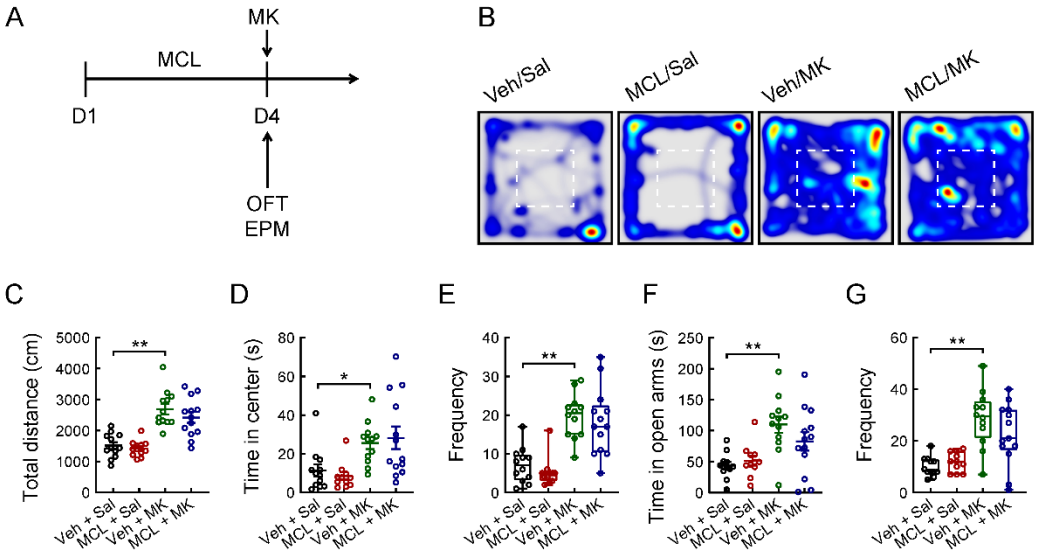
A, D: Quantification of mean number of intersections of microglial processes at distances (in 2 μm increments) from the soma center in the prefrontal cortex (PFC) and hippocampus (HPC). B, E: Quantification of total length of microglial processes. C, F: Quantification of microglial soma area in PFC and HPC of the four groups. Statistical analyses were performed via two-way ANOVA with Bonferroni's *post hoc* test. ***P*<0.01. MK, MK-801; PLX-depl, PLX3397-depletion; Sal, saline; Veh, vehicle.



Supplementary Figure S2 Rapid repopulation and replenishment of newborn microglia in mouse brain after removal of CSF1R inhibitor PLX3397

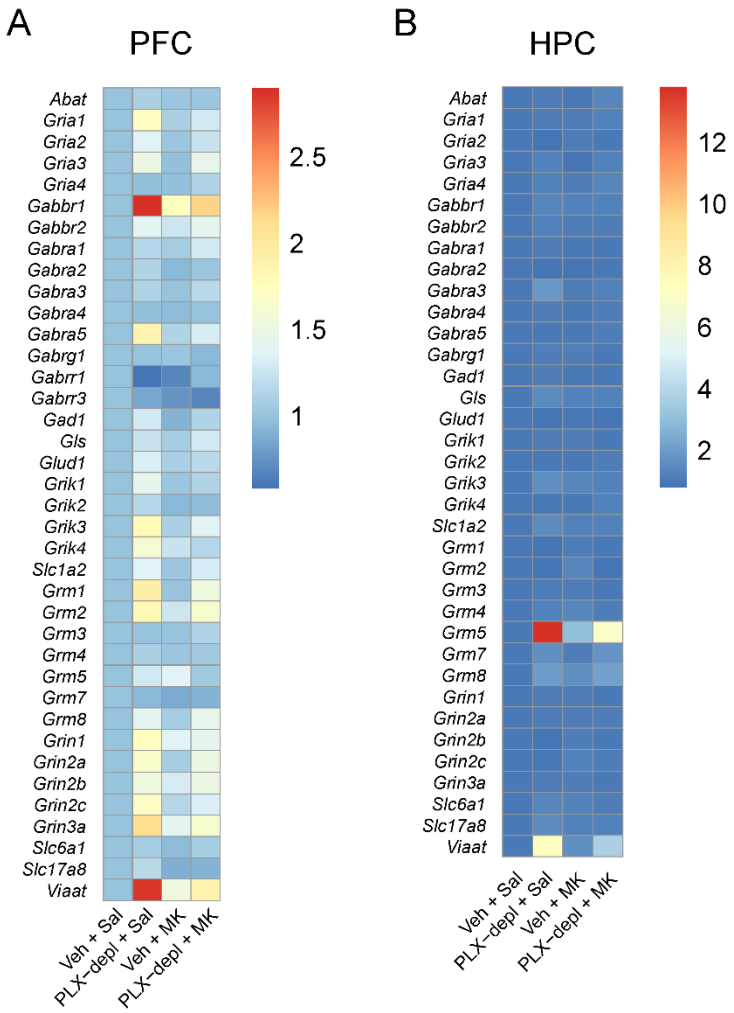
A: Schematic of experimental design. Representative low-magnification and high-magnification photomicrographs illustrating microglial changes (Iba1 immunoreactivity) in PFC (B, C) and HPC (E, F) after PLX3397 (1 mg/mL in drinking water) administration for 14 days to deplete microglia, followed by PLX3397 withdrawal for 1, 3, 7, 14, or 21 days. Control mice were treated with vehicle. Quantification of microglial density in PFC (D) and HPC (G) after PLX3397 withdrawal for 1, 3, 7, 14, or 21 days (n=4–5 for each time point). Statistical analyses were performed via one-way ANOVA with Bonferroni's *post hoc* test. **P<0.01

compared to Control; ##P<0.01 compared to 1 d. Density of black dots represents relative density of Iba1-ir cells in the brain. Each dot represents approximately two Iba1-ir cells. Means and SEM values in D and G are for combined data from two or more independent experiments. Scale bars=1 000 μm in B, E; 50 μm in C; 100 μm in F.



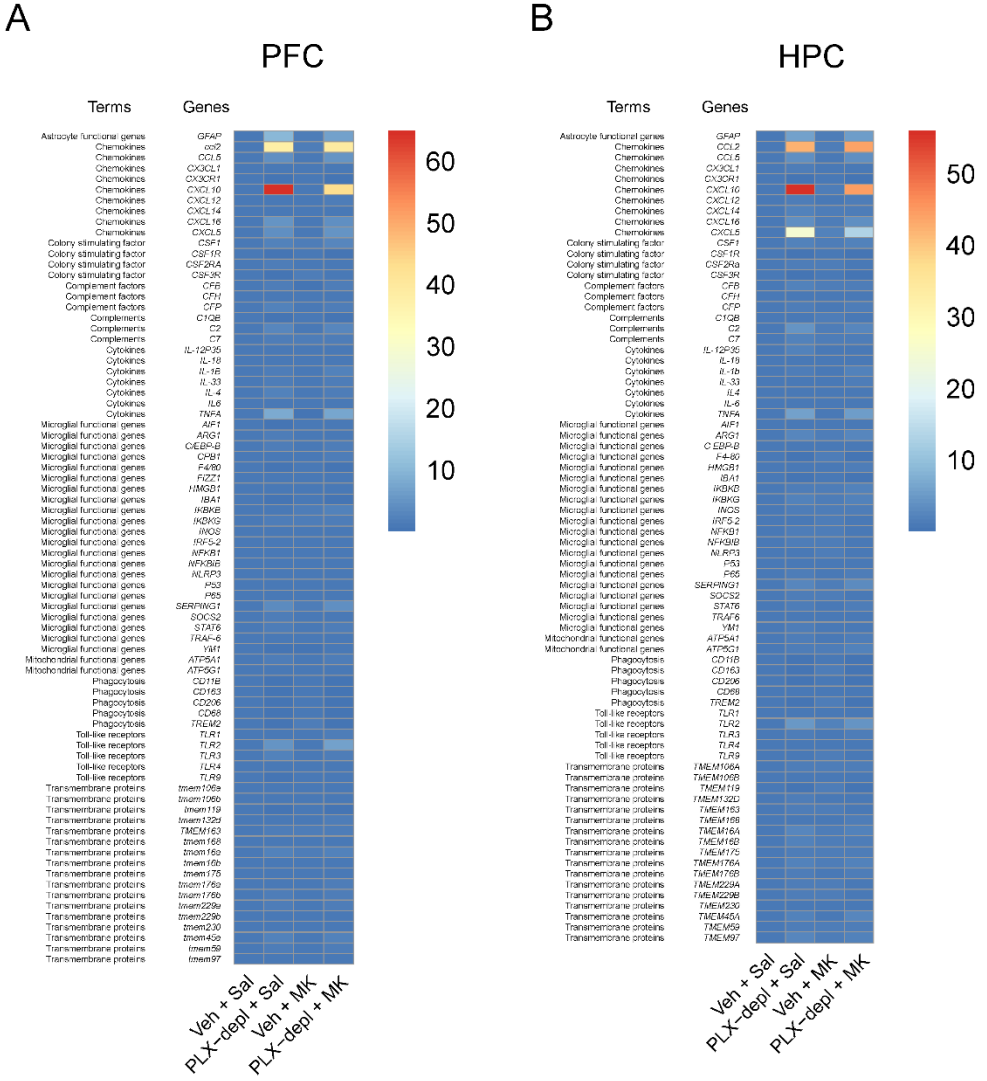
Supplementary Figure S3 Effects of minocycline on MK-801-induced hyperlocomotion in mice

A: Schematic of experimental design. B: Heatmaps showing cumulative duration spent by each group in compartment during the open-field test (OFT). Dashed lines represent central areas. C: Total distance moved by each group (n=11–13/group) in open-field box. D: Time spent by each group in central area during 5 min OFT. E: Comparison of frequency of entries into central area of open-field among four groups after MCL and/or MK administration. F: Time spent in open arms during 5 min elevated plus-maze (EPM) test in four groups. G: Frequency of entries into open arms by each group after MCL and/or MK administration. Statistical analyses were performed via two-way ANOVA with Bonferroni's *post hoc* test (n=48). *P<0.05; **P<0.01. MCL, minocycline. MK, MK-801; Sal, saline; Veh, vehicle.



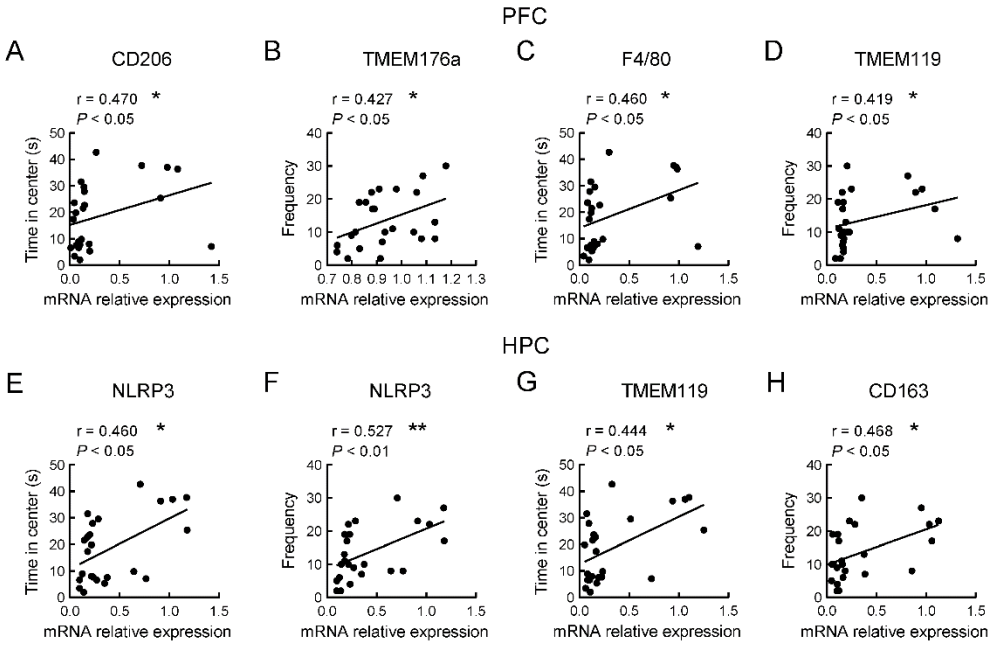
Supplementary Figure S4 Heatmaps showing expression of all candidate glutamate- and GABA-related genes in PFC (A) and HPC (B) after PLX3397 and MK-801 treatment

* Compared to Veh+Sal; *P<0.05; **P<0.01; # compared to Veh+MK; #P<0.05; ##P<0.01. MK, MK-801; PLX-depl, PLX3397-depletion; Sal, saline; Veh, vehicle.



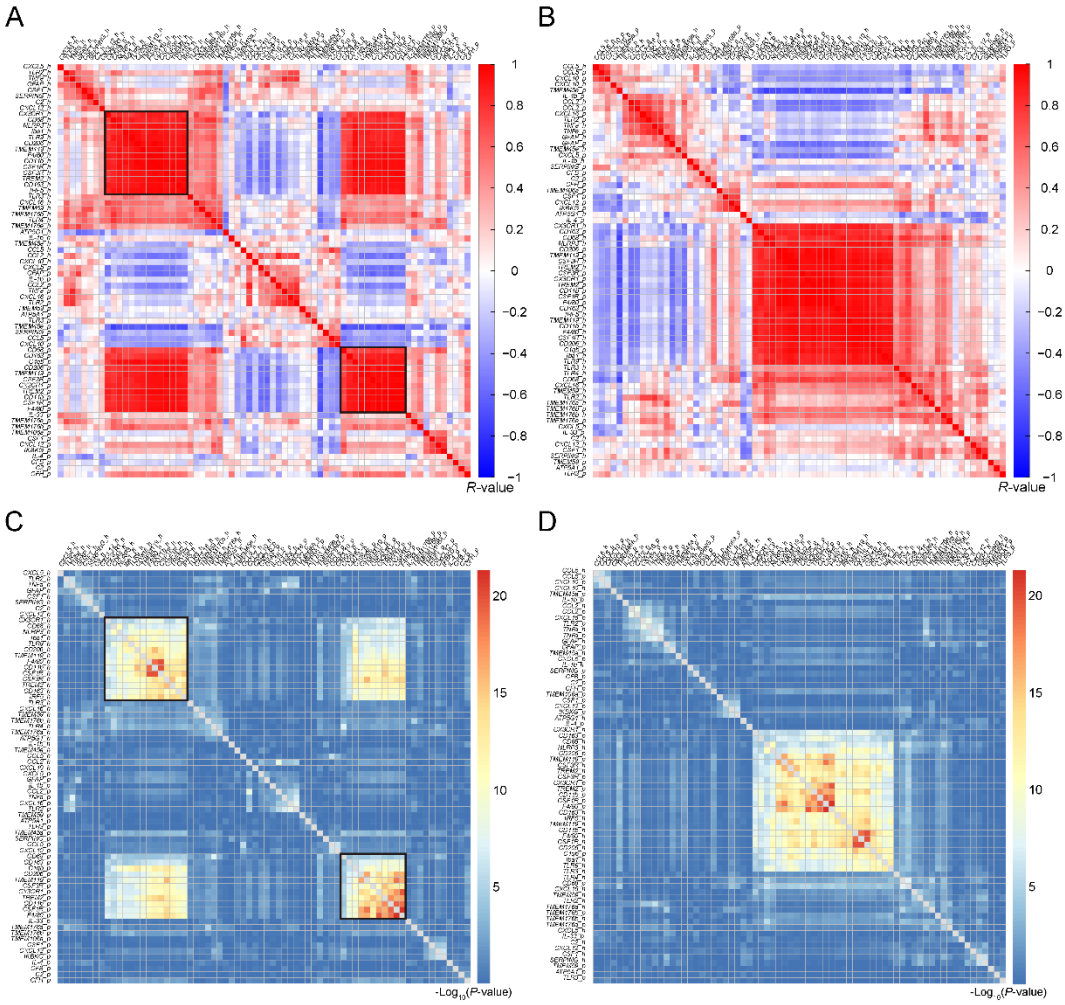
Supplementary Figure S5 Heatmaps showing relative expression of all candidate inflammation-related genes in PFC and HPC after PLX3397 and MK-801 treatment

* Compared to Veh+Sal; **P*<0.05; ***P*<0.01; # compared to Veh+MK; #*P*<0.05; ##*P*<0.01. MK, MK-801; PLX-depl, PLX3397-depletion; Sal, saline; Veh, vehicle.



Supplementary Figure S6 Correlations between inflammation-related gene expression changes in the brain and behaviors during OFT in mice after PLX3397 and MK-801 administration

A-D: Correlation between inflammation-related gene (*CD206*, *TMEM176a*, *F4/80*, and *TMEM119*) expression levels in PFC and anxiolytic-like behaviors in mice. E-H: Correlation between inflammation-related gene (*NLRP3*, *TMEM119*, and *CD163*) expression levels in HPC and behaviors in OFT. Correlation analysis was performed using Spearman correlation (n=24). *P<0.05; **P<0.01.



Supplementary Figure S7 Correlation matrices of differentially expressed inflammation-related genes in PFC and HPC after PLX3397 and MK-801 administration

A-B: Heatmaps showing pairwise correlations among differentially expressed inflammation-related genes in PFC ("_p" suffix) and HPC ("_h" suffix). Color corresponds to Spearman correlation coefficients, with red (blue) indicating positive (negative) correlation (n=24). C-D: Correlation matrices of differentially expressed inflammation-related genes in PFC and HPC. Color scale indicates $-\log_{10}(P\text{-value})$. P-value was calculated using Spearman correlation test with a significance threshold of $P \leq 0.05$ (indicated by dotted line of $-\log_{10}(P\text{-value})=1.3$). Hierarchical clustering was applied to gene expression data from PFC and HPC, respectively (A, C). Hierarchical clustering was applied to whole matrix (B, D). Black boxes indicate those genes that cluster together. Values in A-D are for combined data from two or more independent experiments.

Supplementary Table S1 Primer sequences used for qRT-PCR experiments

Gene name	Primer name	Primer sequence
4-aminobutyrate transaminase	Abat-F	CTGAACACAATCCAGAATGCAGA
	Abat-R	GGTTGTAACCTATGGGCACAG
allograft inflammatory factor 1	AIF1-F	ATCAACAAGCAATTCCTCGATGA
	AIF1-R	CAGCATTCGCTTCAAGGACATA
glutamate receptor, ionotropic, AMPA1 (Gria1)	AMPA1-F	TCCCCAACAATATCCAGATAGGG
	AMPA1-R	AAGCCGCATGTTCCTGTGATT
glutamate receptor, ionotropic, AMPA2 (Gria2)	AMPA2-F	AATGGACGTGTTATGACTCCAGA
	AMPA2-R	CTGACATTCATTCCCATGCCA
glutamate receptor, ionotropic, AMPA3 (Gria3)	AMPA3-F	ACCATCAGCATAGGTGGACTT
	AMPA3-R	ACGTGGTAGTTCAAATGGAAGG
glutamate receptor, ionotropic, AMPA4 (Gria4)	AMPA4-F	GGGAGGTGACTCCAAGGACA
	AMPA4-R	CCAGTGATGGATAACCTGGCT
arginase 1	ARG1-F	CCCGACTTCTGGGACTTCTG
	ARG1-R	AGTAGGTTCCGAAGACTGGGT
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1	ATP5A1-F	TCTCCATGCCTCTAACACTCG
	ATP5A1-R	CCAGGTCAACAGACGTGTCAG
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c1	ATP5G1-F	CCAGAGGCCCCATCTAAGC
	ATP5G1-R	CCCCAGAATGGCATAGGAGAAG
CCAAT/enhancer binding protein, beta	C/EBP-β-F	ACCGGGTTTCGGGACTTGA
	C/EBP-β-R	GTTGCGTAGTCCCGTGTCCA
complement component 1, q subcomponent, beta polypeptide	C1qb-F	ATAAAGGGGGAGAAAGGGCT

	C1qb-R	CGTTGCGTGGCTCATAGTT
complement component 2	C2-F	CGGTGGTAATTTCACCCTCAG
	C2-R	GGTGTGATGTGAGCTAGACCT
complement component 7	C7-F	CAACTGCAAGTGGGACTCCTA
	C7-R	CAGCAACTGAACGCCTTCG
chemokine (C-C motif) ligand 2	CCL2-F	TTAAAAACCTGGATCGGAACCAA
	CCL2-R	GCATTAGCTTCAGATTTACGGGT
chemokine (C-C motif) ligand 5	CCL5-F	ACTCCCTGCTGCTTTGCCTAC
	CCL5-R	GAGGTTCCTTCGAGTGACA
integrin alpha M	CD11b-F	ATGGACGCTGATGGCAATACC
	CD11b-R	TCCCCATTCACGTCTCCCA
cluster of differentiation 163	CD163-F	CCTTGGAAACAGAGACAGGC
	CD163-R	TCCACACGTCCAGAACAGTC
mannose receptor (cluster of differentiation 206)	CD206-F	CTCTGTTCAGCTATTGGACGC
	CD206-R	CGGAATTTCTGGGATTCAGCTTC
cluster of differentiation 68	CD68-F	TGTCTGATCTTGCTAGGACCG
	CD68-R	GAGAGTAACGGCCTTTTTGTGA
complement factor B	CFB-F	GAGCGCAACTCCAGTGCTT
	CFB-R	GAGGGACATAGGTACTCCAGG
complement component factor h	CFH-F	AGGCTCGTGGTCAGAACAAC
	CFH-R	GTTAGACGCCACCCATTTTCC
complement factor properdin	CFP-F	TTCACCCAGTATGAGGAGTCC
	CFP-R	GCTGACCATTGTGGAGACCT
carboxypeptidase B1	CPB1-F	AGGCATGGATTCAACAAGTTGC
	CPB1-R	AGCCTCTCTCACAAACCACTG

colony stimulating factor 1	CSF1-F	GGCTTGGCTTGGGATGATTCT
	CSF1-R	GAGGGTCTGGCAGGTACTC
colony stimulating factor 1 receptor	CSF1R-F	TGTCATCGAGCCTAGTGGC
	CSF1R-R	CGGGAGATTCAGGGTCCAAG
colony stimulating factor 2 receptor, alpha	CSF2RA-F	CTGCTCTTCTCCACGCTACTG
	CSF2RA-R	GAGACTCGCCGGTGTATCC
colony stimulating factor 3 receptor	CSF3R-F	CTGATCTTCTTGCTACTCCCCA
	CSF3R-R	GGTGTAGTTCAAGTGAGGCAG
chemokine (C-X3-C motif) ligand 1	CX3CL1-F	ACGAAATGCGAAATCATGTGC
	CX3CL1-R	CTGTGTCGTCTCCAGGACAA
chemokine (C-X3-C) receptor 1	CX3CR1 -F	GAGTATGACGATTCTGCTGAGG
	CX3CR1 -R	CAGACCGAACGTGAAGACGAG
chemokine (C-X-C motif) ligand 10	CXCL10-F	CCAAGTGCTGCCGTCATTTTC
	CXCL10-R	GGCTCGCAGGGATGATTTCAA
chemokine (C-X-C motif) ligand 12	CXCL12-F	TGCATCAGTGACGGTAAACCA
	CXCL12-R	TTCTTCAGCCGTGCAACAATC
chemokine (C-X-C motif) ligand 14	CXCL14-F	GAAGATGGTTATCGTCACCACC
	CXCL14-R	CGTTCCAGGCATTGTACCACT
chemokine (C-X-C motif) ligand 16	CXCL16-F	CCTTGTCTCTTGCGTTCTTCC
	CXCL16-R	TCCAAAGTACCCTGCGGTATC
chemokine (C-X-C motif) ligand 5	CXCL5-F	GTTCCATCTCGCCATTCATGC
	CXCL5-R	GCGGCTATGACTGAGGAAGG
EGF-like module containing, mucin-like, hormone receptor-like sequence 1 (Emr1)	F4/80-F	TGACTCACCTTGTGGTCCTAA

	F4/80-R	CTTCCCAGAATCCAGTCTTTCC
parasite-induced macrophage novel gene 1 protein	FIZZ1-F	CCAATCCAGCTAACTATCCCTCC
	FIZZ1-R	ACCCAGTAGCAGTCATCCCA
gamma-aminobutyric acid (GABA) B receptor 1	GABBR1-F	ACGTCACCTCGGAAGGTTG
	GABBR1-R	CACAGGCAGGAAATTGATGGC
gamma-aminobutyric acid (GABA) B receptor 2	GABBR2-F	AAGACCCCATAGAGGACATCAA
	GABBR2-R	GGGTGGTACGTGTCTGTGG
gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1	GABRA1-F	AAAAGTCGGGGTCTCTCTGAC
	GABRA1-R	CAGTCGGTCCAAAATTCTTGTGA
gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2	GABRA2-F	GGACCCAGTCAGGTTGGTG
	GABRA2-R	TCCTGGTCTAAGCCGATTATCAT
gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3	GABRA3-F	ATGTGGCACTTTTATGTGACCA
	GABRA3-R	CCCCAGGTTCTTGTCGTCTTG
gamma-aminobutyric acid (GABA) A receptor, subunit alpha 4	GABRA4-F	ACAATGAGACTCACCATAAGTGC
	GABRA4-R	GGCCTTTGGTCCAGGTGTAG
gamma-aminobutyric acid (GABA) A receptor, subunit alpha 5	GABRA5-F	TGACCCAAACCCTCCTTGTCT
	GABRA5-R	GTGATGTTGTCATTGGTCTCGT
gamma-aminobutyric acid (GABA) A receptor, subunit gamma 1	GABRg1-F	TGTGGAGTCAAACTAGAGGAGTG
	GABRg1-R	TTCCCAGATGCAGGGTTAGTA
gamma-aminobutyric acid (GABA) C receptor, subunit rho 1	GABRR1-F	CGAGGAGCACACGACGATG
	GABRR1-R	GTGAAGTCCATGTCAACCTCTG
gamma-aminobutyric acid (GABA) receptor, rho 3	GABRR3-F	TTACCTCAGGCACTATTGGAAGG

	GABRR3-R	CGGGATGTACTCGAAGCATGATA
glutamic acid decarboxylase 1	Gad1-F	CACAGGTCACCCTCGATTTTT
	Gad1-R	ACCATCCAACGATCTCTCTCATC
glial fibrillary acidic protein	GFAP-F	TGGAGGAGGAGATCCAGTTC
	GFAP-R	AGCTGCTCCCGGAGTTCT
glutaminase	Gls-F	CTACAGGATTGCGAACATCTGAT
	Gls-R	ACACCATCTGACGTTGTCTGA
glutamate dehydrogenase 1	Glud1-F	CCCAACTTCTTCAAGATGGTGG
	Glud1-R	AGAGGCTCAACACATGGTTGC
high mobility group box 1	HMGB1-F	GGCGAGCATCCTGGCTTATC
	HMGB1-R	GGCTGCTTGTCATCTGCTG
hypoxanthine guanine phosphoribosyl transferase	HPRT-F	GACCGGTCCCGTCATGC
	HPRT-R	TCATAACCTGGTTCATCATCGC
ionized calcium binding adapter molecule 1	Iba1-F	GGATTTGCAGGGAGGAAAA
	Iba1-R	TGGGATCATCGAGGAATTG
inhibitor of kappaB kinase beta	IKBKB-F	ACAGCCAGGAGATGGTACG
	IKBKB-R	CAGGGTGACTGAGTCGAGAC
inhibitor of kappaB kinase gamma	IKBKG-F	AAGCACCCCTGGAAGAACC
	IKBKG-R	CCTGCTCTGAAGGCAGATGTA
interleukin 12a	IL-12p35-F	ATGACCCTGTGCCTTGGTAG
	IL-12p35-R	GATTCTGAAGTGCTGCGTTG
interleukin 18	IL-18-F	AGAAGACTCTTGCGTCAACTTC
	IL-18-R	AACGAAGAGAACTTGGTCATTTAT
interleukin 1 beta	IL-1β-F	GATCCACACTCTCCAGCTGCA
	IL-1β-R	CAACCAACAAGTGATATTCTCCATG

interleukin 33	IL-33-F	TCCAACTCCAAGATTTCCCCG
	IL-33-R	CATGCAGTAGACATGGCAGAA
interleukin 4	IL-4-F	GTCTGTAGGGCTTCCAAGGT
	IL-4-R	CGAAAGAGTCTCTGCAGCTC
interleukin 6	IL-6-F	TAGTCCTTCCTACCCCAATTTCC
	IL-6-R	TTGGTCCTTAGCCACTCCTTC
inducible nitric oxide synthase	iNOS-F	TGACGGCAAACATGACTTCAG
	iNOS-R	GCCATCGGGCATCTGGTA
interferon regulatory factor 5	IRF5-F	AGAGACAGGGAAGTACACTGAAG
	IRF5-R	TGGAAGTCACGGCTTTTGTTAAG
glutamate receptor, ionotropic, kainate 1 (Grik1)	KA1-F	TCACACCCTACGAGTGGTATAAC
	KA1-R	AGCTCCAACGCCAAACCAG
glutamate receptor, ionotropic, kainate 2 (Grik2)	KA2-F	CAGCGTCGGCTCAAACATAAG
	KA2-R	GGTTTCTTTACCTGGCAACCTT
glutamate receptor, ionotropic, kainate 3 (Grik3)	KA3-F	AGGTCCTAATGTCACTGACTCTC
	KA3-R	TGCCATAAAGGGTCCTATCAGAC
glutamate receptor, ionotropic, kainate 4 (Grik4)	KA4-F	CCCTGAGGATTGCTGCTATCT
	KA4-R	CACCCTTGGGGAGGATCTGA
solute carrier family 1 (glial high affinity glutamate transporter) (Slc1a2)	mGLT1-F	GCACGAGAGCTATGGTGTATTAC
	mGLT1-R	GTTTGGGATTACCTGGGTGGA
glutamate receptor, metabotropic 1 (Grm1)	mGluR1-F	TGGAACAGAGCATTGAGTTCATC
	mGluR1-R	CAATAGGCTTCTTAGTCCTGCC
glutamate receptor, metabotropic 2 (Grm2)	mGluR2-F	GCTCCCACAGCTATCACCG
	mGluR2-R	TCATAACGGGACTTGTCGCTC
glutamate receptor, metabotropic 3 (Grm3)	mGluR3-F	CTGGAGGCCATGTTGTTTGC

	mGluR3-R	CATCCACTTTAGTCAACGATGCT
glutamate receptor, metabotropic 4 (Grm4)	mGluR4-F	CCCATACCCATTGTCAAGTTGG
	mGluR4-R	TGTAGCGCACAAAAGTGACCA
glutamate receptor, metabotropic 5 (Grm5)	mGluR5-F	ACGACCATGACGACCTTCG
	mGluR5-R	GGCAGGTGATACCCCTGTC
glutamate receptor, metabotropic 7 (Grm7)	mGluR7-F	ACACGGATCGCAAATGCAC
	mGluR7-R	CTCCCCGGTAGTCAGCACA
glutamate receptor, metabotropic 8 (Grm8)	mGluR8-F	ATGGTTTGTGAGGGAAAGCG
	mGluR8-R	GAATGGGCATACTCCTGGCT
nuclear factor of kappa light polypeptide gene enhancer in B cells 1	NFKB1-F	ATGGCAGACGATGATCCCTAC
	NFKB1-R	TGTTGACAGTGGTATTTCTGGTG
nuclear factor of kappa light polypeptide gene enhancer in B cells (NF-kB) inhibitor, beta	NFKBIB-F	GCGGATGCCGATGAATGGT
	NFKBIB-R	TGACGTAGCCAAAGACTAAGGG
NLR family, pyrin domain containing 3	NLRP3-F	ATTACCCGCCCGAGAAAGG
	NLRP3-R	TCGCAGCAAAGATCCACACAG
glutamate receptor, ionotropic, NMDA1 (zeta 1) (Grin1)	NMDA1-F	ATGCACCTGCTGACATTCG
	NMDA1-R	TATTGGCCTGGTTTACTGCCT
glutamate receptor, ionotropic, NMDA2A (epsilon 1) (Grin2a)	NMDA2A-F	ACGTGACAGAACGCGAACTT
	NMDA2A-R	TCAGTGCGGTTCATCAATAACG
glutamate receptor, ionotropic, NMDA2B (epsilon 2) (Grin2b)	NMDA2B-F	GCCATGAACGAGACTGACCC
	NMDA2B-R	GCTTCCTGGTCCGTGTCATC
glutamate receptor, ionotropic, NMDA2C (epsilon 3) (Grin2c)	NMDA2C-F	GGGATCTGCCATAACGAGAAG
	NMDA2C-R	GCACTGAGTGTCGAAGTTTCCA

glutamate receptor ionotropic, NMDA3A (Grin3a)	NMDA3A-F	AGAGCCAGGGCGAAATGATG
	NMDA3A-R	GGAAACTCGTGGCGCACTA
tumor protein p53	p53-F	GCGTAAACGCTTCGAGATGTT
	p53-R	TTTTTATGGCGGGAAGTAGACTG
nuclear factor NF-kappa-B p65 subunit	p65-F	GATTGAAGAGAAGCGCAAAA
	p65-R	CAGAAGTTGAGTTTCGGGTA
serine peptidase inhibitor, clade G, member 1	SERPING1-F	TAGAGCCTTCTCAGATCCCGA
	SERPING1-R	ACTCGTTGGCTACTTTACCCA
solute carrier family 6 (neurotransmitter transporter), member 1 (Slc6a1)	SLC6-F	GAAAGCTGTCTGATTCTGAGGTG
	SLC6-R	AGCAAACGATGATGGAGTCCC
suppressor of cytokine signaling 2	SOCS2-F	AGTTCGCATTCAGACTACCTACT
	SOCS2-R	TGGTACTCAATCCGCAGGTTAG
signal transducer and activator of transcription 6	STAT6-F	CTCTGTGGGGCCTAATTTCCA
	STAT6-R	GCATCTGAACCGACCAGGAAC
toll-like receptor 1	TLR1-F	TGAGGGTCCTGATAATGTCCTAC
	TLR1-R	AGAGGTCCAAATGCTTGAGGC
toll-like receptor 2	TLR2-F	GCAAACGCTGTTCTGCTCAG
	TLR2-R	AGGCGTCTCCCTCTATTGTATT
toll-like receptor 3	TLR3-F	GTGAGATACAACGTAGCTGACTG
	TLR3-R	TCCTGCATCCAAGATAGCAAGT
toll-like receptor 4	TLR4-F	ACTGTTCTTCTCCTGCCTGACA
	TLR4-R	GGACTTTGCTGAGTTTCTGATCC
toll-like receptor 9	TLR9-F	ATGGTTCTCCGTCGAAGGACT

	TLR9-R	GAGGCTTCAGCTCACAGGG
transmembrane protein 106a	Tmem106a-F	AGCTCACCTCTCGGAAGGAT
	Tmem106a-R	AGTCACAAAGCTGGAACTAGC
transmembrane protein 106b	Tmem106b-F	ATGGCGTCTGTGTTTGTCTG
	Tmem106b-R	CGTAGCTGACATAGGCTGATTTT
transmembrane protein 119	Tmem119-F	CCTACTCTGTGTCACTCCCG
	Tmem119-R	CACGTACTGCCGGAAGAAATC
transmembrane protein 132d	Tmem132d-F	CCGTGCTCATCAGCCTAGC
	Tmem132d-R	GGTGACCGGGAGGTAGGTAG
transmembrane protein 163	Tmem163-F	GGGTTGGAAGACCGAGGTTTA
	Tmem163-R	GCCAGGGTGACAATAATGGACA
transmembrane protein 168	Tmem168-F	TCACTGCGATACTGTGTTAGTCA
	Tmem168-R	GCCACAAGTAAGTTGATCCTGG
transmembrane protein 16a	Tmem16a-F	CCCGTGCCAGTCACCTTTTT
	Tmem16a-R	TCATCTGCTTCCGTTTCCAGT
transmembrane protein 16b	Tmem16b-F	TTTATGATTGCCCTGACGTTCTC
	Tmem16b-R	GAGGTTGATGATGACTGCTGTT
transmembrane protein 175	Tmem175-F	TCCCCTTGTCATACCTGCTGA
	Tmem175-R	AGACTCCCTTTGGCCCATCA
transmembrane protein 176a	Tmem176a-F	GCCGGATGCTCATTGCTAAG
	Tmem176a-R	ATGGCCTATGTAGAGGGTTCC
transmembrane protein 176b	Tmem176b-F	CCAGTCCGCTCACATCAGC

	Tmem176b-R	CTGGGTCACCCCTAGAGACAG
transmembrane protein 229a	Tmem229a-F	GCCTCTACTTCTACGGGATGC
	Tmem229a-R	GGTAGGGTGAAGAGAAACCCA
transmembrane protein 229b	Tmem229b-F	ATGCTATCCACGGCTACTTCT
	Tmem229b-R	TGGAGGTGCCATAGATGAAGA
transmembrane protein 230	Tmem230-F	CTCCCCAGCAGTAAAGTCAAAT
	Tmem230-R	ACGGTAGCAAGGGCAATGG
transmembrane protein 45a	Tmem45a-F	TGGGCTTTTGGTGGACTATGA
	Tmem45a-R	CCAGCTATACCAGTGAGAGACA
transmembrane protein 59	Tmem59-F	CGCTGCTGCTGTTGACTATG
	Tmem59-R	GTAGGTGTGCAAGGGGTAGG
transmembrane protein 97	Tmem97-F	TCTACTTCGTCTCGCACATCC
	Tmem97-R	GAAGGACTTGAACCACACTGG
tumor necrosis factor alpha	TNFα-F	AATGGCCTCCCTCTCATCAGT
	TNFα-R	CTACAGGCTTGTCACTCGAA
tumor necrosis factor receptor-associated factor 6	TRAF6-F	AAAGCGAGAGATTCTTTCCCTG
	TRAF-6-R	ACTGGGGACAATTCACTAGAGC
triggering receptor expressed on myeloid cells 2	TREM2-F	CTGGAACCGTCACCATCACTC
	TREM2-R	CGAAACTCGATGACTCCTCGG
vesicular glutamate transporter-3 (Slc17a8)	VGLUT3-F	AGAATGCCGTGGGAGACTC
	VGLUT3-R	CAGTCACAGATGTACCGCTTG
vasicular inhibitory amino acid transporter	VIAAT-F	ACCTCCGTGTCCAACAAGTC
	VIAAT-R	CAAAGTCGAGATCGTCGCAGT

secretory protein precursor	Ym1-F	CAGGTCTGGCAATTCTTCTGAA
	Ym1-R	GTCTTGCTCATGTGTGTAAGTGA

References

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