

SUPPLEMENTARY INFORMATION

Microglia Transcriptional Profiling in Major Depressive Disorder Shows Inhibition of Cortical Gray Matter Microglia

Scheepstra *et al.*

Supplementary Table 1. List of donors used for RNA sequencing of microglia isolated from control or MDD GM or WM.

| Donor | Region | Diagnosis | Sex | Age | PMD | pH CSF | Cause of death | RQN |
|-------|--------|-----------|-----|-----|-------|--------|--|-----|
| 1 | CC, OC | MDD | m | 68 | 8:55 | 6.8 | sudden death (pneumonia or cardiac arrest) | 4.8 |
| 2 | CC, OC | control | f | 78 | 7:10 | 6.3 | euthanasia for somatic disease (infarction) | 5.5 |
| 3 | CC | MDD | f | 88 | 10:00 | 6.3 | burns, dehydration | 4.7 |
| 4 | CC, OC | control | m | 70 | 8:45 | 6.4 | pharyngeal cancers | 6.2 |
| 5 | CC, OC | MDD | m | 47 | 5:55 | 6.7 | euthanasia for psychiatric disorder | 5.8 |
| 6 | CC, OC | control | m | 68 | 5:50 | 6.5 | cancer | 5.1 |
| 7 | CC, OC | MDD | m | 58 | 4:30 | 6.8 | euthanasia for psychiatric disorder | 7.8 |
| 8 | CC, OC | control | m | 89 | 8:12 | 6.6 | heart failure | 6.6 |
| 9 | CC, OC | control | f | 84 | 7:40 | 7.5 | sepsis, terminal renal insufficiency | 5.0 |
| 10 | CC, OC | control | m | 83 | 5:05 | 7.1 | euthanasia for somatic disease (urothelial carcinoma) | 5.5 |
| 11 | CC, OC | MDD | f | 68 | 6:25 | 6.3 | euthanasia for somatic disease (colon carcinoma) | 4.5 |
| 12 | CC, OC | MDD | f | 69 | 6:55 | 6.3 | congestive heart failure | 4.5 |
| 13 | CC, OC | MDD | f | 77 | 8:40 | 6.8 | euthanasia for psychiatric disorder | 5.9 |
| 14 | CC, OC | MDD | m | 50 | 9:40 | 6.8 | euthanasia for psychiatric disorder | 7.1 |
| 15 | CC, OC | control | f | 60 | 5:30 | 7.1 | euthanasia for somatic disease (mamma carcinoma) | 6.8 |
| 16 | CC, OC | MDD | f | 67 | 8:40 | 7.1 | euthanasia for psychiatric disorder | 4.3 |
| 17 | CC, OC | MDD | m | 48 | 12:45 | 6.8 | euthanasia for psychiatric disorder | 4.2 |
| 18 | OC | control | m | 80 | 9:30 | n/a | respiratory failure due to traumatic cervical paraplegia | 3.9 |
| 19 | CC, OC | MDD | f | 85 | 4:30 | 6.9 | euthanasia for somatic disease (thalamus infarction) | 6.2 |
| 20 | CC, OC | MDD | m | 61 | 5:45 | n/a | euthanasia for somatic disease (multiple infarctions) | 6.2 |
| 21 | CC, OC | control | f | 83 | 6:50 | 6.8 | euthanasia for somatic disease (multi morbidity) | 6.2 |
| 22 | CC, OC | control | f | 55 | 7:30 | n/a | euthanasia for somatic disease (severe pain) | 7.3 |
| 23 | OC | MDD | f | 43 | 11:20 | n/a | suicide | 5.5 |

Age: age at death (years), PMD: post-mortem delay (hours), CSF: cerebrospinal fluid, CC: corpus callosum (WM), OC: occipital cortex (GM), MDD: major depressive disorder, f: female, m: male, n/a: data not available, RQN: RNA quality number.

Supplementary Table 2. List of donors used for additional characterization of microglia from control or MDD GM; RT-qPCR, IHC or isolation of synaptosomes from fresh-frozen GM tissue.

| Donor | Diagnosis | Sex | Age | PMD | pH CSF | Cause of death | Application |
|-------|-----------|-----|-----|--------|--------|--|----------------------------|
| 24 | control | f | 81 | 6:40 | 7.2 | euthanasia for somatic disease | RT-qPCR, synaptosomes |
| 25 | control | m | 84 | 5:35 | 7.0 | heart failure | synaptosomes |
| 26 | MDD | m | 88 | 6:37 | 6.3 | multiple epileptic seizures | RT-qPCR |
| 27 | MDD | f | 93 | 4:20 | 6.8 | pneumonia | RT-qPCR, IHC, synaptosomes |
| 28 | control | m | 88 | 4:43 | 6.2 | gastro-intestinal bleeding | RT-qPCR, synaptosomes |
| 29 | MDD | f | 83 | 4:05 | 6.8 | euthanasia for somatic disease | RT-qPCR, synaptosomes |
| 30 | control | m | 83 | 5:45 | 6.4 | pneumonia | RT-qPCR, synaptosomes |
| 31 | MDD | m | 83 | 10:40 | 6.5 | acute heart failure | RT-qPCR, synaptosomes |
| 32 | control | f | 78 | 4:35 | 6.4 | bronchopneumonia | RT-qPCR, synaptosomes |
| 33 | control | m | 90 | 5:45 | 6.4 | unknown | RT-qPCR, synaptosomes |
| 34 | MDD | f | 73 | 5:45 | 6.7 | euthanasia for somatic disease | RT-qPCR, synaptosomes |
| 35 | control | m | 80 | 4:25 | 6.6 | euthanasia for somatic disease | RT-qPCR, synaptosomes |
| 36 | control | m | 89 | 6:50 | 6.2 | urosepsis | RT-qPCR, synaptosomes |
| 37 | MDD | m | 89 | 4:35 | 6.7 | metastasized prostate carcinoma | RT-qPCR, synaptosomes |
| 38 | MDD | m | 68 | 13:05 | 6.8 | sudden death possibly related to panlobular emphysema, pneumonia or cardiac arrest | RT-qPCR, IHC, synaptosomes |
| 39 | control | f | 78 | 7:10 | 6.3 | euthanasia for somatic disease | RT-qPCR, synaptosomes |
| 40 | control | f | 60 | 8:10 | 6.6 | metastasized mammary carcinoma | RT-qPCR, synaptosomes |
| 41 | control | f | 76 | 4:45 | 6.4 | adenocarcinoma | RT-qPCR, synaptosomes |
| 42 | MDD | f | 66 | 7:55 | n/a | euthanasia for psychiatric disorder | RT-qPCR, synaptosomes |
| 43 | control | m | 73 | 8:00 | 5.4 | invasive fungal infection and bacterial pneumonia | RT-qPCR |
| 44 | control | f | 75 | 9:10 | 6.6 | euthanasia for somatic disease | RT-qPCR, synaptosomes |
| 45 | MDD | m | 69 | 4:40 | 6.6 | multiple organ failure | RT-qPCR, synaptosomes |
| 46 | MDD | f | 88 | 10:00 | 6.3 | burns, dehydration | RT-qPCR, synaptosomes |
| 47 | MDD | f | 69 | 6:55 | 6.3 | congestive heart failure | RT-qPCR, IHC, synaptosomes |
| 48 | MDD | m | 69 | 8:00 | 6.7 | palliative sedation/cardiac decompensation | RT-qPCR |
| 49 | MDD | m | 48 | 6:10 | 6.8 | euthanasia for psychiatric disorder | IHC, synaptosomes |
| 50 | control | m | 49 | <12:40 | n/a | sudden death | IHC |
| 51 | control | f | 61 | 05:15 | n/a | glioblastoma | IHC |
| 52 | control | m | 49 | 09:50 | n/a | sudden death | IHC |
| 53 | control | f | 41 | 13:30 | n/a | lung bleeding | IHC |
| 54 | control | f | 73 | 13:35 | 6.3 | respiratory insufficiency | IHC |
| 55 | MDD | f | 84 | 08:45 | 6.0 | cachexia | IHC |
| 56 | control | f | 73 | 07:45 | n/a | palliative sedation | IHC |
| 57 | MDD | f | 47 | 06:05 | n/a | euthanasia for psychiatric disorder | IHC |
| 58 | control | f | 95 | 05:40 | 6.5 | cachexia and dehydration | IHC |
| 59 | control | m | 73 | 04:25 | 7.0 | pneumonia | IHC |
| 60 | MDD | m | 47 | 05:20 | 6.7 | euthanasia for psychiatric disorder | IHC |
| 61 | control | m | 68 | 05:50 | 6.5 | cancer | IHC |
| 62 | MDD | m | 58 | 04:30 | 6.8 | physician-assisted suicide (depression) | IHC |

| | | | | | | | |
|----|---------|---|----|-------|-----|--------------------------------|-----|
| 63 | control | f | 84 | 07:40 | 7.5 | sepsis | IHC |
| 64 | MDD | f | 68 | 06:20 | 6.3 | euthanasia for colon carcinoma | IHC |
| 65 | control | f | 81 | 05:15 | n/a | palliative sedation | IHC |
| 66 | MDD | f | 74 | 06:25 | 7.0 | euthanasia for crohn's disease | IHC |
| 67 | MDD | m | 91 | 06:10 | 6.4 | pneumonia | IHC |
| 68 | MDD | f | 84 | 05:20 | 6.4 | metastatic breast cancer | IHC |
| 69 | control | m | 89 | 03:05 | 6.7 | euthanasia for somatic disease | IHC |

Age: age at death (years), PMD: post-mortem delay (hours), CSF: cerebrospinal fluid, m: male, f: female, n/a: data not available, IHC: immunohistochemical staining.

Supplementary Table 3. List of primers used for RT-qPCR.

| Gene | Forward sequence (5'–3') | Reverse sequence (5'–3') |
|--------------|--------------------------|--------------------------|
| <i>CD47</i> | CTGCTCACCAATACCCTGTAAA | CGGGAACATCTGATGGACTAAG |
| <i>CD200</i> | CCATTCTCCAAAGGACCTGAA | GAGTAGCTCAGATGGCAGTAAA |
| <i>EF1A</i> | AAGCTGGAAGATGGCCCTAAA | AAGCGACCCAAAGGTGGAT |
| <i>GAPDH</i> | TGCCACCACCAACTGCTTAGC | GGCATGGACTGTGGTCATGA |

Supplementary Table 4. Complete list of DE genes as determined by RNA sequencing of microglia isolated from control or MDD GM. Negative log₂ (fold change) values indicate downregulation of a gene in MDD microglia compared to control microglia.

| Gene | Description | log ₂ (fold change) | p-value | Adjusted p-value |
|-------------------|--|--------------------------------|----------|------------------|
| <i>CD163</i> | CD163 molecule | -4.033276639 | 1.71E-09 | 2.99E-05 |
| <i>BIRC5</i> | baculoviral IAP repeat containing 5 | -4.024832553 | 5.89E-05 | 0.01880208 |
| <i>ADAMTS2</i> | ADAM metalloproteinase with thrombospondin type 1 motif 2 | -3.998384782 | 8.35E-06 | 0.00813844 |
| <i>HJURP</i> | Holliday junction recognition protein | -3.949108787 | 0.000151 | 0.0327919 |
| <i>MKI67</i> | marker of proliferation Ki-67 | -3.855385849 | 1.37E-06 | 0.00239659 |
| <i>TOP2A</i> | topoisomerase (DNA) II alpha | -3.660150714 | 2.74E-05 | 0.01300933 |
| <i>CD163L1</i> | CD163 molecule like 1 | -3.659046006 | 1.77E-07 | 0.00077563 |
| <i>TBC1D8</i> | TBC1 domain family member 8 | -3.436749801 | 1.06E-08 | 9.32E-05 |
| <i>ERC2</i> | ELKS/RAB6-interacting/CAST family member 2 | -3.315667791 | 5.71E-07 | 0.00118824 |
| <i>FAM20A</i> | FAM20A, Golgi-associated secretory pathway pseudokinase | -3.081153366 | 4.80E-07 | 0.00118824 |
| <i>TICRR</i> | TOPBP1 interacting checkpoint and replication regulator | -3.068774817 | 0.000107 | 0.02706959 |
| <i>MAP3K6</i> | mitogen-activated protein kinase kinase kinase 6 | -2.984372851 | 1.95E-05 | 0.01069706 |
| <i>SLAMF8</i> | SLAM family member 8 | -2.902361547 | 4.69E-05 | 0.01684365 |
| <i>SH3PXD2B</i> | SH3 and PX domains 2B | -2.891863085 | 3.46E-05 | 0.01412911 |
| <i>PLAC8</i> | placenta specific 8 | -2.817148942 | 6.76E-06 | 0.00813844 |
| <i>ST14</i> | suppression of tumorigenicity 14 | -2.811994832 | 5.20E-07 | 0.00118824 |
| <i>SPC24</i> | SPC24, NDC80 kinetochore complex component | -2.787138134 | 0.000108 | 0.02706959 |
| <i>PPA1</i> | pyrophosphatase (inorganic) 1 | -2.784179033 | 0.000127 | 0.02942714 |
| <i>AL136303.1</i> | miscellaneous small RNA AL136303.1 | -2.673872807 | 1.48E-05 | 0.00996499 |
| <i>CASC5</i> | kinetochore scaffold 1 | -2.595230112 | 8.27E-06 | 0.00813844 |
| <i>GPR82</i> | G protein-coupled receptor 82 | -2.531714906 | 2.86E-07 | 0.00100251 |
| <i>TMEM163</i> | transmembrane protein 163 | -2.464765933 | 6.67E-05 | 0.02069323 |
| <i>MYO1G</i> | myosin IG | -2.290296802 | 5.24E-05 | 0.01711641 |
| <i>EMR2</i> | adhesion G protein-coupled receptor E2 | -2.072679207 | 2.94E-05 | 0.0135946 |
| <i>CDHR1</i> | cadherin related family member 1 | -2.042381 | 3.22E-05 | 0.0141149 |
| <i>RNASE2</i> | ribonuclease A family member 2 | -1.914944582 | 1.94E-05 | 0.01069706 |
| <i>LDHAP4</i> | lactate dehydrogenase A pseudogene 4 | -1.914371688 | 1.79E-05 | 0.01069706 |
| <i>SLC11A1</i> | solute carrier family 11 member 1 | -1.903586134 | 2.15E-08 | 0.00012584 |
| <i>FLVCR2</i> | feline leukemia virus subgroup C cellular receptor family member 2 | -1.851283337 | 8.98E-06 | 0.00829011 |
| <i>PIM1</i> | Pim-1 proto-oncogene, serine/threonine kinase | -1.812879567 | 5.27E-05 | 0.01711641 |
| <i>JAK3</i> | Janus kinase 3 | -1.776812687 | 0.000124 | 0.02934378 |
| <i>LAP3P2</i> | leucine aminopeptidase 3 pseudogene 2 | -1.616978229 | 2.24E-05 | 0.01158683 |
| <i>ECHDC3</i> | enoyl-CoA hydratase domain containing 3 | -1.605224756 | 1.13E-05 | 0.00898407 |
| <i>SPP1</i> | secreted phosphoprotein 1 | -1.597525974 | 6.09E-07 | 0.00118824 |
| <i>LMNB1</i> | lamin B1 | -1.562844706 | 4.89E-05 | 0.01684365 |
| <i>CENPF</i> | centromere protein F | -1.545739674 | 0.000132 | 0.03019859 |
| <i>FAM157A</i> | family with sequence similarity 157 member A | -1.484249279 | 0.000236 | 0.04596507 |
| <i>AC097382.5</i> | long non-coding RNA AC097382.5 | -1.431426649 | 0.000224 | 0.04469214 |
| <i>SPATA6</i> | spermatogenesis-associated 6 | -1.391270765 | 2.73E-06 | 0.00435265 |
| <i>SCO2</i> | SCO2, cytochrome c oxidase assembly protein | -1.38097554 | 4.78E-05 | 0.01684365 |
| <i>CMAHP</i> | cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene | -1.375687563 | 8.44E-05 | 0.02415648 |

| | | | | |
|------------------|--|--------------|----------|------------|
| <i>CD93</i> | CD93 molecule | -1.365055369 | 3.89E-05 | 0.01550849 |
| <i>PSTPIP2</i> | proline-serine-threonine phosphatase-interacting protein 2 | -1.321644311 | 4.09E-05 | 0.01579452 |
| <i>FPR1</i> | formyl peptide receptor 1 | -1.303164108 | 1.01E-05 | 0.00884333 |
| <i>MPC2</i> | mitochondrial pyruvate carrier 2 | -1.292970072 | 7.54E-06 | 0.00813844 |
| <i>DSE</i> | dermatan sulfate epimerase | -1.268020241 | 0.000117 | 0.02820328 |
| <i>SCIN</i> | scinderin | -1.251171981 | 3.32E-05 | 0.01412911 |
| <i>SERPINA1</i> | serpin family A member 1 | -1.244392579 | 7.95E-06 | 0.00813844 |
| <i>FCGR1C</i> | Fc fragment of IgG receptor 1c | -1.242888014 | 2.54E-05 | 0.01235894 |
| <i>TMED8</i> | transmembrane p24 trafficking protein family member 8 | -1.241212519 | 1.06E-05 | 0.00884333 |
| <i>LAP3</i> | leucine aminopeptidase 3 | -1.219554183 | 6.92E-05 | 0.02095073 |
| <i>MAP3K8</i> | mitogen-activated protein kinase kinase kinase 8 | -1.212883362 | 2.02E-05 | 0.01074965 |
| <i>PTPN2</i> | protein tyrosine phosphatase, non-receptor type 2 | -1.197039435 | 1.29E-05 | 0.00946874 |
| <i>FCGR3A</i> | Fc fragment of IgG receptor IIIa | -1.156241319 | 7.79E-06 | 0.00813844 |
| <i>TMEM176A</i> | transmembrane protein 176A | -1.133125006 | 0.000144 | 0.03166717 |
| <i>CD14</i> | CD14 molecule | -1.127194451 | 0.000161 | 0.03433271 |
| <i>ATP2B4</i> | ATPase plasma membrane Ca ²⁺ transporting 4 | -1.108357516 | 1.22E-05 | 0.00927314 |
| <i>IKZF2</i> | IKAROS family zinc finger 2 | -1.084739226 | 3.43E-05 | 0.01412911 |
| <i>NLRC5</i> | NLR family CARD domain containing 5 | -1.067884159 | 8.53E-05 | 0.02415648 |
| <i>TLR2</i> | Toll-like receptor 2 | -1.059732048 | 3.13E-05 | 0.01410614 |
| <i>TMEM2</i> | transmembrane protein 2 | -1.051314799 | 0.00014 | 0.03146604 |
| <i>SNX20</i> | sorting nexin 20 | -1.04059865 | 0.000262 | 0.04991326 |
| <i>FCGR1A</i> | Fc fragment of IgG receptor 1a | -1.037044615 | 1.78E-05 | 0.01069706 |
| <i>C1QB</i> | complement C1q B chain | -1.036530996 | 4.14E-05 | 0.01579452 |
| <i>ACER3</i> | alkaline ceramidase 3 | -1.001508523 | 0.000186 | 0.03786151 |
| <i>VSIG4</i> | V-set and immunoglobulin domain containing 4 | -0.97948561 | 0.000231 | 0.04561077 |
| <i>PTPN1</i> | protein tyrosine phosphatase, non-receptor type 1 | -0.967747613 | 6.72E-05 | 0.02069323 |
| <i>PYGL</i> | phosphorylase, glycogen, liver | -0.961317092 | 1.41E-05 | 0.00987079 |
| <i>C1QC</i> | complement C1q C chain | -0.926671471 | 0.00011 | 0.02706959 |
| <i>C1QA</i> | complement C1q A chain | -0.890137724 | 0.000107 | 0.02706959 |
| <i>SPTLC2</i> | serine palmitoyltransferase long chain base subunit 2 | -0.874791093 | 1.86E-05 | 0.01069706 |
| <i>LTB4R</i> | leukotriene B4 receptor | -0.850525541 | 0.000162 | 0.03433271 |
| <i>RBPJ</i> | recombination signal-binding protein for immunoglobulin kappa J region | -0.784031474 | 7.78E-06 | 0.00813844 |
| <i>SSH2</i> | slingshot protein phosphatase 2 | -0.740051694 | 0.000111 | 0.02706959 |
| <i>NCK2</i> | NCK adaptor protein 2 | -0.717253425 | 0.000178 | 0.03699494 |
| <i>RNF144B</i> | ring finger protein 144B | -0.676892567 | 8.17E-05 | 0.02389107 |
| <i>SRGAP3</i> | SLIT-ROBO Rho GTPase activating protein 3 | -0.666013914 | 9.96E-05 | 0.02624851 |
| <i>NIFK</i> | nucleolar protein interacting with the FHA domain of MKI67 | -0.665674605 | 0.000198 | 0.04001036 |
| <i>NOP9</i> | NOP9 nucleolar protein | -0.598216747 | 4.87E-05 | 0.01684365 |
| <i>TMEM101</i> | transmembrane protein 101 | -0.580044505 | 0.000143 | 0.03166717 |
| <i>ARPC2</i> | actin-related protein 2/3 complex subunit 2 | -0.305770615 | 4.58E-05 | 0.01684365 |
| <i>LTBP3</i> | latent transforming growth factor beta binding protein 3 | 0.486067263 | 0.0001 | 0.02624851 |
| <i>BCL9L</i> | B-cell CLL/lymphoma 9-like | 0.510843649 | 8.89E-05 | 0.02477421 |
| <i>C7orf26</i> | chromosome 7 open reading frame 26 | 0.526736445 | 1.65E-05 | 0.01069706 |
| <i>TFCP2L1</i> | transcription factor CP2 like 1 | 0.82117496 | 7.49E-05 | 0.0222737 |
| <i>SHROOM1</i> | shroom family member 1 | 0.833192106 | 0.000179 | 0.03699494 |
| <i>LINC01091</i> | long intergenic non-protein coding RNA 1091 | 1.192932326 | 0.000127 | 0.02942714 |

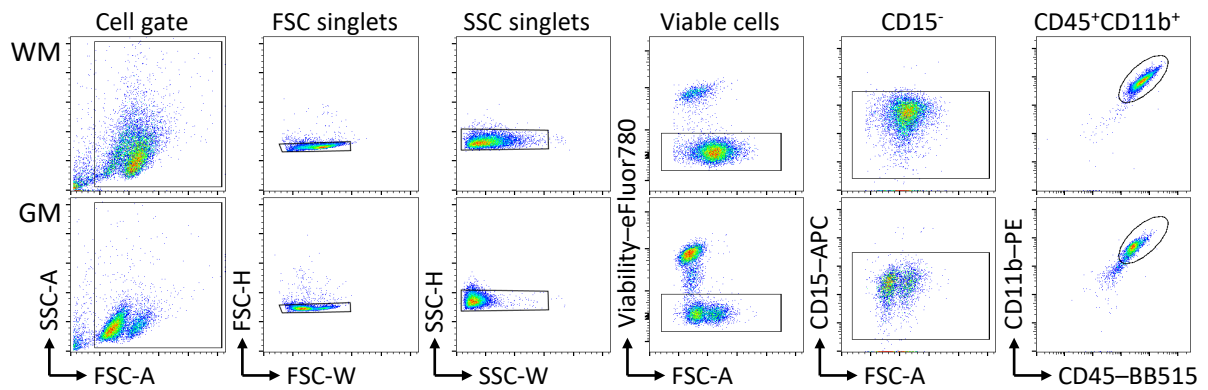
| | | | | |
|----------------------|---|-------------|----------|------------|
| <i>CNTNAP2</i> | contactin-associated protein-like 2 | 1.446998088 | 9.91E-05 | 0.02624851 |
| <i>LIMCH1</i> | LIM and calponin homology domains 1 | 1.675085155 | 0.00026 | 0.04991326 |
| <i>SCHIP1</i> | schwannomin-interacting protein 1 | 1.755426485 | 9.44E-05 | 0.02588543 |
| <i>RP11-580I16.2</i> | RP11-580I16.2 | 1.842657102 | 2.49E-05 | 0.01235894 |
| <i>PTPRB</i> | protein tyrosine phosphatase, receptor type B | 1.95547077 | 5.10E-05 | 0.01711641 |

Supplementary Table 5. Gene score resampling (GSR) of MDD cortical microglia gene expression compared to control microglia.

| GO term | Description | Size | Multi F. | Corrected p-value |
|------------|--|------|----------|-------------------|
| GO:0019864 | IgG binding | 9 | 0.0302 | 8.14E-09 |
| GO:0042116 | macrophage activation | 32 | 0.855 | 1.46E-08 |
| GO:0019724 | B cell-mediated immunity | 63 | 0.859 | 0.00000266 |
| GO:0038094 | Fc-gamma receptor signaling pathway | 72 | 0.843 | 0.00000262 |
| GO:0016064 | immunoglobulin-mediated immune response | 62 | 0.861 | 0.00000532 |
| GO:0101003 | Ficolin 1-rich granule membrane | 59 | 0.64 | 0.00000491 |
| GO:0002455 | humoral immune response mediated by circulating immunoglobulin | 32 | 0.655 | 0.0000213 |
| GO:0006953 | acute-phase response | 32 | 0.696 | 0.0000403 |
| GO:0038096 | Fc-gamma receptor signaling pathway involved in phagocytosis | 68 | 0.843 | 0.0000446 |
| GO:0050663 | cytokine secretion | 39 | 0.852 | 0.0000953 |
| GO:0050764 | regulation of phagocytosis | 71 | 0.885 | 0.0000972 |
| GO:0099024 | plasma membrane invagination | 43 | 0.764 | 0.000137 |
| GO:0033116 | endoplasmic reticulum-Golgi intermediate compartment membrane | 66 | 0.449 | 0.000266 |
| GO:0010324 | membrane invagination | 50 | 0.786 | 0.000335 |
| GO:0046915 | transition metal ion transmembrane transporter activity | 38 | 0.618 | 0.000536 |
| GO:0030670 | phagocytic vesicle membrane | 68 | 0.87 | 0.000522 |
| GO:0006911 | phagocytosis, engulfment | 34 | 0.703 | 0.000558 |
| GO:0002102 | podosome | 34 | 0.533 | 0.000558 |
| GO:0006879 | cellular iron ion homeostasis | 60 | 0.838 | 0.0016 |
| GO:0030449 | regulation of complement activation | 41 | 0.71 | 0.00192 |

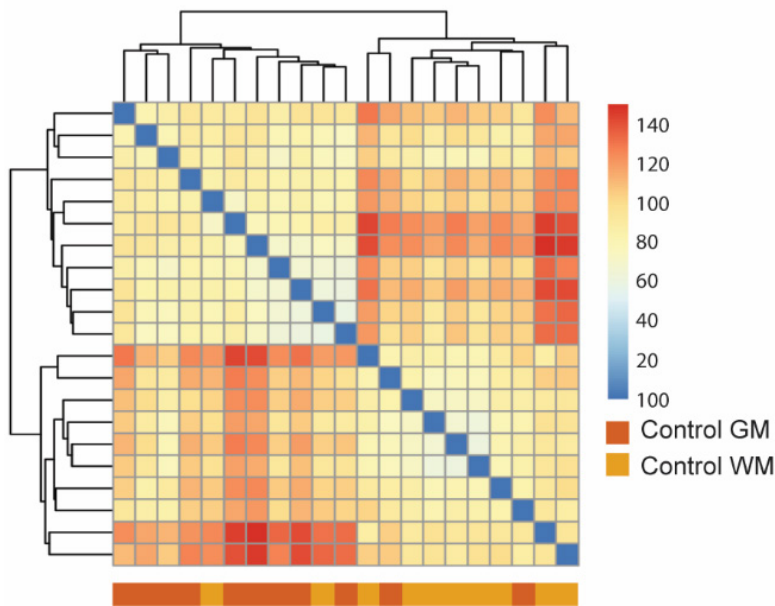
GSR was performed using ErmineJ. GO was set between 5 and 75 genes, 200,000 iterations, false discovery rate (FDR) <0.001.

Supplementary Figure 1.



Supplementary Figure 1. Flow cytometry gating strategy for human microglia in white matter (WM) and gray matter (GM). Representative dot plots showing the gating strategy used for Figure 1A with from left to right: cell gating by forward scatter (FCS) and sideward scatter (SSC), FCS-width/height duplet exclusion, SSC-width/height duplet exclusion, gating of viable cells, gating of CD15⁻ events, and gating of CD45⁺CD11b⁺ events.

Supplementary Figure 2.



Supplementary Figure 2. Hierarchical clustering of gene expression data obtained from WM and GM microglia of control brains.