

Supplemental materials

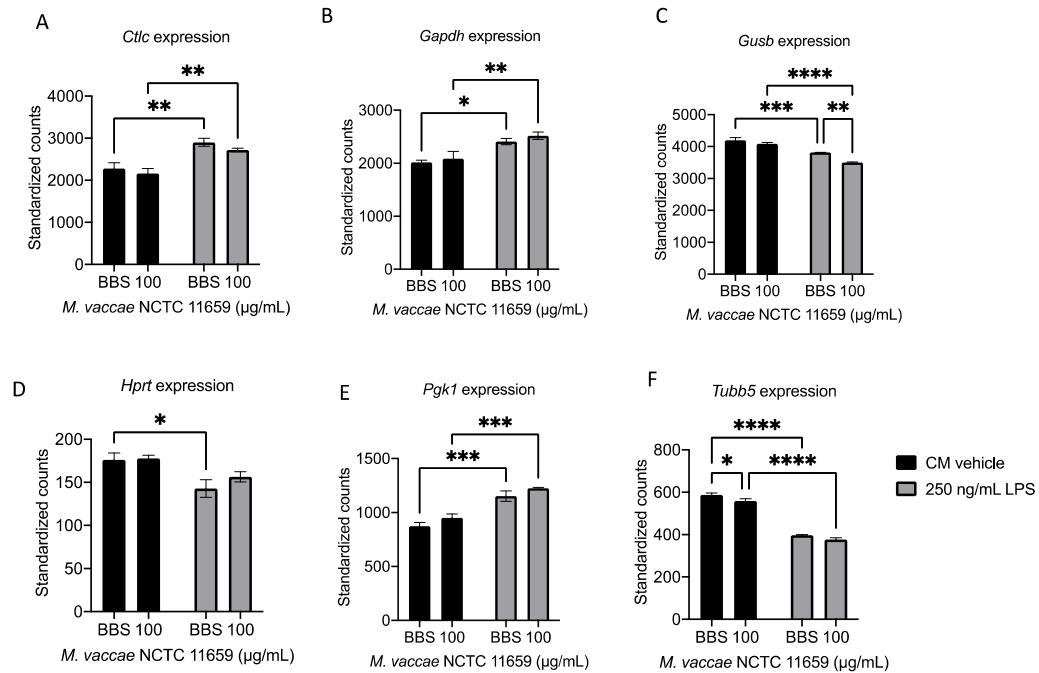


Figure S1. Treating murine BV-2 microglial cells with *M. vaccae* NCTC 11659 (100 µg/mL, 48 h) or sterile borate-buffered saline (BBS) vehicle control conditions and lipopolysaccharide (LPS; 250 ng/mL, 24 h) or a cell culture media (CM) vehicle control condition resulted in differential expression of all internal housekeeping genes in the nCounter Mouse Inflammation v2 Panel. Graphs illustrate effects of treatment on (A) *Ctltc* mRNA expression, (B) *Gapdh* mRNA expression, (C) *Gusb* mRNA expression, (D) *Hprt* mRNA expression, (E) *Pgk1* mRNA expression, and (F) *Tubb5* mRNA expression. Data were analyzed using a two-way ANOVA followed by Fisher's LSD test using a single pooled error value, if appropriate, at a two-tailed alpha level of 0.05. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$. For all experimental conditions, there were 3 technical replicates ($n = 3$) from $N = 1$ experiment. Abbreviations: BBS, borate-buffered saline; CM, culture media; *Ctltc*, gene encoding clathrin heavy chain; *Gapdh*, gene encoding glyceraldehyde 3-phosphate dehydrogenase; *Gusb*, gene encoding beta glucuronidase; *Hprt*, gene encoding hypoxanthine-guanine phosphoribosyltransferase; LPS, lipopolysaccharide; *Pgk1*, gene encoding phosphoglycerate kinase; *Tubb*, gene encoding tubulin beta chain.

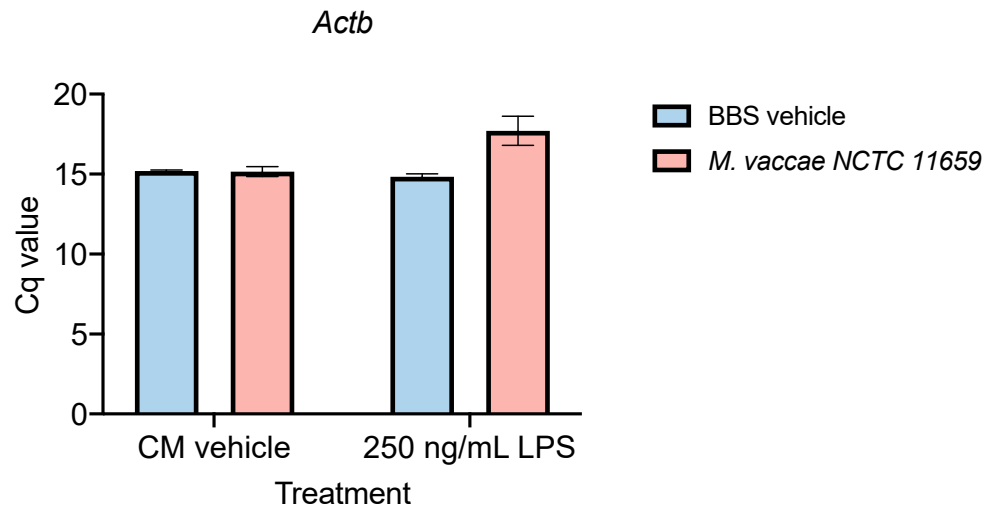


Figure S2. Effects of treatment of murine BV-2 microglial cells with *M. vaccae* NCTC 11659 (100 μ g/mL or sterile borate-buffered saline vehicle control condition; 48 h) and lipopolysaccharide (0, 250 ng/mL; 24 h) or a cell culture media (CM) vehicle control condition on the expression of *Actb*. Abbreviations: BBS, borate-buffered saline. LPS, lipopolysaccharide.

M. vaccae NCTC 11659/CMV vs. BBS/CMV

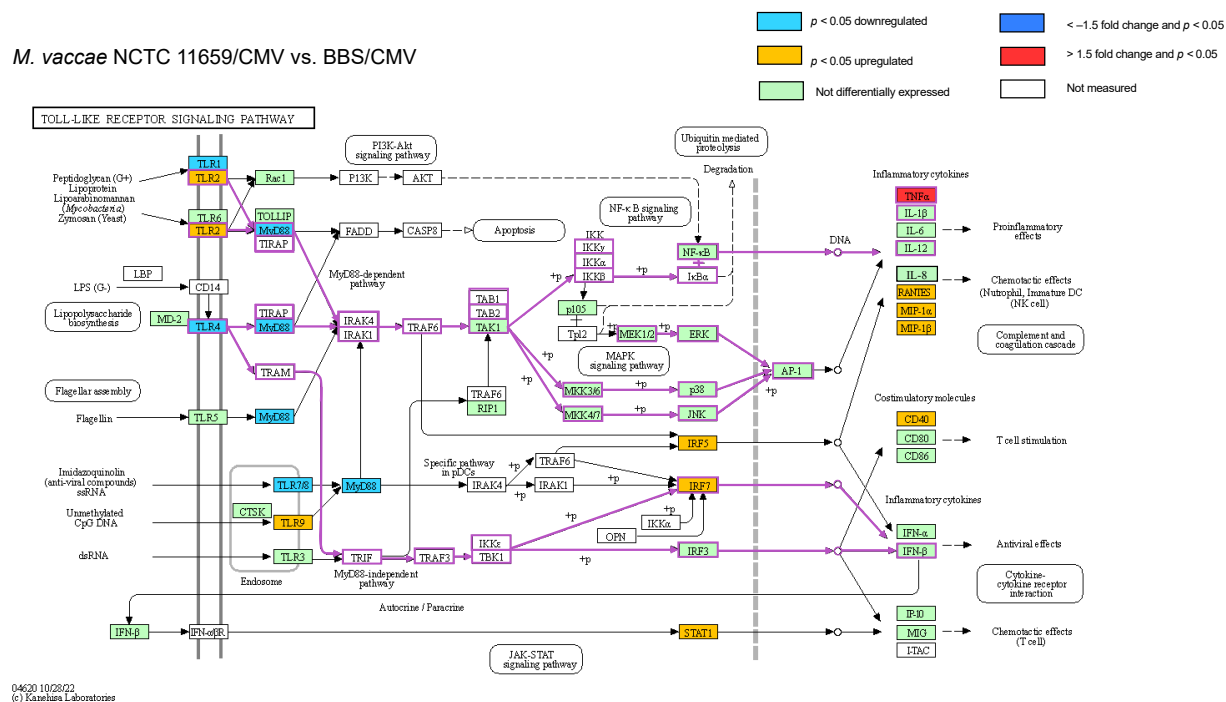


Figure S3. Toll-like receptor signaling KEGG pathway color-coded to reflect the effects of 100 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659 on gene expression. Genes highlighted in blue were downregulated by 100 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659, genes highlighted in red were upregulated by 100 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659, genes highlighted in green were not differentially expressed, and genes in white were not measured. Genes highlighted in light blue had a significant decrease in expression ($p < 0.05$) following treatment with 100 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659 but did not have a 1.5-fold change. Genes highlighted in orange had a significant increase in expression ($p < 0.05$) following treatment with 100 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659 but did not have a 1.5-fold change. The purple line indicates TLR2 and TLR4 signaling pathways.

BBS/LPS vs. BBS/CMV

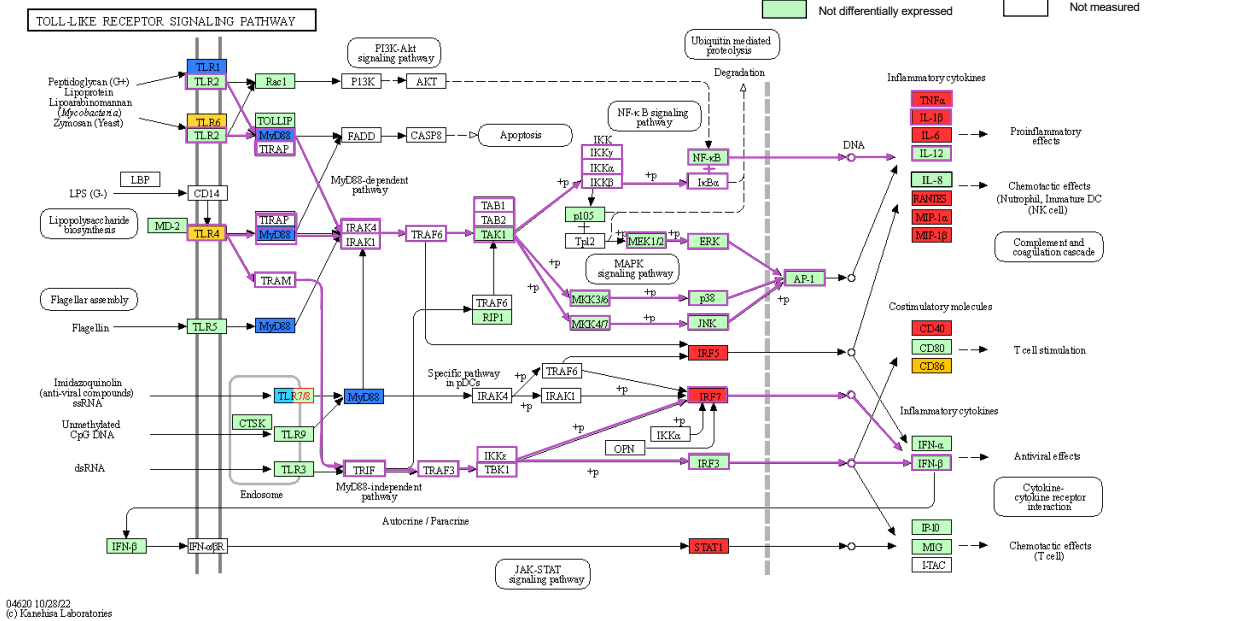


Figure S4. Toll-like receptor signaling KEGG pathway color-coded to reflect the effects of 250 ng/mL lipopolysaccharide (LPS) on gene expression. Genes highlighted in blue were downregulated by 250 ng/mL LPS and had at least a 1.5-fold change, genes highlighted in red were upregulated by 250 ng/mL LPS with at least a 1.5-fold change, genes highlighted in green were not differentially expressed, and genes in white were not measured. Genes highlighted in light blue had a significant decrease in expression ($p < 0.05$) following treatment with 250 ng/mL LPS treatment ($p < 0.05$) but did not have a 1.5-fold change. Genes highlighted in orange had a significant increase in expression ($p < 0.05$) following treatment with 250 ng/mL LPS treatment ($p < 0.05$) but did not have a 1.5-fold change. The purple line indicates TLR2 and TLR4 signaling pathways.

M. vaccae NCTC 11659/LPS vs. BBS/LPS

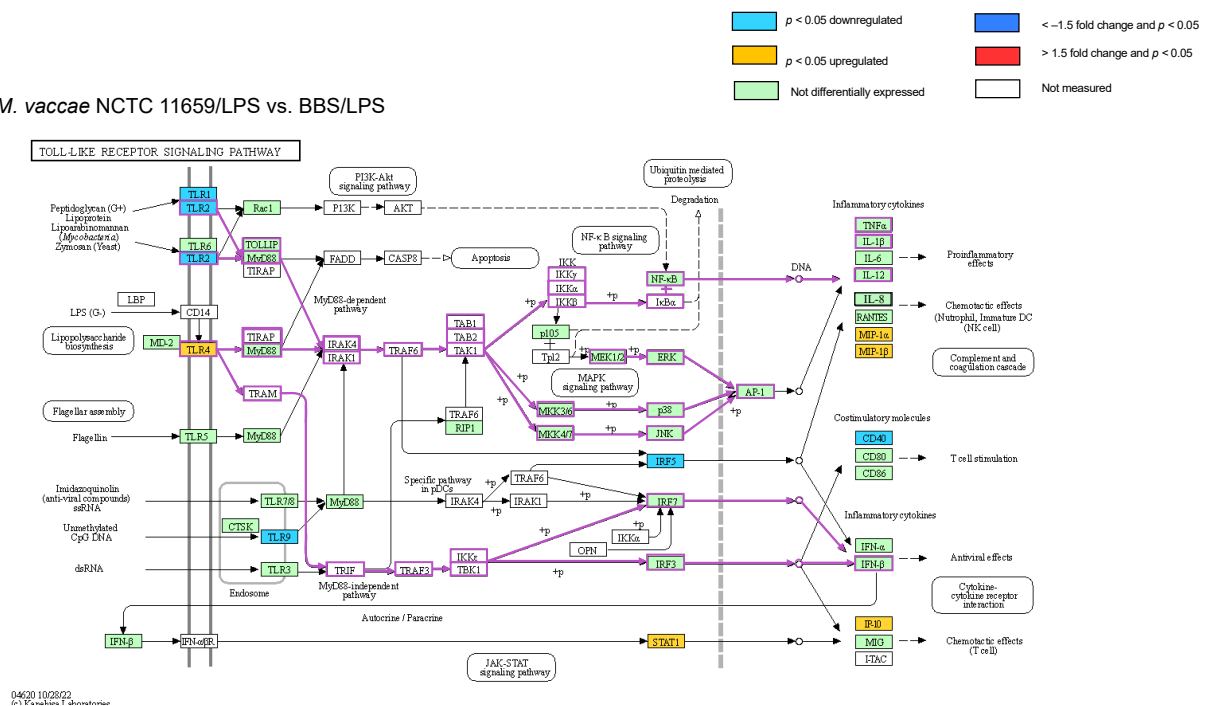


Figure S5. Toll-like receptor signaling KEGG pathway color-coded to reflect the effects of 100 µg/mL *M. vaccae* NCTC 11659 in the presence of 250 ng/mL lipopolysaccharide (LPS) on gene expression. Genes highlighted in blue were downregulated by 100 µg/mL *M. vaccae* NCTC 11659, genes highlighted in red were upregulated by 100 µg/mL *M. vaccae* NCTC 11659, genes highlighted in green were not differentially expressed, and genes in white were not measured. Genes highlighted in light-blue cells had a significant decrease in expression ($p < 0.05$) following treatment with 100 µg/mL *M. vaccae* NCTC 11659 ($p < 0.05$) but did not have a 1.5-fold change. Genes highlighted in orange had a significant increase in expression ($p < 0.05$) following treatment with 100 µg/mL *M. vaccae* NCTC 11659 ($p < 0.05$) but did not have a 1.5-fold change. The purple line indicates TLR2 and TLR4 signaling pathways.

M. vaccae NCTC 11659/LPS vs. *M. vaccae* NCTC 11659/CMV

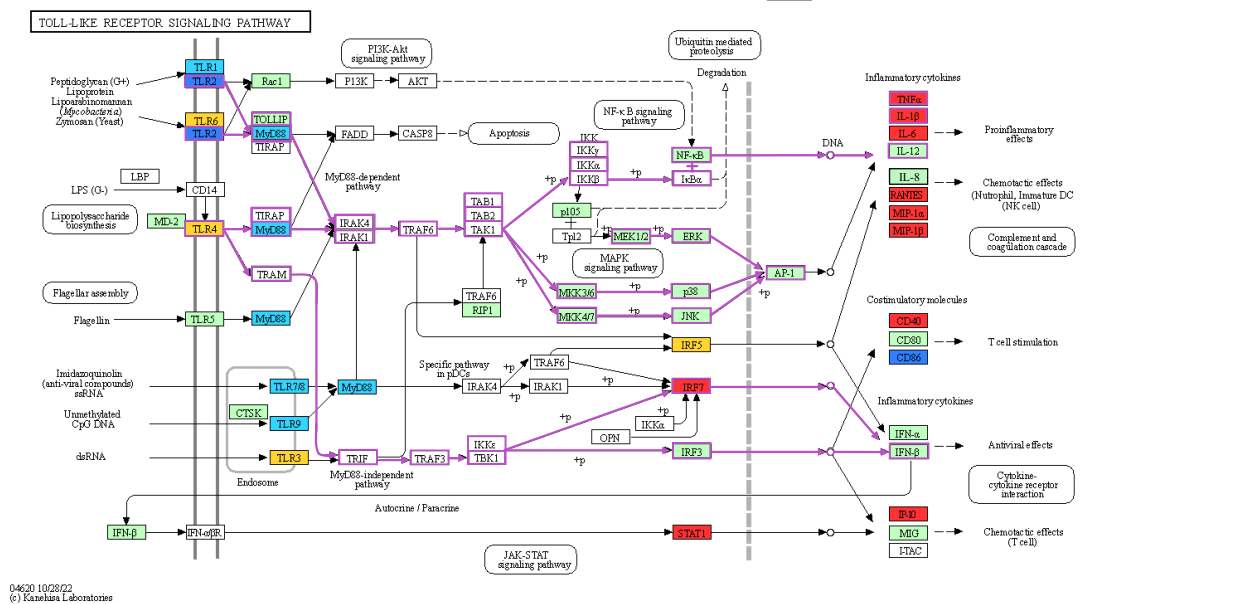


Figure S6. Toll-like receptor signaling KEGG pathway color-coded to reflect the effects of 250 ng/mL lipopolysaccharide (LPS) in the presence of 100 μ g/mL *M. vaccae* NCTC 11659 on gene expression. Genes highlighted in blue were downregulated by 250 ng/mL LPS, genes highlighted in red were upregulated by 250 ng/mL LPS, genes highlighted in green were not differentially expressed, and genes in white were not measured. Genes highlighted in light blue had a significant decrease in expression ($p < 0.05$) following treatment with 250 ng/mL LPS treatment ($p < 0.05$) but did not have a 1.5-fold change. Genes highlighted in orange had a significant increase in expression ($p < 0.05$) following treatment with 250 ng/mL LPS treatment ($p < 0.05$) but did not have a 1.5-fold change. The purple line indicates TLR2 and TLR4 signaling pathways.

Supplemental tables

Table S1. Log2 fold changes among differentially expressed genes in the *M. vaccae* NCTC 11659/CMV versus BBS/CMV comparison.

Gene symbols	Log2 Fold Change
Upregulated	
<i>C3</i>	1.16881
<i>Ccl2</i>	0.698848
<i>Tnf</i>	0.677453
Downregulated	
<i>Arg1</i>	-1.64186
<i>Smad7</i>	-0.62623

Table S2. Genes that had *p*-values less than 0.05 in the *M. vaccae* NCTC 11659/CMV versus BBS/CMV comparison.

Gene Symbol	Log2 Fold Change
Upregulated	
<i>C1ra</i>	0.522863333
<i>Map2k6</i>	0.503656667
<i>Relb</i>	0.495151333
<i>Tlr2</i>	0.474013333
<i>Il1a</i>	0.45724
<i>Tradd</i>	0.441106667
<i>Maff</i>	0.42836
<i>Ccl5</i>	0.41674
<i>Tnfaip3</i>	0.413766667
<i>Cd40</i>	0.33927
<i>Irf1</i>	0.318105
<i>Ccl3</i>	0.304396667
<i>Rock2</i>	0.256366667
<i>Ccl4</i>	0.251118
<i>Nfkb1</i>	0.240120333
<i>Rapgef2</i>	0.234643333
<i>Stat3</i>	0.229596667
<i>Mapkapk2</i>	0.221023333
<i>Irf7</i>	0.20075
<i>Il18</i>	0.197
<i>Cxcr1</i>	0.194853333
<i>Cfb</i>	0.190016667
<i>Nfe2l2</i>	0.166356667

<i>Tlr9</i>	0.16627
<i>Stat1</i>	0.152266667
<i>Ifit2</i>	0.150683333
<i>Itgb2</i>	0.12703
<i>Cebpb</i>	0.118883333
<i>Nod2</i>	0.107374333
<i>Grb2</i>	0.10702
<i>Cxcl2</i>	0.096584
<i>Shc1</i>	0.09582
<i>Mafg</i>	0.093901333
<i>Bcl2l1</i>	0.092198
<i>Mapk1</i>	0.09019
<i>Mapk8</i>	0.086444
<i>Hdac4</i>	0.080853333
<i>Mrc1</i>	0.08044
<i>Mx2</i>	0.067417667
<i>Mx1</i>	0.066616667
<i>Irf5</i>	0.06568
<i>Oasl1</i>	0.05803
<i>Gnaq</i>	0.046157
<i>Tollip</i>	0.043597333
<i>Ptgir</i>	0.041338
<i>Tgfb1</i>	0.040803333
<i>Hif1a</i>	0.03787
Downregulated	
<i>Il15</i>	-0.48629
<i>Oas2</i>	-0.466773333
<i>Fxyd2</i>	-0.465263333
<i>Ripk1</i>	-0.407486667
<i>Tlr1</i>	-0.370292723
<i>Cysltr1</i>	-0.36564
<i>Mef2d</i>	-0.357553
<i>Limk1</i>	-0.339843333
<i>Cxcr4</i>	-0.321923333
<i>Map3k5</i>	-0.318477
<i>Myd88</i>	-0.292906667
<i>Mafk</i>	-0.292616667
<i>Prkcb</i>	-0.292127333
<i>Mknk1</i>	-0.272153333

<i>Ptk2</i>	-0.265663333
<i>Il1rap</i>	-0.255903333
<i>Max</i>	-0.243566667
<i>Ddit3</i>	-0.225653333
<i>Hmgb1</i>	-0.223086667
<i>Ifi2712a</i>	-0.207843333
<i>Stat2</i>	-0.198543333
<i>Ptgs1</i>	-0.190846667
<i>Trem2</i>	-0.18747
<i>Tlr8</i>	-0.177774667
<i>Traf2</i>	-0.166396667
<i>Cxcl10</i>	-0.15852
<i>Tlr4</i>	-0.156593333
<i>C3ar1</i>	-0.15266
<i>Cfl1</i>	-0.150703333
<i>Map2k4</i>	-0.144073333
<i>Hmgn1</i>	-0.140913333
<i>Tgfbr1</i>	-0.135936667
<i>Rela</i>	-0.131246667
<i>Jun</i>	-0.12641
<i>Rhoa</i>	-0.11677
<i>Nr3c1</i>	-0.115952667
<i>Tcf4</i>	-0.115070333
<i>Prkca</i>	-0.114099
<i>Pdgfa</i>	-0.113133333
<i>Fos</i>	-0.109136667
<i>Rac1</i>	-0.10565
<i>Tyrobp</i>	-0.104916667
<i>Keap1</i>	-0.101661333
<i>Gnas</i>	-0.09738
<i>Flt1</i>	-0.094111
<i>C4a</i>	-0.086458333
<i>Mef2c</i>	-0.084173333
<i>Gngt1</i>	-0.071236667
<i>Mapkapk5</i>	-0.06905
<i>Nfatc3</i>	-0.068228
<i>Ppp1r12b</i>	-0.067863333
<i>Raf1</i>	-0.067411333
<i>Map3k7</i>	-0.065804

<i>Gnb1</i>	-0.063546667
<i>Cdc42</i>	-0.05227
<i>Mmp9</i>	-0.051743333
<i>Nlrp3</i>	-0.049161333
<i>Ptgs2</i>	-0.045203333
<i>Pla2g4a</i>	-0.021403993
<i>Mapk3</i>	-0.02038
<i>Ly96</i>	-0.018520667

Table S3. List of abbreviations for all gene symbols

Alox12, arachidonate 12-lipoxygenase
APC, antigen-presenting cell
Arg1, arginase 1
BBS, borate-buffered saline
Birc2, baculoviral IAP repeat-containing 2
Clqb, complement component 1, q subcomponent, beta polypeptide
Clra, complement component 1, r subcomponent A
Cls1, complement component 1, s subcomponent 1
C3, complement component 3
Ccl2, C-C motif chemokine ligand 2
Ccl3, C-C motif chemokine ligand 3
Ccl4, C-C motif chemokine ligand 4
Ccl5, C-C motif chemokine ligand 5
Ccl7, C-C motif chemokine ligand 7
Ccr3, chemokine (C-C motif) receptor 3
Cd163, Cd163 antigen
Cd4, Cd4 antigen
Cd40, Cd40 antigen
Cebpb, CCAAT/enhancer binding protein, beta
Cfb, complement factor B
CMV, cell culture media vehicle
CNS, central nervous system
Csf1, colony-stimulating factor 1
Csf3, colony-stimulating factor 3
Cxcl10, C-X-C motif chemokine ligand 10
Cxcl2, C-X-C motif chemokine ligand 2
Cxcr1, chemokine (C-X-C motif) receptor 1
Cxcr4, chemokine (C-X-C motif) receptor 4
Daxx, fas death domain-associated protein
Ddit3, DNA-damage inducible transcript 3
Fasl, fas ligand; *Fos*, FBJ osteosarcoma oncogene
H2-eb1, histocompatibility 2, class II antigen E beta
Hif1a, hypoxia-inducible factor 1, alpha subunit
Hmgb1, high mobility group box 1
Hmgn1, high mobility group nucleosomal binding domain 1
Hspb1, heat shock protein 1
Ifi2712A, interferon, alpha-inducible protein 27 like 2A
Ifi44, interferon-induced protein 44
Ifit1, interferon-induced protein with tetratricopeptide repeats 1
Ifit2, interferon-induced protein with tetratricopeptide repeats 2
Ifit3, interferon-induced protein with tetratricopeptide repeats 3
Iigp1, interferon-inducible GTPase 1
IL, interleukin
Il12b, interleukin 12b
Il18, interleukin 18

Il1a, interleukin 1 alpha
Il1b, interleukin 1 beta
Il1r1, interleukin 1 receptor, type 1
Il1rn, interleukin 1 receptor antagonist
Il23a, interleukin 23, alpha subunit p19
Il6, interleukin 6
Il6ra, interleukin 6 receptor, alpha
Irf1, interferon regulatory factor 1
Irf5, interferon regulatory factor 5
LPS, lipopolysaccharide
Lta, lymphotoxin A
Ly96, lymphocyte antigen 96
Maff, v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F
M. vaccae, *Mycobacterium vaccae*
Mafg, v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G
Map2k1, mitogen-activated protein kinase kinase 1
Mapkapk2, MAP kinase-activated protein kinase 2
Mef2a, myocyte enhancer factor 2a
Mef2c, myocyte enhancer factor 2C
Mmp9, matrix metalloproteinase 9
Mrc1, mannose receptor, C type 1
Mx1, MX dynamin-like GTPase 1
Mx2, MX dynamin-like GTPase 2
Myc, myelocytomatosis oncogene
Myd88, myeloid differentiation primary response gene 88
NCTC, National Collection of Type Cultures
Nfe2l2, nuclear factor, erythroid derived 2, like 2
Nfkb1, nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105
Nlrp3, NLR family, pyrin domain containing 3
Nod1, nucleotide-binding oligomerization domain containing 1
Nod2, nucleotide-binding oligomerization domain containing 2
Nos2, nitric oxide synthase 2, inducible
Nox1, NADPH oxidase 1
Oas1a, 2'-5' oligoadenylate synthetase 1a
Oas2, 2'-5' oligoadenylate synthetase 2
Oasl1, 2'-5' oligoadenylate synthetase-like 1
PNN, perineuronal net
Ptgir, prostaglandin I receptor (IP)
Ptgs1, prostaglandin-endoperoxide synthase 1
Ptgs2, prostaglandin-endoperoxide synthase 2
Rapgef2, rap guanine nucleotide exchange factor (GEF) 2
Rela, v-rel reticuloendotheliosis viral oncogene homolog A
Relb, avian reticuloendotheliosis viral (v-rel) oncogene related B
Ripk2, receptor (TNFRSF)-interacting serine-threonine kinase 2
Stat1, signal transducer and activator of transcription 1
Stat2, signal transducer and activator of transcription 2

Stat3, signal transducer and activator of transcription 3
TGFβ, transforming growth factor beta
TLR, toll-like receptor
Tlr1, toll-like receptor 1
Tlr2, toll-like receptor 2
Tlr3, toll-like receptor 3
Tlr6, toll-like receptor 6
Tlr8, toll-like receptor 8
Tlr9, toll-like receptor 9
Tnf, tumor necrosis factor
Tnfaip3, tumor necrosis factor, alpha-induced protein 3
Traf2, Tnf receptor-associated factor 2
Treg, regulatory T cell
Trem2, triggering receptor expressed on myeloid cells

Table S4. Log2 fold changes among differentially expressed genes in the BBS/250 ng/mL LPS versus BBS/CMV comparison.

Gene Symbol	Log2 Fold Change
Upregulated	
<i>Cfb</i>	5.60648
<i>Ccl5</i>	5.56549
<i>Ifit1</i>	4.024
<i>Cd40</i>	3.07338
<i>Ifit3</i>	2.99376
<i>Il1b</i>	2.79327
<i>Il6</i>	2.61309
<i>Nos2</i>	2.57817
<i>Maff</i>	2.55533
<i>Tnf</i>	2.4393
<i>Tradd</i>	2.29754
<i>C3</i>	2.26905
<i>Ccl2</i>	2.0218
<i>Irf1</i>	1.98211
<i>Irf7</i>	1.92943
<i>Ccl3</i>	1.85339
<i>Rock2</i>	1.57019
<i>Cxcr1</i>	1.56136
<i>Oasl1</i>	1.54032
<i>Il1a</i>	1.44444
<i>Ccl4</i>	1.37771
<i>Map2k6</i>	1.35468
<i>Mx1</i>	1.27039
<i>Cxcl2</i>	1.23382
<i>Ifit2</i>	1.13021
<i>Tnfaip3</i>	0.975547
<i>Clra</i>	0.929432
<i>Il18</i>	0.830453
<i>Il6ra</i>	0.79481
<i>Ifi44</i>	0.756457
<i>Csfl</i>	0.719692
<i>Irf5</i>	0.713634
<i>Stat1</i>	0.70563
<i>Mx2</i>	0.702039
<i>Keap1</i>	0.671778

<i>Ripk2</i>	0.666244
Downregulated	
<i>Arg1</i>	-2.80374
<i>Smad7</i>	-1.93381
<i>Limk1</i>	-1.83436
<i>Fxyd2</i>	-1.79421
<i>Ptgs1</i>	-1.61283
<i>Hmgn1</i>	-1.53119
<i>Trem2</i>	-1.52992
<i>Max</i>	-1.5075
<i>Myl2</i>	-1.47985
<i>Tlr8</i>	-1.43853
<i>Ripk1</i>	-1.26378
<i>Mef2d</i>	-1.25684
<i>Cysltr1</i>	-1.25576
<i>Hmgb1</i>	-1.22569
<i>Clqb</i>	-1.15706
<i>Cxcr4</i>	-1.12752
<i>Ptger4</i>	-1.11958
<i>Maik</i>	-0.999982
<i>Ptk2</i>	-0.996795
<i>Mmp9</i>	-0.985976
<i>Mknk1</i>	-0.943527
<i>C1s1</i>	-0.855773
<i>Oas2</i>	-0.85333
<i>Cd86</i>	-0.834836
<i>Raf1</i>	-0.834556
<i>Map3k7</i>	-0.819428
<i>Pdgfa</i>	-0.805386
<i>Mrc1</i>	-0.697027
<i>Il1rap</i>	-0.651947
<i>Jun</i>	-0.649737
<i>Tlr1</i>	-0.620468
<i>Rhoa</i>	-0.615622
<i>Flt1</i>	-0.610663
<i>Cfl1</i>	-0.602626
<i>Myd88</i>	-0.593948

Table S5. Genes that had *p*-values less than 0.05 in the BBS/LPS versus BBS/CMV comparison.

Gene Symbol	Log2 Fold Change
Upregulated	
<i>Atf2</i>	0.574514667
<i>Cd4</i>	0.548781333
<i>Gnas</i>	0.532883333
<i>Grb2</i>	0.530340667
<i>Rac1</i>	0.500567
<i>Il10rb</i>	0.494686667
<i>Bcl6</i>	0.492426667
<i>H2-Eb1</i>	0.476682667
<i>Tcf4</i>	0.427876667
<i>Tyrobp</i>	0.426743333
<i>Mafg</i>	0.41568
<i>Mapk14</i>	0.401537333
<i>Map2k4</i>	0.372703333
<i>Map3k1</i>	0.36534
<i>Pla2g4a</i>	0.360026333
<i>Ppp1r12b</i>	0.35498
<i>Cdc42</i>	0.338123333
<i>Tlr7</i>	0.331499333
<i>Birc2</i>	0.321431667
<i>Gnaq</i>	0.304983333
<i>Gngt1</i>	0.302697667
<i>Mapkapk5</i>	0.261233
<i>Mapk1</i>	0.236921
<i>Gnb1</i>	0.234823333
<i>Tollip</i>	0.224343333
<i>C3ar1</i>	0.211985333
<i>Nr3c1</i>	0.202471
<i>Shc1</i>	0.189009
<i>Ly96</i>	0.187679
<i>Mapk3</i>	0.158596667
<i>Tlr4</i>	0.145233333
<i>Tgfb1</i>	0.12621
<i>Rela</i>	0.100826667
<i>Ifi2712a</i>	0.081143333
<i>Nfe2l2</i>	0.078463333

<i>Stat2</i>	0.04284
<i>Clqa</i>	0.024513333
Downregulated	
<i>Ptgir</i>	-0.528952333
<i>Relb</i>	-0.508803333
<i>Elk1</i>	-0.506823333
<i>Map3k5</i>	-0.48829
<i>Nlrp3</i>	-0.487453333
<i>Ddit3</i>	-0.473056667
<i>Il1rn</i>	-0.452563333
<i>Map2k1</i>	-0.436669667
<i>Hdac4</i>	-0.435948
<i>Mapkapk2</i>	-0.427086667
<i>Cebpb</i>	-0.422433667
<i>Ccl7</i>	-0.414796667
<i>Nox1</i>	-0.35121
<i>Ptgs2</i>	-0.3473188
<i>Stat3</i>	-0.31330722
<i>Tlr9</i>	-0.285496667
<i>Hif1a</i>	-0.224553333
<i>Bcl2l1</i>	-0.21676
<i>Oas1a</i>	-0.206146667
<i>Nod1</i>	-0.204346
<i>Hmgb2</i>	-0.18363
<i>Nod2</i>	-0.181143333
<i>Mapk8</i>	-0.16611
<i>Rapgef2</i>	-0.164476667
<i>Myc</i>	-0.147813
<i>Tlr6</i>	-0.132133333
<i>Il1r1</i>	-0.129887333
<i>Nfatc3</i>	-0.124976667
<i>Prkca</i>	-0.062955667
<i>Fos</i>	-0.024766667

Table S6. Log2 fold changes among differentially expressed genes in the *M. vaccae* NCTC 11659/250 ng/mL LPS versus BBS/250 ng/mL LPS condition.

Gene symbols	Log2 Fold Change
Upregulated	
<i>Ccl7</i>	1.10527
<i>Csf3</i>	0.711066
Downregulated	
<i>Cysltr1</i>	-0.630051

Table S7. Genes that had *p*-values less than 0.05 in the *M. vaccae* NCTC 11659/250 ng/mL LPS versus BBS/250 ng/mL LPS comparison.

Gene Symbol	Log2 Fold Change
Upregulated	
<i>Mmp9</i>	0.521552733
<i>Tlr3</i>	0.46441
<i>Ccl2</i>	0.454501667
<i>Cxcr1</i>	0.432406667
<i>Rps6ka5</i>	0.385053333
<i>Fos</i>	0.32347
<i>Il15</i>	0.32142
<i>Rock2</i>	0.321271
<i>C1ra</i>	0.295016667
<i>Hdac4</i>	0.293523333
<i>Nos2</i>	0.289856667
<i>Ripk2</i>	0.271563333
<i>Ptgs2</i>	0.257453333
<i>Mafg</i>	0.246756667
<i>Mknk1</i>	0.23039
<i>Tradd</i>	0.227473333
<i>Il1rn</i>	0.223083333
<i>Myc</i>	0.208986667
<i>Cxcl2</i>	0.191143333
<i>Mapk8</i>	0.191081
<i>Fxyd2</i>	0.185787467
<i>Jun</i>	0.185123333
<i>Map2k4</i>	0.184196667
<i>Ccl4</i>	0.168313333
<i>Tcf4</i>	0.167267667
<i>Cxcl10</i>	0.161426667
<i>Flt1</i>	0.140163333

<i>Mrc1</i>	0.1365
<i>Ccl3</i>	0.13141
<i>Keap1</i>	0.126113333
<i>Stat1</i>	0.11608
<i>Mapk3</i>	0.10595
<i>Cfb</i>	0.098346667
<i>Oasl1</i>	0.08909
<i>Il1a</i>	0.083816667
<i>Pla2g4a</i>	0.080459333
<i>Shc1</i>	0.076493333
<i>Nlrp3</i>	0.065152433
<i>Tlr4</i>	0.043196667
Downregulated	
<i>Tlr9</i>	-0.37297
<i>Mx2</i>	-0.2752792
<i>Cd40</i>	-0.252691667
<i>Bcl6</i>	-0.227363333
<i>Tlr1</i>	-0.225156667
<i>Mx1</i>	-0.219863333
<i>Grb2</i>	-0.206496667
<i>Tnfaip3</i>	-0.162046667
<i>Mapk1</i>	-0.155753333
<i>Maff</i>	-0.14415
<i>Irf5</i>	-0.13144
<i>C3ar1</i>	-0.130933333
<i>Bcl2l1</i>	-0.130643667
<i>Atf2</i>	-0.125656667
<i>Tgfb1</i>	-0.123026667
<i>Il18</i>	-0.12242
<i>Tlr2</i>	-0.122263333
<i>Tyrobp</i>	-0.113626667
<i>C3</i>	-0.110666667
<i>Gnas</i>	-0.089353333
<i>Gnaq</i>	-0.082727667
<i>Il10rb</i>	-0.075986667
<i>Irf1</i>	-0.075463333
<i>Cfl1</i>	-0.07277
<i>Cdc42</i>	-0.06998
<i>Ly96</i>	-0.05652

<i>Oas1a</i>	-0.053942667
<i>Rela</i>	-0.05245
<i>Gnbl</i>	-0.04362

Table S8. Log2 fold changes among differentially expressed genes in the *M. vaccae* NCTC 11659/250 ng/mL LPS versus *M. vaccae* NCTC 11659/CMV condition.

Gene symbol	Log2 Fold Change
Upregulated	
<i>Cfb</i>	5.51481
<i>Ccl5</i>	5.06203
<i>Ifit1</i>	4.22224
<i>Ifit3</i>	2.99882
<i>Nos2</i>	2.76852
<i>Il6</i>	2.70201
<i>Il1b</i>	2.67336
<i>Cd40</i>	2.48141
<i>Tradd</i>	2.08391
<i>Maff</i>	1.98282
<i>Cxcr1</i>	1.79891
<i>Ccl2</i>	1.77745
<i>Irf7</i>	1.76926
<i>Tnf</i>	1.72265
<i>Ccl3</i>	1.6804
<i>Rock2</i>	1.6351
<i>Irf1</i>	1.58854
<i>Oasl1</i>	1.57138
<i>Ccl7</i>	1.43047
<i>Cxcl2</i>	1.32839
<i>Ccl4</i>	1.29491
<i>Il1a</i>	1.07101
<i>Ripk2</i>	1.00964
<i>Map3k5</i>	1.00414
<i>C3</i>	0.989572
<i>Mx1</i>	0.983916
<i>Keap1</i>	0.899553
<i>Il6ra</i>	0.876298
<i>Map2k6</i>	0.873408
<i>Ifit2</i>	0.777177
<i>Ifi44</i>	0.757504
<i>Il1rn</i>	0.719116
<i>Clra</i>	0.701586
<i>Ddit3</i>	0.697734

<i>Il15</i>	0.691392
<i>Csf1</i>	0.680683
<i>Stat1</i>	0.66944
<i>Ptgs2</i>	0.668
<i>Hdac4</i>	0.640543
<i>Nlrp3</i>	0.614881
<i>Csf3</i>	0.609804
<i>Fos</i>	0.591201
Downregulated	
<i>Limk1</i>	-1.59298
<i>Cysltr1</i>	-1.52017
<i>Ptgs1</i>	-1.4189
<i>Myl2</i>	-1.38455
<i>Max</i>	-1.33951
<i>Trem2</i>	-1.31826
<i>Hmgn1</i>	-1.31755
<i>Smad7</i>	-1.30721
<i>C1qb</i>	-1.25213
<i>Arg1</i>	-1.19992
<i>Tlr8</i>	-1.19457
<i>Fxyd2</i>	-1.14316
<i>C1s1</i>	-1.0975
<i>Mef2d</i>	-1.04409
<i>Ptger4</i>	-1.0306
<i>Hmgb1</i>	-0.968003
<i>Ptk2</i>	-0.947579
<i>Ripk1</i>	-0.848458
<i>Map3k7</i>	-0.846216
<i>Cd86</i>	-0.80308
<i>Grb2</i>	-0.801806
<i>Raf1</i>	-0.755615
<i>Bcl6</i>	-0.700543
<i>Pdgfa</i>	-0.685679
<i>Cxcr4</i>	-0.684825
<i>Mafk</i>	-0.642115
<i>Mrc1</i>	-0.640967
<i>Atf2</i>	-0.636656
<i>H2-Eb1</i>	-0.613079
<i>Tlr2</i>	-0.594341

Table S9. Genes that had *p*-values less than 0.05 in the *M. vaccae* NCTC 11659/250 ng/mL LPS versus *M. vaccae* NCTC 11659/CMV comparison.

Gene Symbol	Log2 Fold Change
Upregulated	
<i>Elk1</i>	0.553416667
<i>Irf5</i>	0.516513333
<i>Map2k1</i>	0.513035667
<i>Il18</i>	0.511036667
<i>Prkcb</i>	0.502143
<i>Tlr3</i>	0.502013333
<i>Ptgir</i>	0.4707
<i>Rps6ka5</i>	0.458906667
<i>Myc</i>	0.455173333
<i>Prkca</i>	0.453177
<i>Tnfaip3</i>	0.399733333
<i>Cxcl10</i>	0.37518
<i>Mx2</i>	0.359341467
<i>Mapk8</i>	0.341558
<i>Nox1</i>	0.323453333
<i>Ifi27l2a</i>	0.27288
<i>Nfatc3</i>	0.271963667
<i>Oas1a</i>	0.267537
<i>Cebpb</i>	0.267276667
<i>Hif1a</i>	0.263643333
<i>Hmgb2</i>	0.256328333
<i>C4a</i>	0.248158333
<i>Stat2</i>	0.228993333
<i>Tlr4</i>	0.224303333
<i>Nod1</i>	0.210726667
<i>Mapkapk2</i>	0.188243333
<i>Traf2</i>	0.16002
<i>Rela</i>	0.15726
<i>Tlr6</i>	0.122373667
<i>Clqa</i>	0.11133
<i>Mapk3</i>	0.101563333
<i>Tgfbr1</i>	0.088243333
Downregulated	

<i>Mef2c</i>	-0.564018667
<i>Cd4</i>	-0.538076667
<i>Cfl1</i>	-0.52469
<i>Il10rb</i>	-0.521076667
<i>Gnas</i>	-0.498796667
<i>Rhoa</i>	-0.491613333
<i>Tlr1</i>	-0.475331667
<i>Rac1</i>	-0.450123333
<i>Mknk1</i>	-0.440986667
<i>Mapk14</i>	-0.438436667
<i>Tyrobp</i>	-0.435796667
<i>Myd88</i>	-0.420828333
<i>Mmp9</i>	-0.412677
<i>Mapk1</i>	-0.412053333
<i>Map3k1</i>	-0.392781
<i>Flt1</i>	-0.376388333
<i>Jun</i>	-0.3382
<i>Gnaq</i>	-0.333230667
<i>Oas2</i>	-0.331556667
<i>Tollip</i>	-0.292194667
<i>Mafg</i>	-0.269578333
<i>Cdc42</i>	-0.242263333
<i>Birc2</i>	-0.21882
<i>Pla2g4a</i>	-0.211443893
<i>Nfkb1</i>	-0.196643
<i>Tlr9</i>	-0.18426
<i>Tlr7</i>	-0.154416667
<i>Tcf4</i>	-0.15361
<i>Gnb1</i>	-0.14455
<i>Shc1</i>	-0.144303333
<i>Nfe2l2</i>	-0.127403333
<i>Tgfb1</i>	-0.12099
<i>Gngt1</i>	-0.113633333
<i>C3ar1</i>	-0.110406667
<i>Ly96</i>	-0.100955
<i>Mapkapk5</i>	-0.10086

Table S10. Sample size for real-time reverse transcription polymerase chain reaction (RT-PCR).

LPS Treatment	Bacterial Treatment	Sample Size (<i>n</i>)
0 ng/mL	BBS	3
	100 µg/mL <i>M. vaccae</i> NCTC 11659	2
250 ng/mL	BBS	2
	100 µg/mL <i>M. vaccae</i> NCTC 11659	3

Table S11. Total RNA concentrations in each sample prior to assessment using the NanoString nCounter system.

Sample Name	RNA concentration (ng/µl)
Sample 1 (BBS1/CMV)	4.5
Sample 2 (BBS2/CMV)	2.5
Sample 3 (BBS3/CMV)	4.7
Sample 4 (Mv1/CMV)	4.4
Sample 5 (Mv2/CMV)	4.4
Sample 6 (Mv3/CMV)	4.1
Sample 7 (BBS/LPS1)	5.1
Sample 8 (BBS/LPS2)	5.1
Sample 9 (BBS/LPS3)	4.8
Sample 10 (Mv/LPS1)	4.9
Sample 11 (Mv/LPS2)	5.6
Sample 12 (Mv/LPS3)	4.9

Abbreviations: BBS, borate-buffered saline; CMV, culture media vehicle; LPS, lipopolysaccharide; Mv, *Mycobacterium vaccae* NCTC 11659.