

S1. List of abbreviations for all gene symbols

AGER, advanced glycosylation end-product specific receptor

ALOX5, arachidonate 5-lipoxygenase

AREG, amphiregulin

ATF2, activating transcription factor 2

BCL2L1, BCL2 like 1

BCL6, BCL6 transcription repressor

BIRC2, baculoviral IAP repeat containing 2

C1QA, complement C1q A chain

C1QB, complement C1q B chain

C1S, complement C1s

C2, complement C2

C3, complement C3

C3AR1, complement C3a receptor 1

C4A, complement C4A (Rodgers blood group)

C5, complement C5

CCL13, C-C motif chemokine ligand 13

CCL17, C-C motif chemokine ligand 17

CCL19, C-C motif chemokine ligand 19

CCL2, C-C motif chemokine ligand 2

CCL20, C-C motif chemokine ligand 20

CCL21, C-C motif chemokine ligand 21

CCL22, C-C motif chemokine ligand 22

CCL23, C-C motif chemokine ligand 23

CCL24, C-C motif chemokine ligand 24

CCL3, C-C motif chemokine ligand 3

CCL4, C-C motif chemokine ligand 4

CCL5, C-C motif chemokine ligand 5

CCL8, C-C motif chemokine ligand 8

CCR1, C-C motif chemokine receptor 1

CCR2, C-C motif chemokine receptor 2

CCR7, C-C motif chemokine receptor 7

CD163, CD163 molecule

CD4, CD4 molecule

CD40, CD40 molecule

CD86, CD86 molecule

CEBPB, CCAAT enhancer binding protein beta

CFB, complement factor B

CFD, complement factor D

CFL1, cofilin 1

CREB1, cAMP responsive element binding protein 1

CSF1, colony stimulating factor 1

CSF3, colony stimulating factor 3

CXCL1, C-X-C motif chemokine ligand 1

CXCL10, C-X-C motif chemokine ligand 10

CXCL2, C-X-C motif chemokine ligand 2
CXCL3, C-X-C motif chemokine ligand 3
CXCL5, C-X-C motif chemokine ligand 5
CXCL6, C-X-C motif chemokine ligand 6
CXCR2, C-X-C motif chemokine receptor 2
CXCR4, C-X-C motif chemokine receptor 4
CYSLTR1, cysteinyl leukotriene receptor 1
DAXX, death domain associated protein
DDIT3, DNA damage inducible transcript 3
DEFA1, defensin alpha 1
ELK1, ETS transcription factor ELK1
FOS, Fos proto-oncogene, AP-1 transcription factor subunit
FXRD2, FXRD domain containing ion transport regulator 2
GNAQ, G protein subunit alpha q
GNAS, GNAS complex locus
GRB2, growth factor receptor bound protein 2
HDAC4, histone deacetylase 4
HIF1A, hypoxia inducible factor 1 subunit alpha
HLA-DRA, major histocompatibility complex, class II, DR alpha
HLA-DRB1, major histocompatibility complex, class II, DR beta 1
HMGB1, high mobility group box 1
HMGB2, high mobility group box 2
HMGNI, high mobility group nucleosome binding domain 1
HRAS, HRas proto-oncogene, GTPase
HSPB1, heat shock protein family B (small) member 1
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
IL10, interleukin 10
IL10RB, interleukin 10 receptor subunit beta
IL11, interleukin 11
IL12B, interleukin 12B
IL15, interleukin 15
IL18, interleukin 18
IL1A, interleukin 1 alpha
IL1B, interleukin 1 beta
IL1R1, interleukin 1 receptor type 1
IL1RAP, interleukin 1 receptor accessory protein
IL1RN, interleukin 1 receptor antagonist
IL23A, interleukin 23 subunit alpha
IL23R, interleukin 23 receptor
IL6R, interleukin 6 receptor
IL8, C-X-C motif chemokine ligand 8
IRF1, interferon regulatory factor 1
IRF3, interferon regulatory factor 3

IRF5, interferon regulatory factor 5
IRF7, interferon regulatory factor 7
ITGB2, integrin subunit beta 2
KEAP1, kelch like ECH associated protein 1
LIMK1, LIM domain kinase 1
LTB, lymphotoxin beta
LTB4R, leukotriene B4 receptor
LTB4R2, leukotriene B4 receptor 2
LY96, lymphocyte antigen 96
MAFF, MAF bZIP transcription factor F
MAFG, MAF bZIP transcription factor G
MAFK, MAF bZIP transcription factor K
MAP2K1, mitogen-activated protein kinase kinase 1
MAP2K4, mitogen-activated protein kinase kinase 4
MAP2K6, mitogen-activated protein kinase kinase 6
MAP3K1, mitogen-activated protein kinase kinase kinase 1
MAP3K5, mitogen-activated protein kinase kinase kinase 5
MAP3K7, mitogen-activated protein kinase kinase kinase 7
MAPK1, mitogen-activated protein kinase 1
MAPK14, mitogen-activated protein kinase 14
MAPK3, mitogen-activated protein kinase 3
MAPK8, mitogen-activated protein kinase 8
MAPKAPK2, MAPK activated protein kinase 2
MAPKAPK5, MAPK activated protein kinase 5
MAX, MYC associated factor X
MEF2C, myocyte enhancer factor 2C
MEF2D, myocyte enhancer factor 2D
MKNK1, MAPK interacting serine/threonine kinase 1
MMP9, matrix metalloproteinase 9
MRC1, mannose receptor C-type 1
MX1, MX dynamin like GTPase 1
MX2, MX dynamin like GTPase 2
MYC, MYC proto-oncogene, bHLH transcription factor
MYD88, MYD88 innate immune signal transduction adaptor
NFATC3, nuclear factor of activated T cells 3
NFE2L2, nuclear factor, erythroid 2 like 2
NFKB1, nuclear factor kappa B subunit 1
NLRP3, NLR family pyrin domain containing 3
NOD1, nucleotide binding oligomerization domain containing 1
NOD2, nucleotide binding oligomerization domain containing 2
NR3C1, nuclear receptor subfamily 3 group C member 1
OAS2, 2'-5'-oligoadenylate synthetase 2
OASL, 2'-5'-oligoadenylate synthetase like
OXER1, oxoeicosanoid receptor 1
PDGFA, platelet derived growth factor subunit A
PLA2G4A, phospholipase A2 group IVA

PLCB1, phospholipase C beta 1
PPP1R12B, protein phosphatase 1 regulatory subunit 12B
PRKCA, protein kinase C alpha
PRKCB, protein kinase C beta
PTGER2, prostaglandin E receptor 2
PTGER4, prostaglandin E receptor 4
PTGIR, prostaglandin I2 receptor
PTGS1, prostaglandin-endoperoxide synthase 1
PTGS2, prostaglandin-endoperoxide synthase 2
PTK2, protein tyrosine kinase 2
RAC1, Rac family small GTPase 1
RAF1, Raf-1 proto-oncogene, serine/threonine kinase
RAPGEF2, Rap guanine nucleotide exchange factor 2
RELA, RELA proto-oncogene, NF-kB subunit
RELB, RELB proto-oncogene, NF-kB subunit
RHOA, ras homolog family member A
RIPK1, receptor interacting serine/threonine kinase 1
RIPK2, receptor interacting serine/threonine kinase 2
ROCK2, Rho associated coiled-coil containing protein kinase 2
RPS6KA5, ribosomal protein S6 kinase A5
SHC1, SHC adaptor protein 1
SMAD7, SMAD family member 7
STAT1, signal transducer and activator of transcription 1
STAT2, signal transducer and activator of transcription 2
STAT3, signal transducer and activator of transcription 3
TCF4, transcription factor 4
TGFB1, transforming growth factor beta 1
TGFB2, transforming growth factor beta 2
TGFBR1, transforming growth factor beta receptor 1
TLR1, toll like receptor 1
TLR2, toll like receptor 2
TLR4, toll like receptor 4
TLR5, toll like receptor 5
TLR6, toll like receptor 6
TLR7, toll like receptor 7
TLR8, toll like receptor 8
TNF, tumor necrosis factor
TNFAIP3, TNF alpha induced protein 3
TNFSF14, TNF superfamily member 14
TOLLIP, toll interacting protein
TRADD, TNFRSF1A associated via death domain
TRAF2, TNF receptor associated factor 2
TREM2, triggering receptor expressed on myeloid cells 2
TWIST2, twist family bHLH transcription factor 2
TYROBP, transmembrane immune signaling adaptor TYROBP

S2. Supplemental results

S2.1. Cell viability

Analysis revealed no main effect of either *M. vaccae* NCTC 11659 ($F_{(4, 30)} = 0.8854$, $p = 0.4845$) or LPS ($F_{(1, 30)} = 0.4101$, $p = 0.5268$), nor was there an interaction effect ($F_{(4, 30)} = 0.2806$, $p = 0.8882$; Fig. S1).

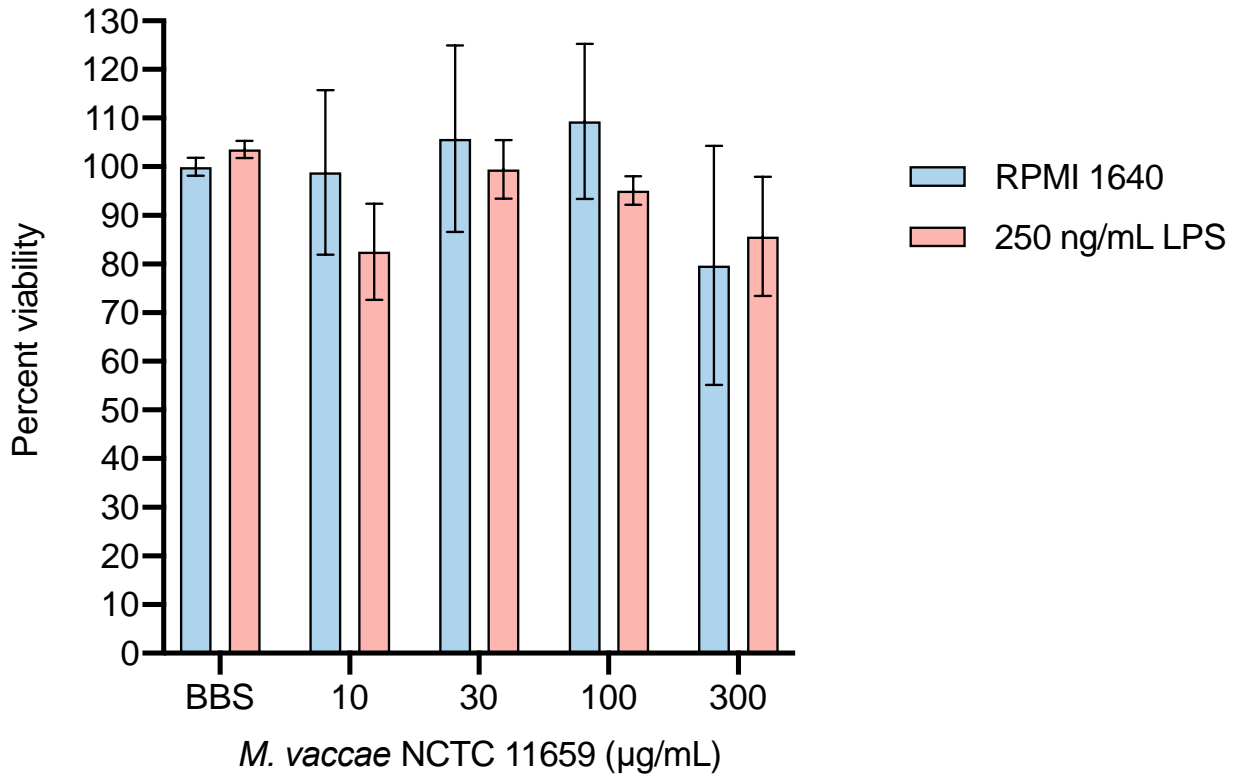


Figure S1. Treating THP-1-derived macrophages with *M. vaccae* NCTC 11659 (0, 10, 30, 100, or 300 µg/mL; 48 h) and lipopolysaccharide (0, 250 ng/mL; 24 h) did not change cell viability. Data are expressed as percent viable cells relative to the BBS/RPMI 1640 condition. Cell viability was assessed by flow cytometry gating of live singlets based on forward and side scatter (FSC/SSC). Sample sizes can be found in Table S1. Abbreviations: BBS, borate-buffered saline; LPS, lipopolysaccharide.

S2.2. Analysis of NanoString housekeeping genes

S2.2.1. CTLC

Analysis revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(2, 29)} = 5.464$, $p = 0.0097$). Dunnett's multiple comparisons test revealed significant differences between BBS/RPMI 1640 vs. 300 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 ($p = 0.0018$), BBS/RPMI 1640 vs. BBS/250 ng/mL LPS ($p < 0.0001$), 30 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 vs. 30 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p < 0.0001$), and 300 µg/mL *M. vaccae* NCTC

11659/RPMI 1640 vs. 300 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p = 0.0042$). Fig. S2.

S2.2.2. *GAPDH*

Analysis revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(2, 29)} = 21.84$, $p < 0.0001$). Dunnett's multiple comparisons test revealed significant differences between BBS/RPMI 1640 vs. BBS/250 ng/mL LPS ($p < 0.0001$), BBS/250 ng/mL LPS vs. 30 µg/mL *M. vaccae* NCTC 11659 ($p < 0.0001$), and BBS/250 ng/mL LPS vs. 300 µg/mL *M. vaccae* NCTC 11659 ($p < 0.0001$; Fig. S2).

S2.2.3. *GUSB*

Analysis revealed an *M. vaccae* NCTC 11659 main effect ($F_{(2, 29)} = 15.31$, $p < 0.0001$), but no main effect of LPS nor an interaction effect. Dunnett's multiple comparisons test revealed significant differences between BBS/RPMI 1640 vs. 300 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 ($p = 0.0111$) and BBS/250 ng/mL LPS vs. 300 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p = 0.0035$; Fig. S2).

S2.2.4. *HPRT1*

Analysis revealed an LPS main effect ($F_{(1, 29)} = 36.53$, $p < 0.0001$), but no main effect of *M. vaccae* NCTC 11659 nor an interaction effect. Dunnett's multiple comparisons test revealed significant differences between 30 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 vs. 30 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p = 0.0138$) and 300 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 vs. 300 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p = 0.0010$; Fig. S2).

S2.2.5. *PGK1*

Analysis revealed an *M. vaccae* NCTC 11659 main effect ($F_{(2, 29)} = 38.89$, $p < 0.0001$), but no main effect of LPS nor an interaction effect. Dunnett's multiple comparisons test revealed significant differences between BBS/RPMI 1640 vs. 30 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 ($p < 0.0001$), BBS/RPMI 1640 vs. 300 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 ($p < 0.0001$), BBS/250 ng/mL LPS vs. 30 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p = 0.0027$), and BBS/250 ng/mL LPS vs. 300 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p = 0.0002$; Fig. S2).

S2.2.6. *TUBB*

Analysis revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(2, 29)} = 4.294$, $p < 0.0233$). Dunnett's multiple comparisons test revealed significant differences between BBS/RPMI 1640 vs. BBS/250 ng/mL LPS ($p < 0.0001$), 30 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 vs. 30 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p < 0.0001$), and 300 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 vs. 300 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS ($p < 0.0001$; Fig. S2).

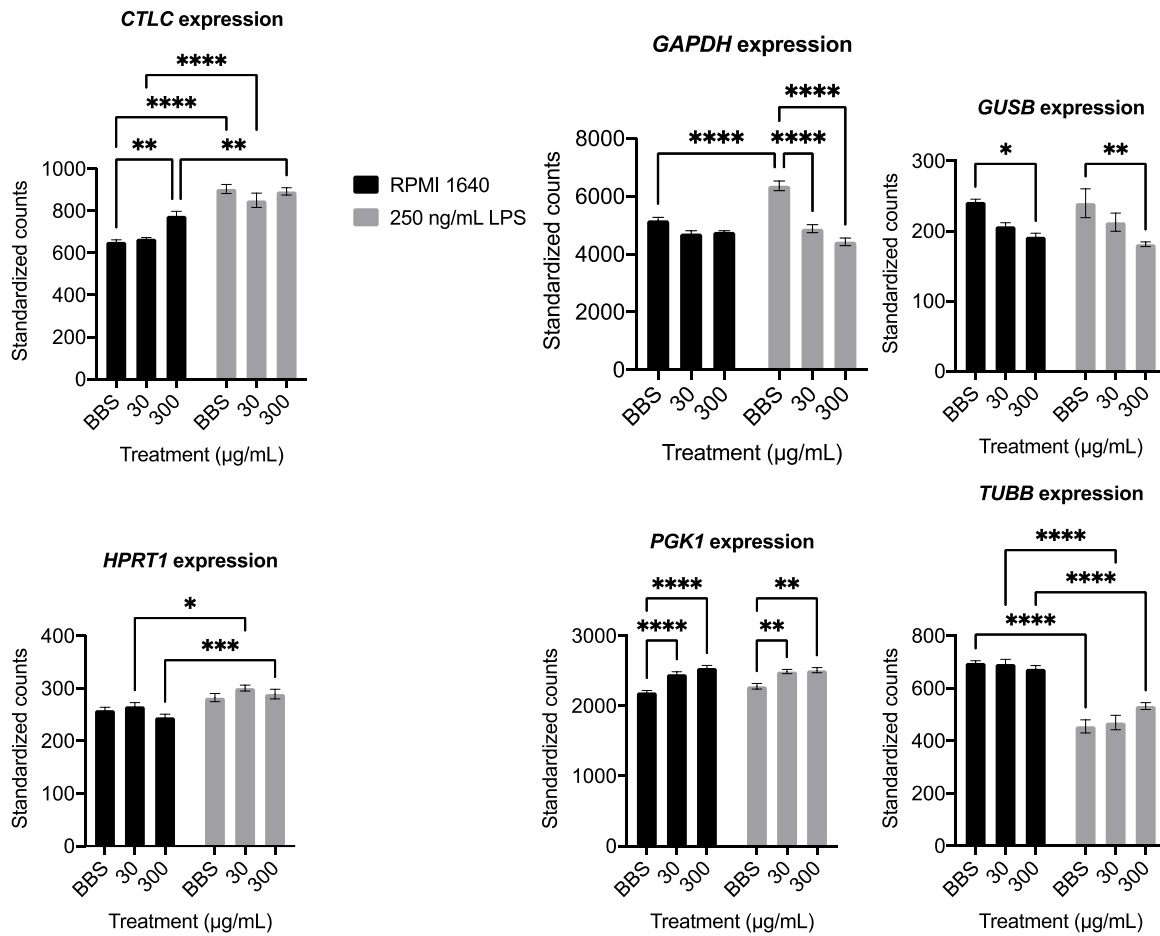


Figure S2. Treating human THP-1 monocyte-derived macrophages with *M. vaccae* NCTC 11659 (48 h) and lipopolysaccharide (LPS; 250 ng/mL, 24 h) resulted in differential expression of all internal housekeeping genes in *Experiment 1*. Abbreviations: BBS, borate-buffered saline; LPS, lipopolysaccharide.

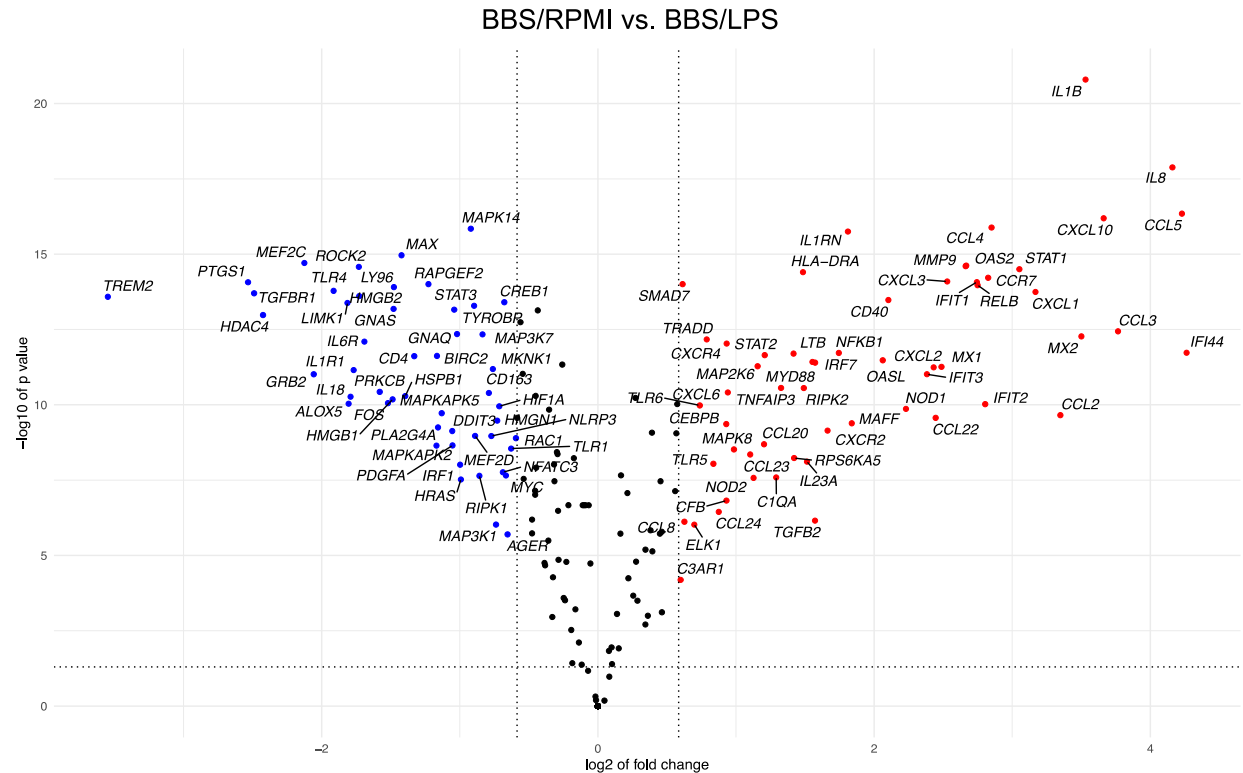


Figure S3. Volcano plot illustrating that lipopolysaccharide (LPS; 250 ng/mL, 24 h) induced an inflammatory gene expression phenotype in human THP-1 derived macrophages. The x axis is the log base 2 of the fold change and the y axis is the negative log base 10 of the p -value. Each dot in the figure represents a specific gene. The blue dots in the upper left quadrant of the volcano plot represent the genes that were expressed at lower levels in the BBS vehicle/250 ng/mL LPS group relative to the BBS vehicle/RPMI 1640 vehicle group. The red dots in the upper right quadrant of the volcano plot represent the genes in the BBS vehicle/250 ng/mL LPS group that were expressed at higher levels relative to the BBS vehicle/RPMI 1640 vehicle group. The black dots represent genes that were not differentially expressed between the groups (i.e., the absolute value of the log base 2 of fold change < 1.5 or p -value > 0.05). The dashed vertical lines represent log base 2 fold changes of approximately -0.6 or 0.6 (i.e., genes with an absolute fold change of at least 1.5). The horizontal dashed line is the negative log base 10 of p -value alpha level of 0.05. The volcano plot was generated using the ggplot2 and ggrepel packages. See S1. List of abbreviations for all gene symbols for a complete list of definitions of gene symbols (S1, Supplementary Material online).

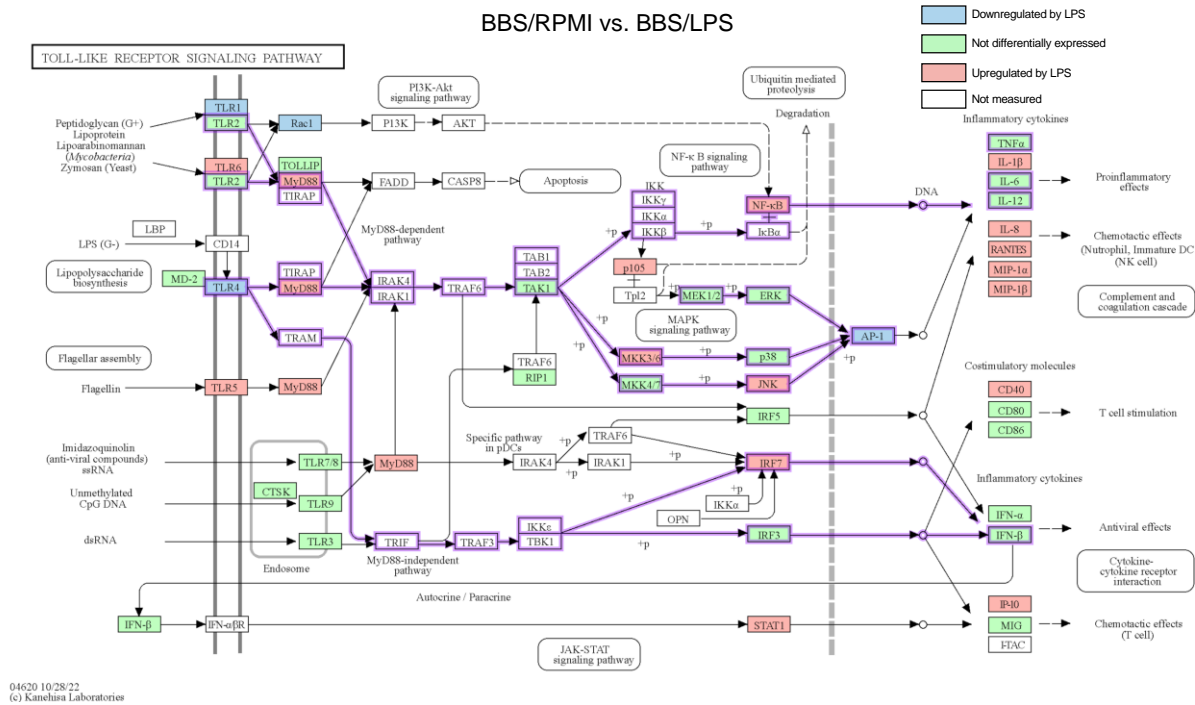


Figure S4. Toll-Like Receptor Signaling KEGG pathway color coded to reflect the effects of 250 ng/mL lipopolysaccharide (LPS). Purple lines indicate TLR2 and TLR4 signaling pathways. Genes highlighted in blue were downregulated by 250 ng/mL LPS, genes highlighted in green were not differentially expressed, genes highlighted in red were upregulated by 250 ng/mL LPS, and genes in white were not measured.

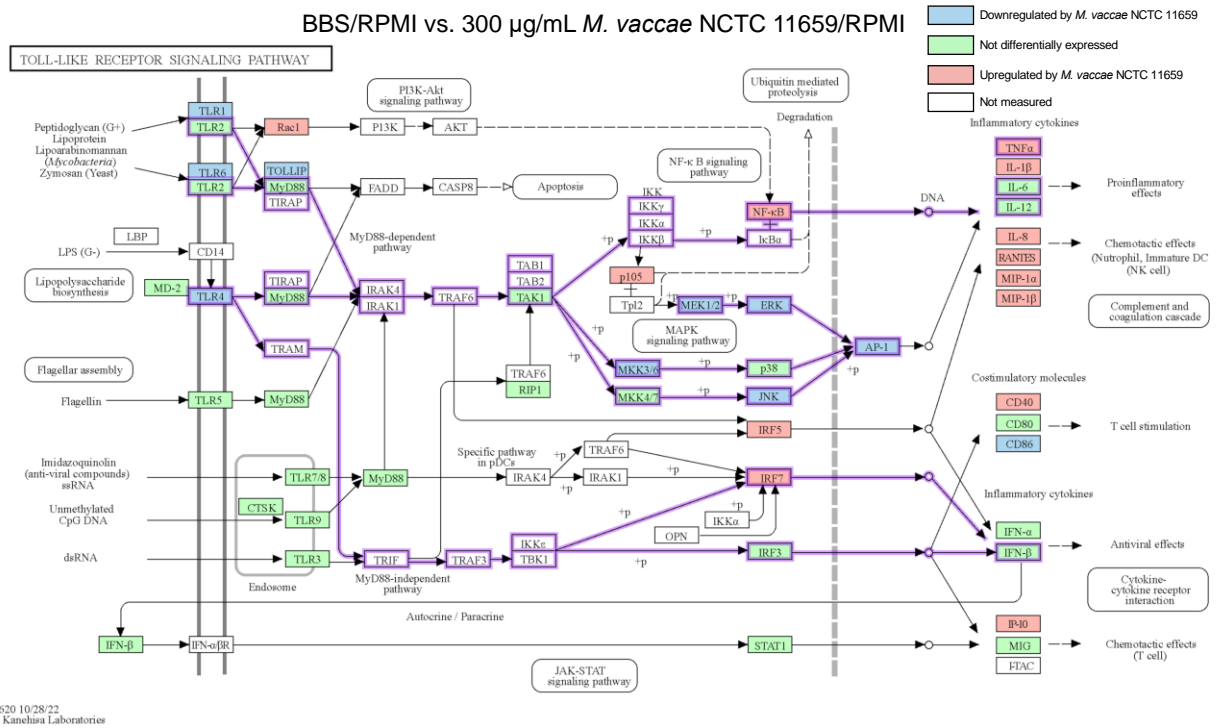


Figure S5. Toll-Like Receptor Signaling KEGG pathway color coded to reflect the effects of 300 μ g/mL *M. vaccae* NCTC 11659. Purple lines indicate TLR2 and TLR4 signaling pathways. Genes highlighted in blue were downregulated by 300 μ g/mL *M. vaccae* NCTC 11659, genes highlighted in green were not differentially expressed, genes highlighted in red were upregulated by 300 μ g/mL *M. vaccae* NCTC 11659, and genes in white were not measured.

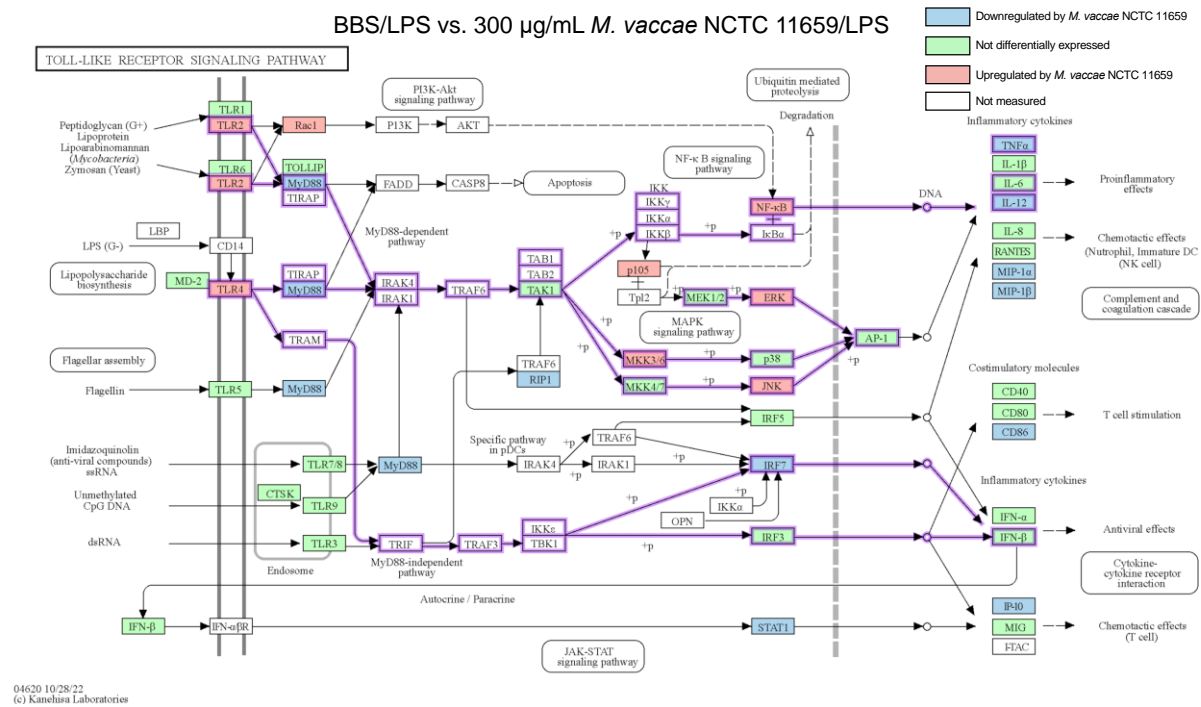


Figure S6. Toll-Like Receptor Signaling KEGG pathway color coded to reflect the effects of *M. vaccae* NCTC 11659 in the presence of 250 ng/mL lipopolysaccharide (LPS). Purple lines indicate TLR2 and TLR4 signaling pathways. Genes highlighted in blue were downregulated by 300 μ g/mL *M. vaccae* NCTC 11659, genes highlighted in green were not differentially expressed, genes highlighted in red were upregulated by 300 μ g/mL *M. vaccae* NCTC 11659, and genes in white were not measured.

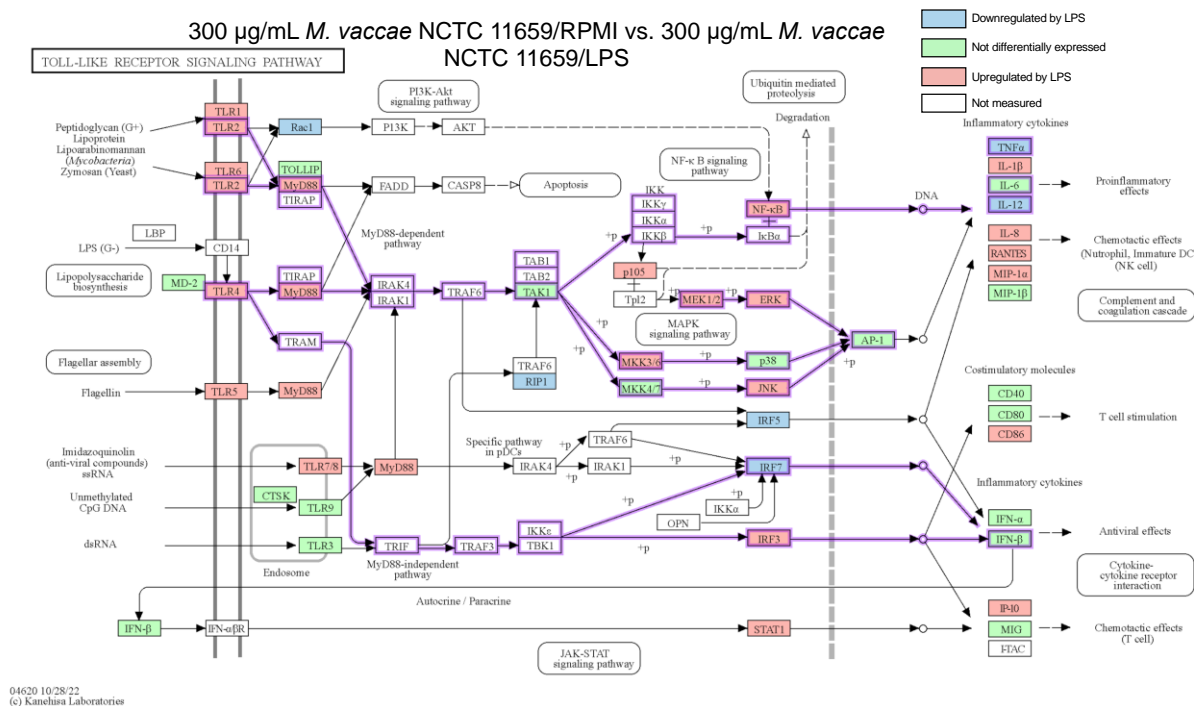


Figure S8. Toll-Like Receptor Signaling KEGG pathway color coded to reflect the effects of 250 ng/mL lipopolysaccharide (LPS) in the presence of 300 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659. Purple lines indicate TLR2 and TLR4 signaling pathways. Genes highlighted in blue were downregulated by 250 ng/mL LPS, genes highlighted in green were not differentially expressed, genes highlighted in red were upregulated by 250 ng/mL LPS, and genes in white were not measured.

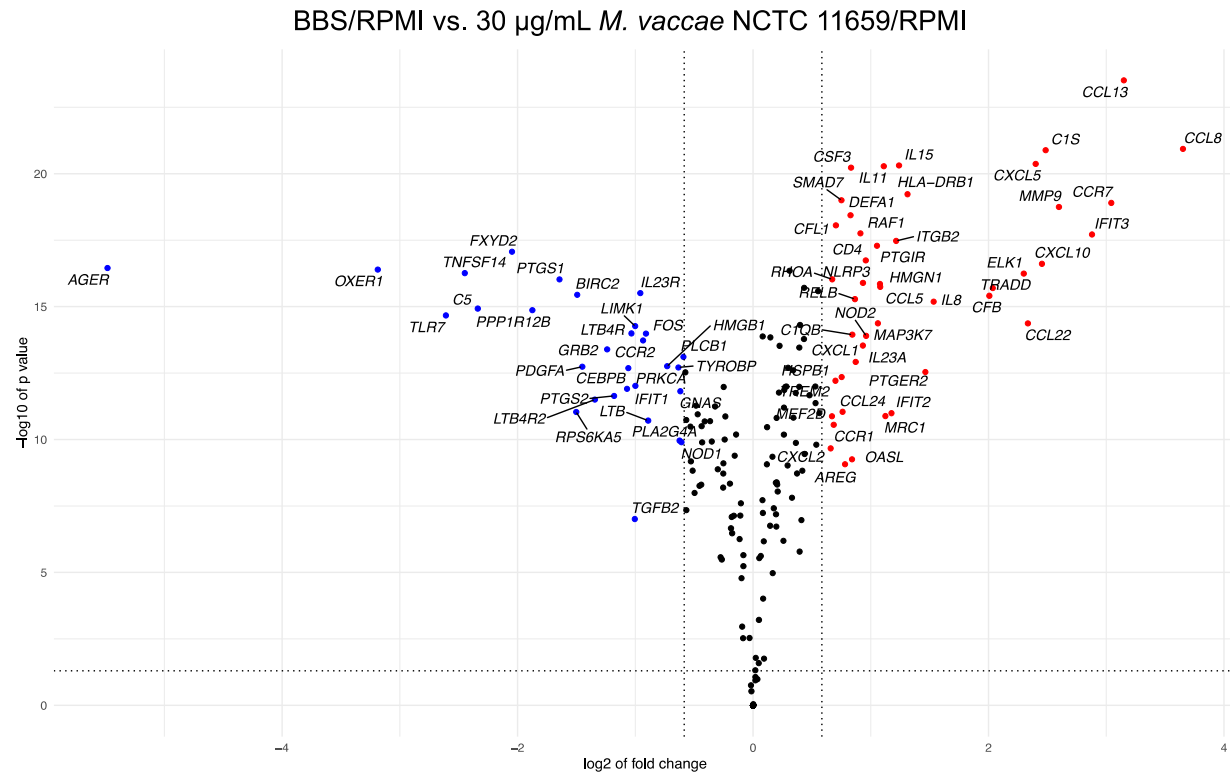


Figure S9. Volcano plot illustrating that, in the RPMI 1640 vehicle control condition, *M. vaccae* NCTC 11659 (30 μ g/mL) results in differential expression of both proinflammatory and anti-inflammatory markers in human THP-1-derived macrophages. The x axis is the log base 2 of the fold change and the y axis is the negative log base 10 of the *p*-value. Each dot in the figure represents a specific gene. The blue dots in the upper left quadrant of the volcano plot represent the genes that were expressed at lower levels in 30 μ g/mL *M. vaccae* NCTC 11659/RPMI 1640 vehicle group relative to the BBS vehicle/RPMI 1640 vehicle group. The red dots in the upper right quadrant of the volcano plot represent the genes in the 30 μ g/mL *M. vaccae* NCTC 11659/RPMI 1640 vehicle group that were expressed at higher levels relative to the BBS vehicle/RPMI 1640 vehicle group. The black dots represent genes that were not differentially expressed between the groups (i.e., the absolute value of the log base 2 of fold change < 1.5 or *p*-value > 0.05). The dashed vertical lines represent log base 2 fold changes of approximately -0.6 or 0.6 (i.e., genes with a fold change of at least 1.5). The horizontal dashed line is the negative log base 10 of adjusted *p*-value alpha level of 0.05. The volcano plot was generated using the ggplot2 and ggrepel packages. See S1. List of abbreviations for all gene symbols for a complete list of definitions of gene symbols (S1, Supplementary Material online).

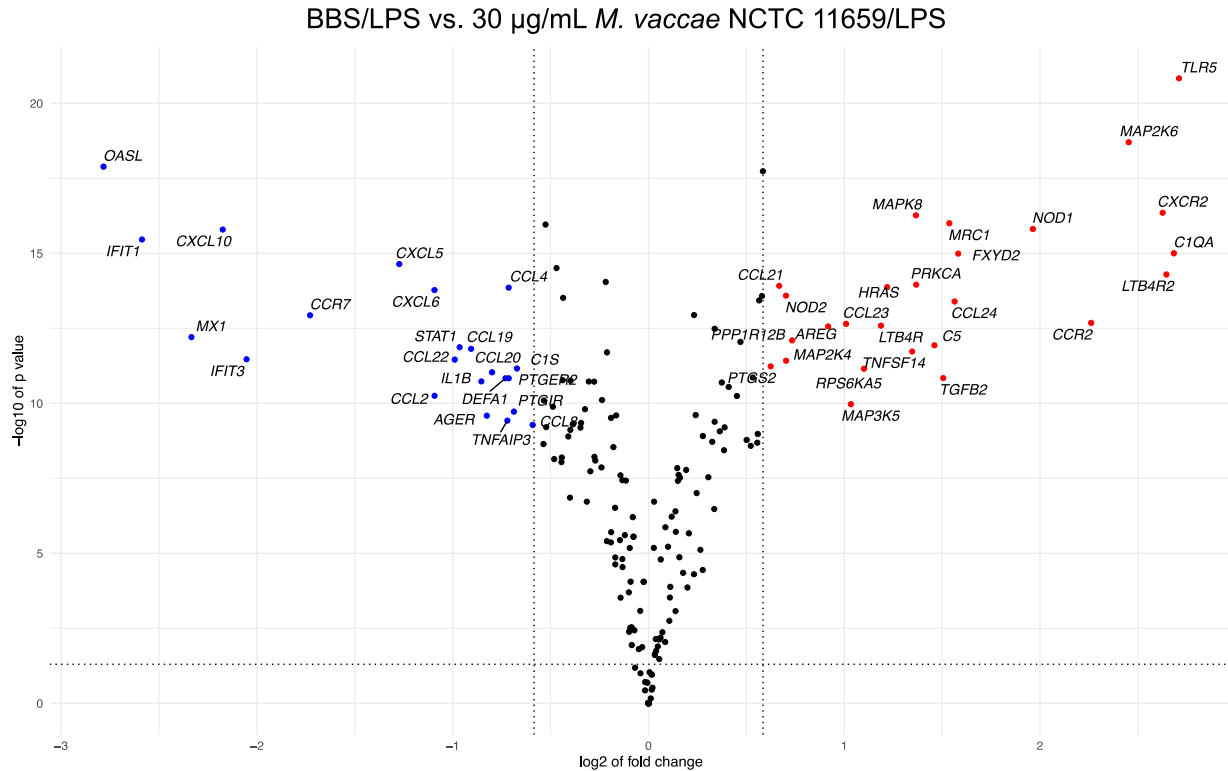


Figure S10. Volcano plot illustrating that, in the lipopolysaccharide (LPS; 250 ng/mL) challenge condition, *M. vaccae* NCTC 11659 (30 μ g/mL) shifted human THP-1-derived macrophages toward an anti-inflammatory phenotype, for example, with increased *TGFB2*, *MRC1* expression and decreased *IL1B* and *STAT1* expression when assessed 24 h after LPS challenge. The x axis is the log base 2 of the fold change and the y axis is the negative log base 10 of the *p*-value. Each dot in the figure represents a specific gene. The blue dots in the upper left quadrant of the volcano plot represent the genes that were expressed at lower levels in 30 μ g/mL *M. vaccae* NCTC 11659/250 ng/mL LPS group relative to BBS vehicle/250 ng/mL LPS group. The red dots in the upper right quadrant of the volcano plot represent the genes in 30 μ g/mL *M. vaccae* NCTC 11659/250 ng/mL LPS group that were expressed at higher levels relative to the BBS vehicle/250 ng/mL LPS group. The black dots represent genes that were not differentially expressed between the groups (i.e., the absolute value of the log base 2 of fold change < 1.5 or adjusted *p*-value > 0.05). The dashed vertical lines represent log base 2 fold changes of approximately -0.6 or 0.6 (i.e., genes with a fold change of at least 1.5). The horizontal dashed line is the negative log base 10 of *p*-value alpha level of 0.05. The volcano plot was generated using the ggplot2 and ggrepel packages. See S1. *List of abbreviations for all gene symbols* for a complete list of definitions of gene symbols (S1, Supplementary Material online).

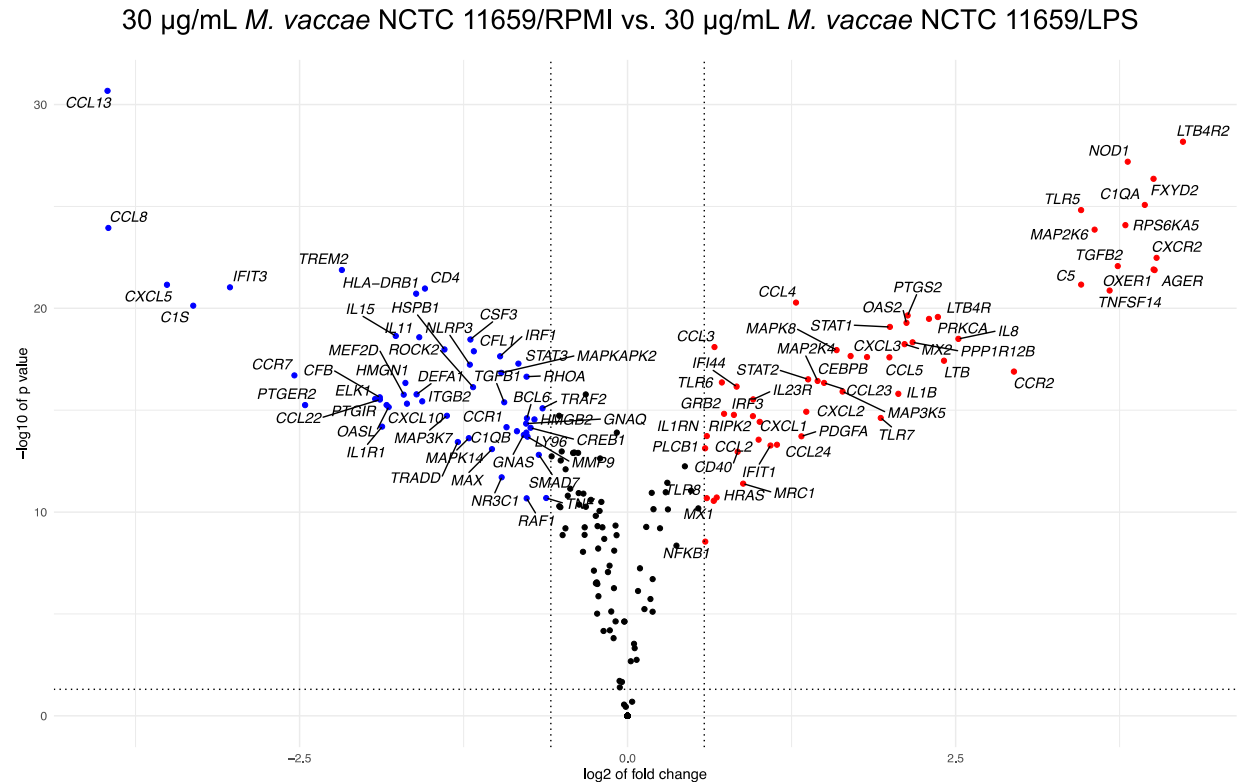


Figure S11. Volcano plot illustrating that, under the *M. vaccae* NCTC 11659 (30 $\mu\text{g/mL}$) treatment condition, lipopolysaccharide (LPS; 250 ng/mL) downregulated a number of genes involved in the LPS-induced $\text{NF}\kappa\text{B}$ signaling cascade in THP-1-derived macrophages, including *LY96*, *MAP3K7*, *MAPK14*, *TNF*, and downregulated genes associated with LPS induction of *NLRP3*, a key component of the *NLRP3* inflammasome. The x axis is the log base 2 of the fold change and the y axis is the negative log base 10 of the *p*-value. Each dot in the figure represents a specific gene. The blue dots in the upper left quadrant of the volcano plot represent the genes that were expressed at lower levels in 30 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/250 ng/mL LPS group relative to *M. vaccae* NCTC 11659/RPMI 1640 vehicle control group. The red dots in the upper right quadrant of the volcano plot represent the genes in the 30 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/250 ng/mL LPS group that were expressed at higher levels relative to the 30 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/RPMI 1640 vehicle control group. The black dots represent genes that were not differentially expressed between the groups (i.e., the absolute value of the log base 2 of fold change < 1.5 or adjusted *p*-value > 0.05). The dashed vertical lines represent log base 2 fold changes of approximately -0.6 or 0.6 (i.e., genes with a fold change of at least 1.5). The horizontal dashed line is the negative log base 10 of *p*-value alpha level of 0.05. The volcano plot was generated using the ggplot2 and ggrepel packages. See S1. List of abbreviations for all gene symbols for a complete list of definitions of gene symbols (S1, Supplementary Material online).

S2.3. Analysis of *ACTB* housekeeping gene for real time RT-PCR

Analysis revealed a main effect of *M. vaccae* NCTC 11659 ($F_{(4, 134)} = 4.556$, $p = 0.0018$) and LPS ($F_{(3, 134)} = 42.75$, $p < 0.0001$). Dunnett's multiple comparisons test revealed significant differences between BBS/RPMI 1640 and BBS/0.5 ng/mL LPS ($p = 0.0038$), 10 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/RPMI 1640 and 10 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/0.5 ng/mL LPS ($p <$

0.0001), 10 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/RPMI 1640 and 10 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/2.5 ng/mL LPS ($p < 0.0001$), 10 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/RPMI 1640 and 10 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/250 ng/mL LPS ($p = 0.0036$), 30 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/RPMI 1640 and 30 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/0.5 ng/mL LPS ($p = 0.0002$), 300 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/RPMI 1640 and 300 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/0.5 ng/mL LPS ($p < 0.0001$), and 300 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/RPMI 1640 and 300 $\mu\text{g/mL}$ *M. vaccae* NCTC 11659/2.5 ng/mL LPS ($p = 0.0095$; Fig. S12).

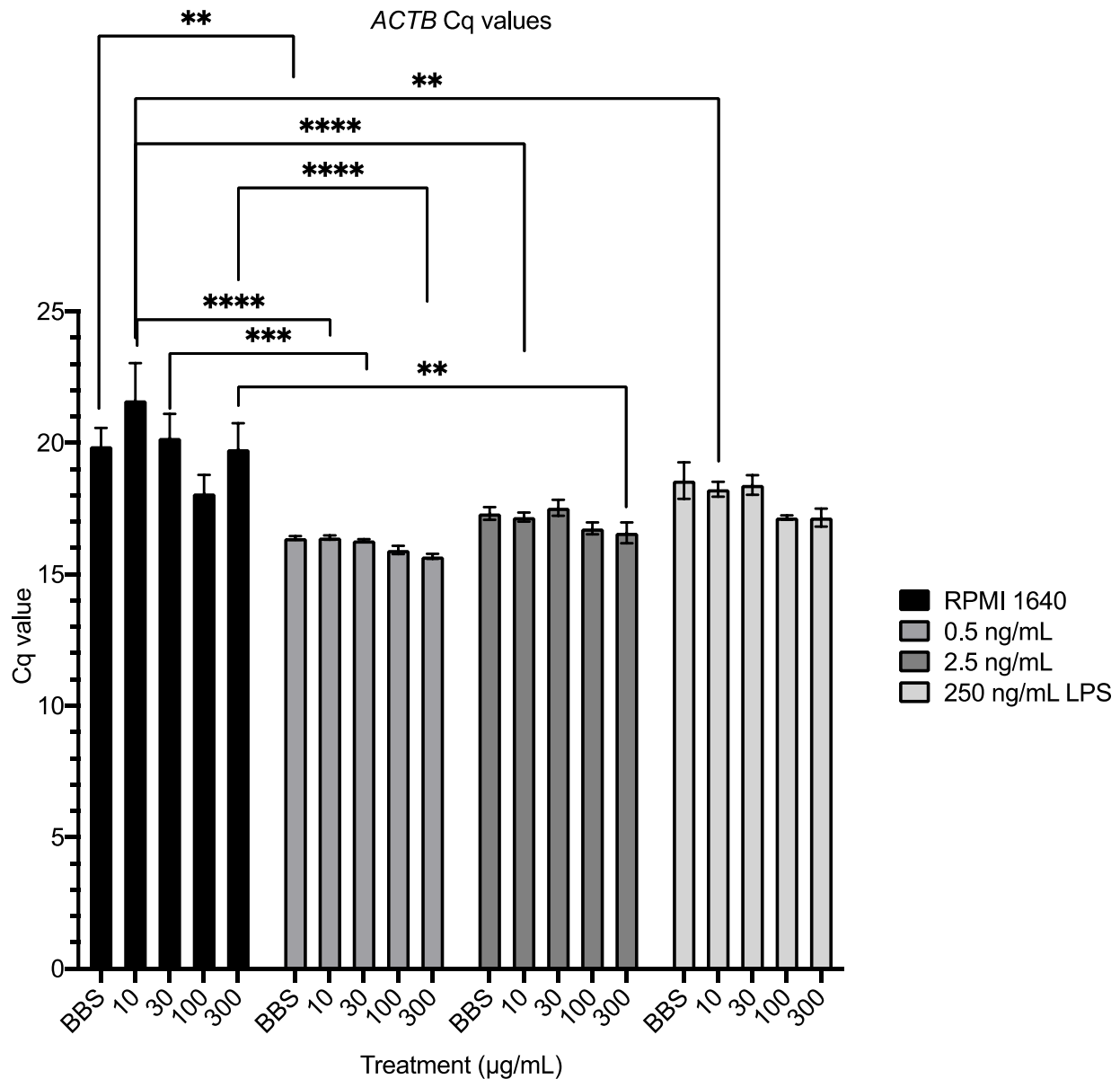


Figure S12. Effects of treatment of THP-1-derived macrophages with *M. vaccae* NCTC 11659 (0, 10, 30, 100, or 300 $\mu\text{g/mL}$; 48 h) and lipopolysaccharide (0, 250 ng/mL; 24 h) on the expression of *ACTB*. Abbreviations: BBS, borate-buffered saline. LPS, lipopolysaccharide.

S2.4. Validation of effects of heat-killed *M. vaccae* NCTC 11659 and LPS on proinflammatory *IL12A*, *IL12B*, and *IL23A* gene expression using real time RT-PCR

In the sections below, we describe results from experiments designed to measure expression of genes encoding major inflammatory cytokines in macrophages by extracting total RNA from THP-1 monocyte-derived macrophages and performing real time PCR as described above. Analysis of the housekeeping gene, *ACTB*, for differential expression across treatment groups found no meaningful differences in expression (Fig. S12, Supplementary Material online).

S2.4.1. *IL12A* mRNA expression

IL-12 production in macrophages is a marker of macrophages with a proinflammatory bias in mice (Orecchioni et al., 2019), and humans (Mantovani et al., 2004). Given IL-12 is a dimer between IL-12p35 (derived from *IL12A*) and IL-12p40 (derived from *IL12B*), *IL12A* and *IL12B* mRNA expression were measured in THP-1 monocyte-derived macrophages after incubating them with various concentrations of *M. vaccae* NCTC 11659 and LPS as described above. Analysis of *IL12A* mRNA expression revealed an *M. vaccae* NCTC 11659 x LPS interaction that approached statistical significance ($F_{(12, 103)} = 1.784$, $p = 0.06$), while main effects of *M. vaccae* NCTC 11659 and LPS were both significant (*M. vaccae* NCTC 11659, $F_{(4, 103)} = 3.732$, $p < 0.01$; LPS, $F_{(3, 103)} = 22.92$, $p < 0.001$). Despite many non-detects in the 0 ng/mL LPS control conditions (i.e., 67.5% of samples were RT-PCR non-detects, Table S1, Supplementary Material online), likely due to the lack of IFN- γ stimulation (Ma et al., 2015; Ma et al., 1996; Grohmann et al., 2001), the trend was for higher concentrations of LPS to increase *IL12A* mRNA expression, and for *M. vaccae* NCTC 11659 to mitigate this effect. Challenging THP-1 monocyte-derived macrophages with 250 ng/mL LPS, relative to the RPMI 1640 control condition, increased *IL12A* mRNA expression in the 300 μ g/mL *M. vaccae* NCTC 11659 condition. *M. vaccae* NCTC 11659 had no effect on *IL12A* mRNA expression at any of the concentrations of LPS studied (Fig. S13A, Supplementary Material online). Post hoc p values for all planned pairwise comparisons can be found in Table S10, Supplementary Material online.

S2.4.2. *IL12B* mRNA expression

Analysis of *IL12B* mRNA expression revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(12, 122)} = 13.02$, $p < 0.001$) as well as main effects of *M. vaccae* NCTC 11659 ($F_{(4, 122)} = 6.189$, $p < 0.001$) and LPS ($F_{(3, 122)} = 666.8$, $p < 0.001$). Exposure of THP-1 monocyte-derived macrophages to *M. vaccae* NCTC 11659, in the absence of LPS or at a low concentration of LPS (0.5 ng/mL), increased *IL12B* mRNA expression in a concentration dependent manner (Fig. S13B, Supplementary Material online). Likewise, exposure of THP-1 monocyte-derived macrophages to LPS, in the absence of *M. vaccae* NCTC 11659, increased *IL12B* mRNA expression in a concentration dependent manner (Fig. S13B, Supplementary Material online). However, pretreatment with *M. vaccae* NCTC 11659 attenuated LPS-induced increases in *IL12B* mRNA expression at the highest concentration of LPS studied (i.e., 250 ng/mL; Fig. S13B, Supplementary Material online). Post hoc p values for all planned pairwise comparisons can be found in Table S10, Supplementary Material online.

S2.4.3. *IL23A* mRNA expression

IL-23, a dimer consisting of IL-12p40 and IL-23p19, production in macrophages is a marker of macrophages with a proinflammatory bias (Yamaguchi et al., 2017; Viola et al., 2019), but see (Hou et al., 2018). *IL23A* (encoding IL-23p19) mRNA expression was measured in THP-1 monocyte-derived macrophages after incubating them with various concentrations of *M. vaccae* NCTC 11659 and LPS as described above. Analysis of *IL23A* mRNA expression revealed an *M.*

vaccae NCTC 11659 x LPS interaction ($F_{(12, 140)} = 13.88, p < 0.001$), an *M. vaccae* NCTC 11659 main effect that approached statistical significance ($F_{(4, 140)} = 2.083, p = 0.086$), and an LPS main effect ($F_{(3, 140)} = 13.02, p < 0.001$). Exposure of THP-1 monocyte-derived macrophages to *M. vaccae* NCTC 11659 in the absence of LPS increased *IL23A* mRNA expression in a concentration dependent manner (Fig. S13C, Supplementary Material online). Likewise, exposure of THP-1 monocyte-derived macrophages to LPS in the absence of *M. vaccae* NCTC 11659 increased *IL23A* mRNA expression in a concentration dependent manner (Fig. S13C, Supplementary Information online). However, pretreatment with *M. vaccae* NCTC 11659 attenuated LPS-induced increases in *IL23A* mRNA expression at the highest concentration of LPS studied (i.e., 250 ng/mL; Fig. S13C, Supplementary Material online). Post hoc p values for all planned pairwise comparisons can be found in Table S10, Supplementary Material online.

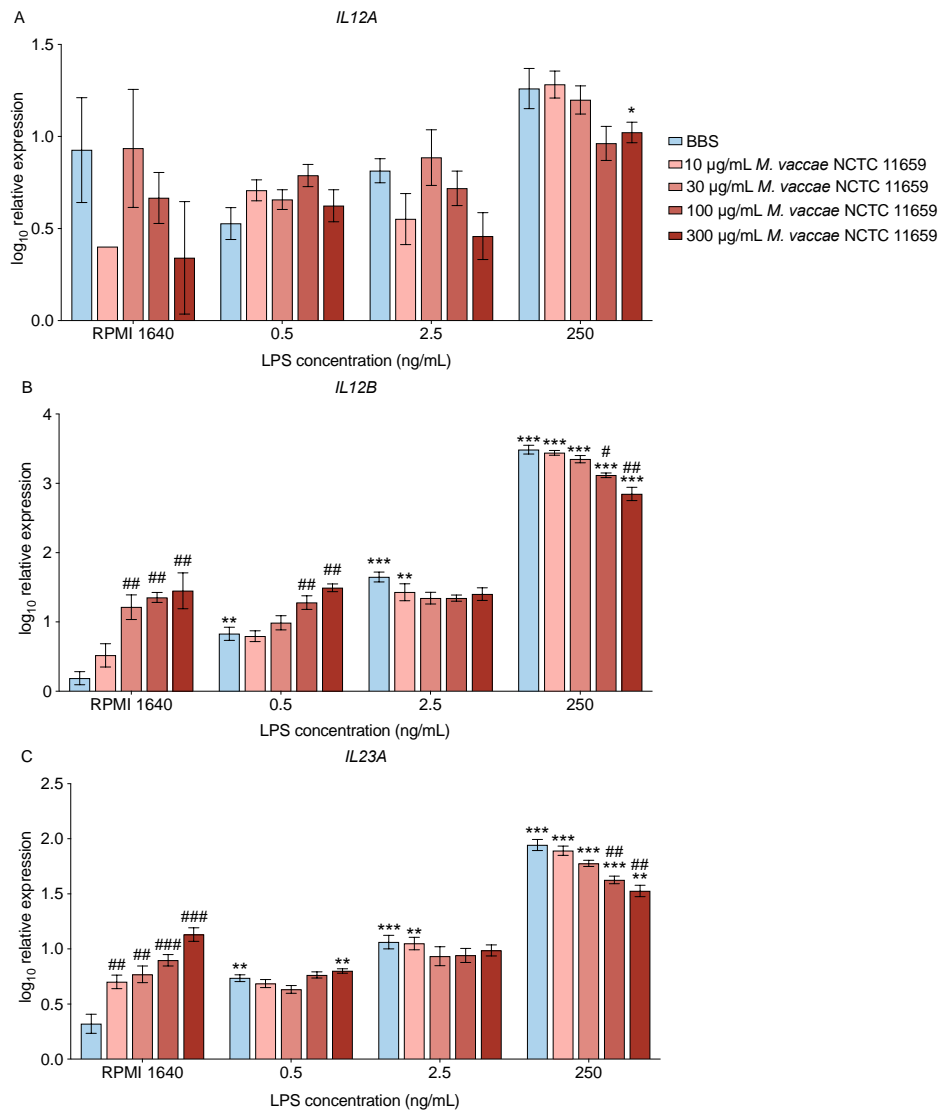


Figure S13. Heat-killed *M. vaccae* NCTC 11659 modulates lipopolysaccharide (LPS)-induced increases in inflammation in THP-1 monocyte-derived macrophages by downregulating inflammatory gene expression. Gene expression was measured using real time reverse

transcription polymerase chain reaction (RT-PCR) and is represented relative to the highest Cq value for each gene using the $2^{-\Delta\Delta C_t}$ method. Data represent means \pm SEM. Numbers on the x-axis indicate the concentration of LPS in ng/mL. Data were analyzed using a two-way ANOVA followed by Dunnett's multiple comparisons tests using a single pooled error value from all 20 treatment groups, if appropriate, at a two-tailed alpha level of 0.05. Darker colors represent sequentially higher concentrations of *M. vaccae* NCTC 11659. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, effect of LPS, within the same *M. vaccae* NCTC 11659 condition, using RPMI 1640 groups as the comparison groups. # $p < 0.05$, ## $p < 0.01$, ### $p < 0.001$, effect of *M. vaccae* NCTC 11659, within the same LPS condition, using the BBS condition as the comparison group. **A)** *IL12A* mRNA expression. **B)** *IL12B* mRNA expression. **C)** *IL23A* mRNA expression. Abbreviations: BBS, borate-buffered saline; LPS, lipopolysaccharide; NCTC, National Collection of Type Cultures. Sample sizes can be found in Table S1, Supplementary Material online.

S2.5. Effects of heat-killed M. vaccae NCTC 11659 and LPS on IL10 and TGFB1 mRNA expression

IL-10 and TGF- β 1 production are biomarkers of macrophages with an anti-inflammatory bias (Viola et al., 2019). *IL10* and *TGFB1* gene expression levels were measured in THP-1 monocyte-derived macrophages after incubating them with various concentrations of *M. vaccae* NCTC 11659 and LPS as described above.

S2.5.1. IL10 mRNA expression

Analysis of *IL10* mRNA expression revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(12, 139)} = 2.971$, $p < 0.001$) as well as main effects of *M. vaccae* NCTC 11659 ($F_{(4, 139)} = 14.81$, $p < 0.001$) and LPS ($F_{(3, 139)} = 4.149$, $p < 0.01$). Exposure of THP-1 monocyte-derived macrophages to *M. vaccae* NCTC 11659 in the absence of LPS increased *IL10* mRNA expression (Fig. S14A, Supplementary Material online). At intermediate concentrations of LPS (i.e., 0.5 and 2.5 ng/mL), *M. vaccae* NCTC 11659 decreased *IL10* mRNA expression (Fig. S14A, Supplementary Material online). Exposure to THP-1-derived macrophages to LPS in the absence of *M. vaccae* NCTC 11659 increased *IL10* mRNA expression in a concentration dependent manner with the exception of the 250 ng/mL concentration of LPS (Fig. S14A, Supplementary Material online). Post hoc p values for planned pairwise comparisons can be found in Table S10, Supplementary Information online.

S2.5.2. TGFB1 mRNA expression

Analysis of *TGFB1* mRNA expression revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(12, 137)} = 2.99$, $p < 0.001$) as well as main effects of *M. vaccae* NCTC 11659 ($F_{(4, 137)} = 4.37$, $p < 0.01$) and LPS ($F_{(3, 137)} = 18.86$, $p < 0.001$). Exposure of THP-1 monocyte-derived macrophages to *M. vaccae* NCTC 11659 affected *TGFB1* mRNA expression only in the 2.5 ng/mL LPS condition, where it decreased *TGFB1* mRNA expression in the 30 μ g/mL concentration of *M. vaccae* NCTC 11659 and increased *TGFB1* mRNA expression at the highest concentration (300 μ g/mL; Fig. S14B, Supplementary Material online). Exposure of THP-1 monocyte-derived macrophages to LPS in the absence of *M. vaccae* NCTC 11659 decreased *TGFB1* expression in the 2.5 ng/mL LPS condition (Fig. S14B, Supplementary Material online). Pretreatment with *M. vaccae* NCTC 11659 (300 μ g/mL) attenuated LPS-induced decreases in *TGFB1* mRNA expression in the 2.5 ng/mL LPS condition (Fig. S14B, Supplementary Information online). Post hoc p values for planned pairwise comparisons can be found in Table S10, Supplementary Material online.

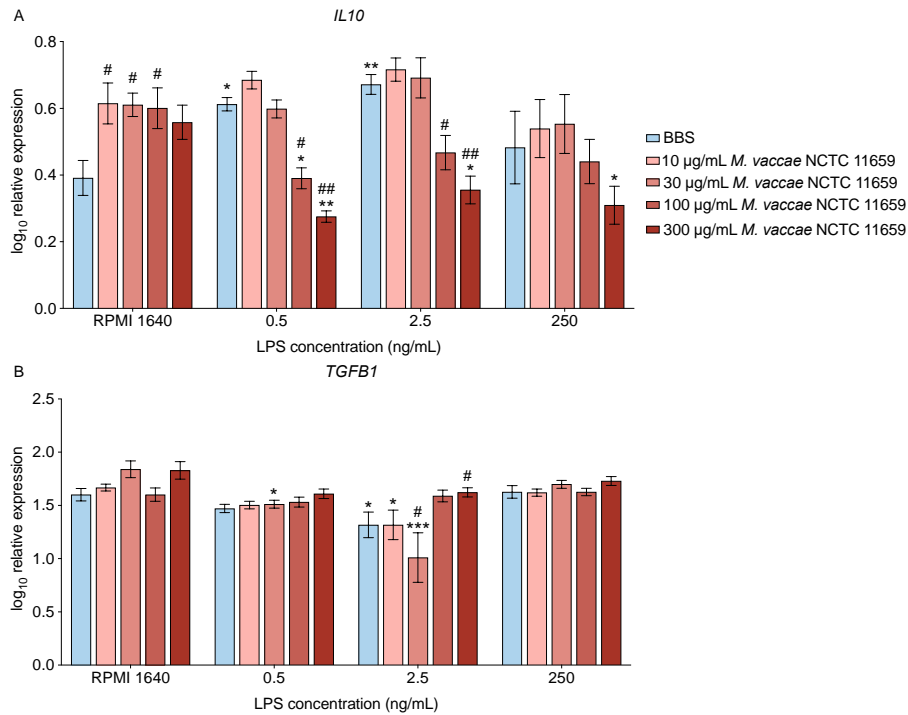


Figure S14. Heat-killed *M. vaccae* NCTC 11659 alone upregulates *IL10* mRNA expression and, among THP-1 monocyte-derived macrophages subsequently stimulated with LPS, downregulates *IL10* mRNA expression and differentially regulates *TGFB1* mRNA expression. Gene expression was measured using real time reverse transcription polymerase chain reaction (RT-PCR) and is represented relative to the highest Cq value for each gene. Data represent means \pm SEM. Numbers on the x-axis indicate the concentration of LPS in ng/mL. Data were analyzed using a two-way ANOVA followed by Dunnett's multiple comparisons test using a single pooled error value from all 20 treatment groups, if appropriate, at a two-tailed alpha level of 0.05. Darker colors represent sequentially higher concentrations of *M. vaccae* NCTC 11659. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, effect of LPS, within the same *M. vaccae* NCTC 11659 condition, using RPMI 1640 groups as the comparison groups. # $p < 0.05$, ## $p < 0.01$, ### $p < 0.001$, effect of *M. vaccae* NCTC 11659, within the same LPS condition, using the BBS condition as the comparison group. **A)** *IL10* mRNA expression upon challenge with different concentrations of *M. vaccae* NCTC 11659 and LPS. **B)** *TGFB1* mRNA expression upon challenge with different concentrations of *M. vaccae* NCTC 11659 and LPS. Abbreviations: BBS, borate-buffered saline; LPS, lipopolysaccharide; NCTC, National Collection of Type Cultures. Sample sizes can be found in Table S1, Supplemental Information online.

*S2.6. Effects of heat-killed *M. vaccae* NCTC 11659 and LPS on *TGFB1:IL12A*, *TGFB1:IL12B*, and *TGFB1:IL23A* ratios*

*S2.6.1. *TGFB1:IL12A* mRNA expression ratio*

As mentioned above, expression levels of *IL12A*, *IL12B*, *IL23A*, and *TGFB1* are important in their own right to characterize the immune environment, but the ratio between anti-inflammatory and inflammatory cytokines in the environment is an important feature of macrophage polarization. For example, high expression of IL-12, but low expression of TGF- β 1, is characteristic of macrophages with a proinflammatory bias (Mantovani et al., 2004; Viola et al., 2019). In contrast, high expression of TGF- β 1, but low expression of IL-12, is characteristic of macrophages with an anti-inflammatory bias, particularly macrophages implicated in anti-inflammatory and immunosuppressive effects (Mantovani et al., 2004; Viola et al., 2019). This suggests that the ratio of *TGFB1* to *IL12A*, *IL12B*, and *IL23A* may be a meaningful measure of macrophage polarization. The ratio of *TGFB1* to *IL12A* expression was calculated in THP-1 monocyte-derived macrophages after incubating them with various doses of *M. vaccae* NCTC 11659 and LPS as described above. In line with low expression of *IL12A* mRNA in the vehicle (0 ng/mL LPS) condition, 67.5% of *TGFB1:IL12A* mRNA expression ratio data were real time RT-PCR non-detects (Table S9, Supplementary Material online). Analysis of the *TGFB1:IL12A* mRNA expression ratio revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(12, 102)} = 2.73$, $p < 0.01$) as well as main effects of *M. vaccae* NCTC 11659 ($F_{(4, 102)} = 6.07$, $p < 0.001$) and LPS ($F_{(3, 102)} = 10.04$, $p < 0.001$). Exposure of THP-1 monocyte-derived macrophages to the highest concentration of *M. vaccae* NCTC 11659 (300 μ g/mL) in the presence of 2.5 ng/mL LPS increased the *TGFB1:IL12A* mRNA expression ratio (Fig. S15A). Exposure of THP-1 monocyte-derived macrophages to LPS in the absence of *M. vaccae* NCTC 11659 did not affect the *TGFB1:IL12A* mRNA expression ratio. Post hoc p values for planned pairwise comparisons can be found in Table S10, Supplementary Material online.

*S2.6.2. *TGFB1:IL12B* mRNA expression ratio*

The ratio of *TGFB1* to *IL12B* expression was calculated in THP-1 monocyte-derived macrophages after incubating them with various doses of *M. vaccae* NCTC 11659 and LPS as described above. Analysis of the *TGFB1:IL12B* mRNA expression ratios revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(12, 119)} = 8.70$, $p < 0.001$); there was no main effect of *M. vaccae* NCTC 11659 ($F_{(4, 119)} = 1.962$, $p = 0.10$), but there was a main effect of LPS ($F_{(3, 119)} = 320.2$, $p < 0.001$). Exposure of THP-1 monocyte-derived macrophages to *M. vaccae* NCTC 11659 in the absence of LPS and in the presence of 0.5 ng/mL LPS dose-dependently decreased the *TGFB1:IL12B* mRNA expression ratio (Fig. S15B). Likewise, exposure of THP-1 monocyte-derived macrophages to LPS in the absence of *M. vaccae* NCTC 11659 dose dependently decreased the *TGFB1:IL12B* mRNA expression ratio (Fig. S15B). In contrast, pretreatment with *M. vaccae* NCTC 11659 increased the *TGFB1:IL12B* mRNA expression ratio in the presence of higher concentrations of LPS (2.5 ng/mL and 250 ng/mL; Fig. S15B), consistent with potential anti-inflammatory effects of *M. vaccae* NCTC 11659 under these conditions. Post hoc p values for planned pairwise comparisons can be found in Table S10, Supplementary Material online.

*S2.6.3. *TGFB1:IL23A* mRNA expression ratio*

The ratio of *TGFB1* to *IL23A* expression was calculated in THP-1 monocyte-derived macrophages after incubating them with various doses of *M. vaccae* NCTC 11659 and LPS as

described above. Analysis of the *TGFB1:IL23A* mRNA expression ratios revealed an *M. vaccae* NCTC 11659 x LPS interaction ($F_{(12, 137)} = 5.909, p < 0.001$); there was no main effect of *M. vaccae* NCTC 11659 ($F_{(4, 137)} = 1.18, p = 0.32$), but there was a main effect of LPS ($F_{(3, 137)} = 123.3, p < 0.001$). Exposure of THP-1 monocyte-derived macrophages to *M. vaccae* NCTC 11659 in the absence of LPS dose dependently decreased the *TGFB1:IL23A* mRNA expression ratio (Fig. S15C). Likewise, exposure of THP-1 monocyte-derived macrophages to LPS in the absence of *M. vaccae* NCTC 11659 dose dependently decreased the *TGFB1:IL23A* mRNA expression ratio (Fig. S15C). In contrast, pretreatment with *M. vaccae* NCTC 11659 increased the *TGFB1:IL23A* mRNA expression ratio in the presence of higher concentrations of LPS (2.5 ng/mL and 250 ng/mL; Fig. S15C), consistent with potential anti-inflammatory effects of *M. vaccae* NCTC 11659 under these conditions. Post hoc *p* values for planned pairwise comparisons can be found in Table S10, Supplemental Information online.

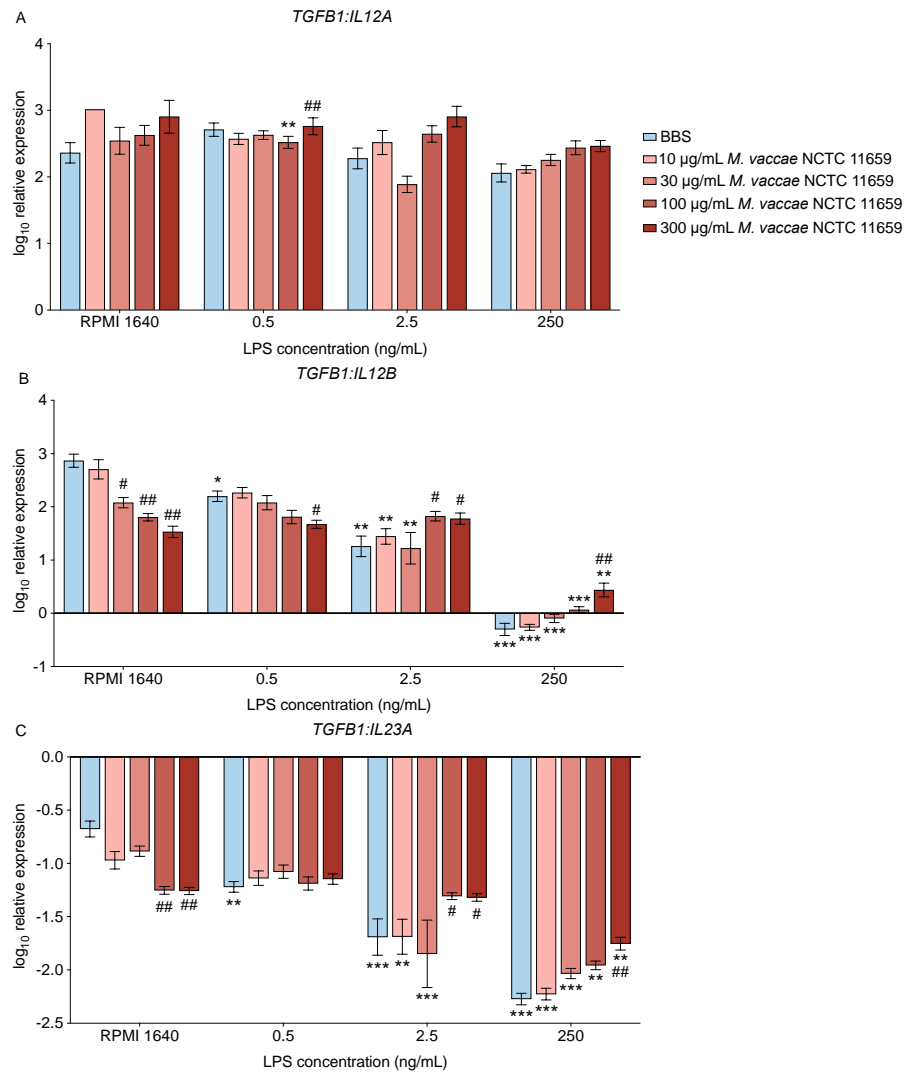


Figure S15. Heat-killed *M. vaccae* NCTC 11659 modulates lipopolysaccharide (LPS)-induced exaggeration of inflammation in THP-1 monocyte-derived macrophages by increasing the ratio of *TGFBI* expression to inflammatory gene expression. Gene expression was measured using real time reverse transcription polymerase chain reaction (RT-PCR) and is represented relative to the highest Cq value for each gene. Data represent means \pm SEM. Numbers on the x-axis indicate the concentration of LPS in ng/mL. Data were analyzed using a two-way ANOVA followed by Dunnett's multiple comparisons test using a single pooled error value from all 20 treatment groups, if appropriate, at a two-tailed alpha level of 0.05. Darker colors represent sequentially higher concentrations of *M. vaccae* NCTC 11659. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, effect of LPS, within the same *M. vaccae* NCTC 11659 condition, using the RPMI 1640 groups as the comparison groups. # $p < 0.05$, ## $p < 0.01$, ### $p < 0.001$, effect of *M. vaccae* NCTC 11659, within the same LPS condition, using the BBS condition as the comparison group. **A)** *TGFBI:IL12A* mRNA expression ratio upon challenge with different concentrations of *M. vaccae* NCTC 11659 and LPS. **B)** *TGFBI:IL12B* mRNA expression ratio upon challenge with different concentrations of *M. vaccae* NCTC 11659 and LPS. **C)** *TGFBI:IL23A* mRNA expression ratio upon challenge with different concentrations of *M. vaccae* NCTC 11659 and

LPS. Abbreviations: BBS, borate-buffered saline; LPS, lipopolysaccharide; NCTC, National Collection of Type Cultures. Sample sizes can be found in Table S1, Supplemental Information online.

S3. Supplemental Materials and Methods

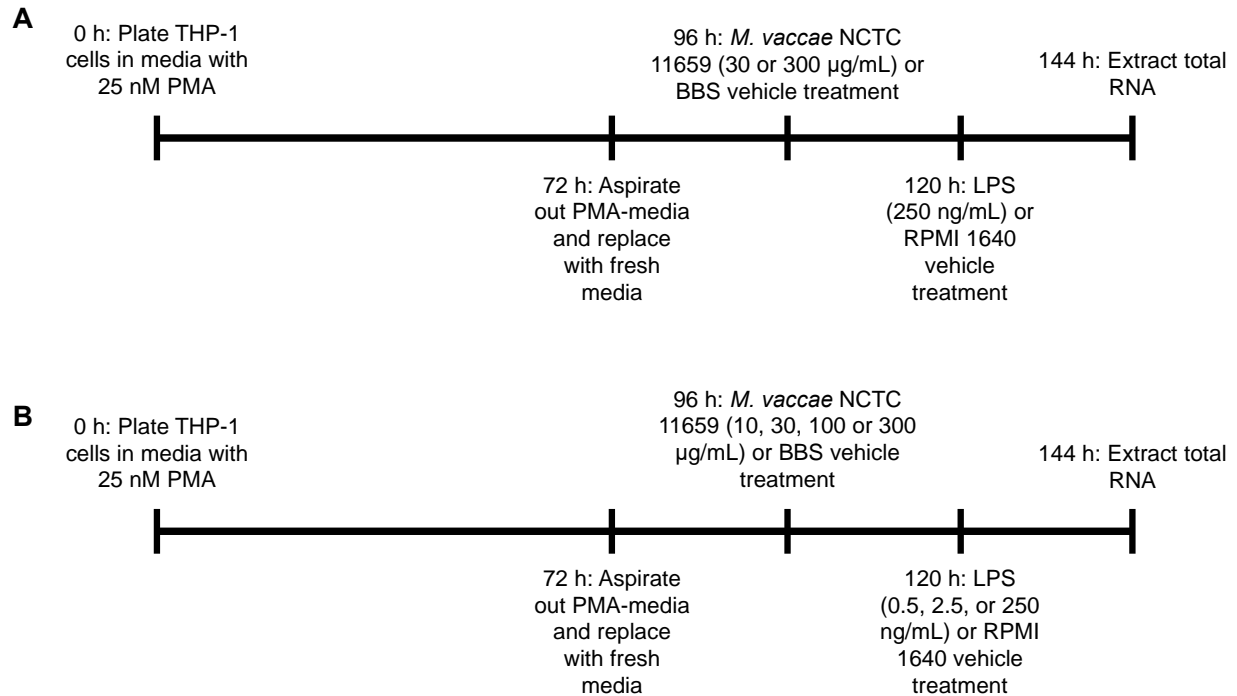


Figure S16. Summary of experimental timelines for (A) *Experiment 1* and (B) *Experiment 2*. Abbreviations: BBS, borate-buffered saline; LPS, lipopolysaccharide; NCTC, National Collection of Type Cultures; PMA, phorbol 12-myristate 13-acetate; RNA, ribonucleic acid.

S3.1. Flow cytometry for assessment of cell viability

Cell plates containing 525 µL/well were centrifuged at 500 x g for 5 minutes at room temperature. After removing cell media, adherent differentiated cells were collected by pipetting 0.5 mL of 5 mM ethylenediaminetetraacetic acid-phosphate buffered solution (EDTA, Cat. No. E4884, Sigma-Aldrich; PBS: sodium chloride, Cat. No. BP358-212, Fisher Scientific, Fair Lawn, New Jersey, USA; potassium phosphate monobasic, Cat. No. P286-1, Fisher Scientific; sodium phosphate dibasic anhydrous, Cat. No. S374-500, Fisher Scientific; potassium chloride, Cat. No. P217-500, Fisher Scientific) into each well and pipetting up and down. Cell viability was assessed by flow cytometry gating of live singlets based on forward and side scatter (FSC/SSC). Flow cytometry was performed with an independent set of cells separate from those used for real time RT-qPCR. Sample sizes for flow cytometry studies are listed in Table S1. Flow cytometry was conducted using a BD Special Order FACSArray™ Bioanalyzer machine (serial no. W91100224, BD Biosciences, Franklin Lakes, NJ, USA). All downstream analysis was carried out using the FlowJo Software (version 10.1, FlowJo, LLC., Ashland, OR, USA).

S3.2. Flow cytometry statistical analysis

Flow cytometry data for cell viability analysis were represented as the percent of cells viable to the mean of the BBS vehicle/RPMI 1640 vehicle group, which was done by taking the gate for live cells. Flow cytometry data were analyzed using two-way ANOVA followed by Dunnett's multiple comparisons test, if appropriate, at a two-tailed alpha level of 0.05.

Table S1. Sample sizes (*n*) for the flow cytometry experiment cell viability in response to *M. vaccae* NCTC 11659 and lipopolysaccharide (LPS). Sample size represents 1 experimental replicate.

LPS Treatment	Bacterial Treatment	Sample Size (<i>n</i>)
0 ng/mL	BBS	5
	10 µg/mL <i>M. vaccae</i> NCTC 11659	5
	30 µg/mL <i>M. vaccae</i> NCTC 11659	5
	100 µg/mL <i>M. vaccae</i> NCTC 11659	5
	300 µg/mL <i>M. vaccae</i> NCTC 11659	5
250 ng/mL	BBS	4
	10 µg/mL <i>M. vaccae</i> NCTC 11659	4
	30 µg/mL <i>M. vaccae</i> NCTC 11659	4
	100 µg/mL <i>M. vaccae</i> NCTC 11659	4
	300 µg/mL <i>M. vaccae</i> NCTC 11659	4
0 ng/mL	BBS	5
	10 µg/mL <i>M. vaccae</i> NCTC 11659	5
	30 µg/mL <i>M. vaccae</i> NCTC 11659	5
	100 µg/mL <i>M. vaccae</i> NCTC 11659	5
	300 µg/mL <i>M. vaccae</i> NCTC 11659	5
250 ng/mL	BBS	4
	10 µg/mL <i>M. vaccae</i> NCTC 11659	4
	30 µg/mL <i>M. vaccae</i> NCTC 11659	4
	100 µg/mL <i>M. vaccae</i> NCTC 11659	4
	300 µg/mL <i>M. vaccae</i> NCTC 11659	4

Table S2. Fold changes among differentially expressed genes for the BBS/250 ng/mL LPS vs BBS/RPMI 1640 comparison in *Experiment 1* using the NanoString platform.

Gene symbol	log2FoldChange
Upregulated	
<i>IFI44</i>	4.262269026
<i>CCL5</i>	4.228568845
<i>IL8</i>	4.159731409
<i>CCL3</i>	3.765570054
<i>CXCL10</i>	3.661646101
<i>IL1B</i>	3.530651461
<i>MX2</i>	3.500801064
<i>CCL2</i>	3.348462814
<i>CXCL1</i>	3.16835941
<i>STAT1</i>	3.051809072
<i>CCL4</i>	2.850338226
<i>CCR7</i>	2.825718296
<i>IFIT2</i>	2.804308939
<i>RELB</i>	2.748962417
<i>IFIT1</i>	2.743794411
<i>OAS2</i>	2.667257557
<i>MMP9</i>	2.662598429
<i>CXCL3</i>	2.529580501
<i>MX1</i>	2.487862151
<i>CCL22</i>	2.445586712
<i>CXCL2</i>	2.431240533
<i>IFIT3</i>	2.382447108
<i>NOD1</i>	2.230599396
<i>CD40</i>	2.103029474
<i>OASL</i>	2.062527622
<i>MAFF</i>	1.837931872
<i>IL1RN</i>	1.810310897
<i>NFKB1</i>	1.744320545
<i>CXCR2</i>	1.663204849
<i>IRF7</i>	1.572842636
<i>TGFB2</i>	1.572199863
<i>MYD88</i>	1.55351638
<i>IL23A</i>	1.514079188
<i>RIPK2</i>	1.491068592
<i>HLA-DRA</i>	1.485166012

<i>RPS6KA5</i>	1.420754255
<i>LTB</i>	1.416792999
<i>TNFAIP3</i>	1.326074938
<i>C1QA</i>	1.291248673
<i>STAT2</i>	1.207951243
<i>CCL20</i>	1.203041045
<i>MAP2K6</i>	1.156471185
<i>NOD2</i>	1.126930781
<i>CCL23</i>	1.102917155
<i>MAPK8</i>	0.985073941
<i>CXCL6</i>	0.940690292
<i>CXCR4</i>	0.932173675
<i>CFB</i>	0.930713986
<i>CEBPB</i>	0.92956128
<i>CCL24</i>	0.875357784
<i>TLR5</i>	0.83638696
<i>TRADD</i>	0.787948598
<i>TLR6</i>	0.737944965
<i>ELK1</i>	0.697904269
<i>CCL8</i>	0.626491937
<i>SMAD7</i>	0.613347757
<i>C3AR1</i>	0.599176377
Downregulated	
<i>TREM2</i>	-3.548187492
<i>PTGS1</i>	-2.532871722
<i>TGFBR1</i>	-2.489080777
<i>HDAC4</i>	-2.424431522
<i>MEF2C</i>	-2.125305204
<i>GRB2</i>	-2.057306367
<i>TLR4</i>	-1.913291151
<i>LIMK1</i>	-1.812929182
<i>ALOX5</i>	-1.804872332
<i>IL18</i>	-1.790840137
<i>IL1R1</i>	-1.76824
<i>ROCK2</i>	-1.730590858
<i>HMGB2</i>	-1.727870056
<i>IL6R</i>	-1.690664298
<i>PRKCB</i>	-1.579542716
<i>FOS</i>	-1.520073498

<i>HMGB1</i>	-1.48640968
<i>GNAS</i>	-1.479297821
<i>LY96</i>	-1.476827195
<i>MAX</i>	-1.421829881
<i>HSPB1</i>	-1.394916551
<i>CD4</i>	-1.329394552
<i>RAPGEF2</i>	-1.226831758
<i>MAPKAPK2</i>	-1.168885773
<i>BIRC2</i>	-1.164865848
<i>PLA2G4A</i>	-1.157716781
<i>MAPKAPK5</i>	-1.130769454
<i>DDIT3</i>	-1.054315672
<i>PDGFA</i>	-1.052492146
<i>TYROBP</i>	-1.040038705
<i>GNAQ</i>	-1.019696587
<i>IRF1</i>	-0.997193312
<i>HRAS</i>	-0.991733602
<i>MAPK14</i>	-0.920002433
<i>STAT3</i>	-0.895976194
<i>MEF2D</i>	-0.888962215
<i>RIPK1</i>	-0.85750619
<i>MAP3K7</i>	-0.835212496
<i>CD163</i>	-0.789549572
<i>NLRP3</i>	-0.77122709
<i>MKNK1</i>	-0.760232478
<i>MAP3K1</i>	-0.737623351
<i>HMGNI</i>	-0.728439309
<i>HIF1A</i>	-0.713836198
<i>NFATC3</i>	-0.687810068
<i>CREB1</i>	-0.677395388
<i>MYC</i>	-0.665728171
<i>AGER</i>	-0.653885323
<i>TLR1</i>	-0.627990698
<i>RAC1</i>	-0.593136501

Table S3. Fold changes among differentially expressed genes for the 300 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 vs BBS/RPMI 1640 comparison in *Experiment 1* using the NanoString platform.

Gene symbol	log2FoldChange
Upregulated	
<i>CCL8</i>	4.89690652
<i>CFB</i>	4.430250149
<i>CCL13</i>	3.870692489
<i>MAFF</i>	3.860842614
<i>IFIT2</i>	3.720039294
<i>MMP9</i>	3.520145054
<i>IFIT3</i>	3.431284527
<i>KEAP1</i>	3.360990863
<i>IL10</i>	3.239398915
<i>C1S</i>	2.862037841
<i>CXCL1</i>	2.782482056
<i>IRF7</i>	2.763613935
<i>CXCL5</i>	2.747719032
<i>CD40</i>	2.639664337
<i>IFI44</i>	2.528043214
<i>TRADD</i>	2.427985433
<i>OASL</i>	2.376190291
<i>IL8</i>	2.225557551
<i>RELB</i>	2.159524239
<i>NFKB1</i>	2.10983004
<i>HLA-DRA</i>	1.910535992
<i>RELA</i>	1.905547488
<i>MAPK3</i>	1.807589712
<i>MAP3K5</i>	1.767905581
<i>CXCL10</i>	1.745745502
<i>C3</i>	1.67081143
<i>SMAD7</i>	1.592342315
<i>CD163</i>	1.547699987
<i>MRC1</i>	1.547476852
<i>ALOX5</i>	1.533939839
<i>RAPGEF2</i>	1.512887703
<i>ITGB2</i>	1.51025086
<i>TRAF2</i>	1.484385294
<i>HLA-DRB1</i>	1.41103933

<i>CXCR4</i>	1.385213822
<i>IL15</i>	1.341519769
<i>IL1B</i>	1.321287767
<i>IL6R</i>	1.307791409
<i>NFE2L2</i>	1.257189249
<i>RHOA</i>	1.224671416
<i>PTGER4</i>	1.218333365
<i>CCL2</i>	1.211098382
<i>GNAQ</i>	1.196668767
<i>IL11</i>	1.196521436
<i>AREG</i>	1.177134361
<i>DAXX</i>	1.176135067
<i>RAC1</i>	1.161219841
<i>CCL3</i>	1.098591596
<i>CCL5</i>	1.055958887
<i>C3AR1</i>	1.033466277
<i>CCL4</i>	1.019245099
<i>TNF</i>	1.010907794
<i>PTGIR</i>	0.993283114
<i>CD4</i>	0.961464272
<i>CSF3</i>	0.889676629
<i>DEFA1</i>	0.884852623
<i>TGFBR1</i>	0.881763235
<i>NFATC3</i>	0.840590723
<i>IRF5</i>	0.801880014
<i>CFD</i>	0.772920032
<i>HSPB1</i>	0.756997065
<i>NOD2</i>	0.745261634
<i>CXCL2</i>	0.743951576
<i>CCR1</i>	0.736963034
<i>ELK1</i>	0.698647747
<i>PRKCB</i>	0.645457851
<i>FXYD2</i>	0.621906369
<i>LTB</i>	0.619950676
Downregulated	
<i>PLA2G4A</i>	-5.144740794
<i>TNFSF14</i>	-5.100462031
<i>MX1</i>	-5.005120687
<i>AGER</i>	-4.778907627

<i>RPS6KA5</i>	-3.392627591
<i>PPP1R12B</i>	-3.33328838
<i>C5</i>	-3.032903984
<i>TGFB2</i>	-2.902286516
<i>IL1RAP</i>	-2.55178396
<i>TLR4</i>	-2.534433312
<i>PTGS2</i>	-2.531511955
<i>OXER1</i>	-2.513443302
<i>NOD1</i>	-2.362597471
<i>PDGFA</i>	-2.359872495
<i>MAP2K1</i>	-2.139549594
<i>TLR5</i>	-1.972131517
<i>OAS2</i>	-1.789295679
<i>CYSLTR1</i>	-1.71961854
<i>IFIT1</i>	-1.697762641
<i>LTB4R</i>	-1.619607434
<i>PRKCA</i>	-1.613126296
<i>FOS</i>	-1.524388349
<i>HRAS</i>	-1.498999247
<i>TCF4</i>	-1.435626898
<i>TLR1</i>	-1.419172567
<i>CXCR2</i>	-1.3854188
<i>MAPK8</i>	-1.287056878
<i>C1QB</i>	-1.28606134
<i>CXCL6</i>	-1.177120774
<i>MYC</i>	-1.174193238
<i>TLR6</i>	-1.125992285
<i>MAX</i>	-1.112550891
<i>CD86</i>	-1.103115614
<i>MEF2C</i>	-1.085875385
<i>IL23R</i>	-1.039724013
<i>TLR7</i>	-0.995868956
<i>MAP2K6</i>	-0.973545549
<i>LTB4R2</i>	-0.962118237
<i>HIF1A</i>	-0.925925934
<i>MAPK1</i>	-0.824273447
<i>MX2</i>	-0.776580478
<i>MKNK1</i>	-0.772712802
<i>IL1R1</i>	-0.767024105

<i>MAPKAPK2</i>	-0.757813202
<i>TOLLIP</i>	-0.755326387
<i>HMGB1</i>	-0.753189183
<i>IL18</i>	-0.737871444
<i>CCR2</i>	-0.733063666
<i>C1QA</i>	-0.723428349
<i>HMGB2</i>	-0.672598711
<i>CCL22</i>	-0.647010509
<i>PTK2</i>	-0.608116411

Table S4. Fold changes among differentially expressed genes for the 300 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS vs BBS/250 ng/mL LPS comparison in *Experiment 1* using the NanoString platform.

Gene symbol	log2FoldChange
Upregulated	
<i>LTB4R2</i>	3.087050466
<i>CXCR2</i>	3.05915473
<i>MAP2K6</i>	2.819087782
<i>NFATC3</i>	2.25194415
<i>IL23A</i>	2.247266952
<i>ALOX5</i>	2.16121367
<i>IL1RAP</i>	1.738176198
<i>MRC1</i>	1.681382612
<i>MAPK1</i>	1.648627325
<i>TGFB2</i>	1.64577741
<i>C5</i>	1.593725862
<i>NOD2</i>	1.50209677
<i>MAPK8</i>	1.491295888
<i>NFKB1</i>	1.460314226
<i>TLR8</i>	1.447373153
<i>LTB4R</i>	1.404433165
<i>HDAC4</i>	1.402348842
<i>MAPK3</i>	1.291189699
<i>IL10</i>	1.289208553
<i>MAP3K1</i>	1.270090708
<i>MYC</i>	1.26044476
<i>CXCR4</i>	1.232853584
<i>GNAQ</i>	1.221348027
<i>IL10RB</i>	1.215773582
<i>RELB</i>	1.193184076
<i>CD163</i>	1.181033116
<i>TLR4</i>	1.104777136
<i>TGFBRI</i>	1.099294031
<i>ROCK2</i>	1.088525522
<i>RHOA</i>	1.080929738
<i>NOD1</i>	1.068606356
<i>SMAD7</i>	1.055497516
<i>CYSLTR1</i>	0.986892275
<i>C2</i>	0.986476297

<i>MAPKAPK5</i>	0.976870297
<i>ELK1</i>	0.971771149
<i>KEAP1</i>	0.959985562
<i>RPS6KA5</i>	0.889956977
<i>PRKCB</i>	0.850548766
<i>HSPB1</i>	0.839812465
<i>MAFG</i>	0.832517482
<i>DAXX</i>	0.757933477
<i>MEF2D</i>	0.739331706
<i>TLR5</i>	0.729232422
<i>TLR2</i>	0.723843162
<i>CCL21</i>	0.710800392
<i>RAC1</i>	0.703406301
<i>AREG</i>	0.687881125
<i>CXCL1</i>	0.655032692
<i>CD4</i>	0.650741458
<i>RELA</i>	0.637369019
<i>CFL1</i>	0.617930885
Downregulated	
<i>OASL</i>	-4.408160277
<i>CXCL10</i>	-4.136442755
<i>C1S</i>	-3.506510094
<i>PTGIR</i>	-3.30655998
<i>IFIT3</i>	-3.292122002
<i>AGER</i>	-3.175492742
<i>CXCL5</i>	-3.164124162
<i>CCL8</i>	-3.156239486
<i>IFIT1</i>	-3.030267348
<i>MX1</i>	-2.996931999
<i>CCL2</i>	-2.96239435
<i>PTGER2</i>	-2.942304023
<i>CSF1</i>	-2.900074092
<i>CCL13</i>	-2.842854299
<i>CCL23</i>	-2.785297352
<i>PTGS2</i>	-2.485993629
<i>TRADD</i>	-2.44295147
<i>IFIT2</i>	-2.175390748
<i>DEFA1</i>	-2.162019224
<i>CXCL6</i>	-2.112661844

<i>GRB2</i>	-2.085292422
<i>MAP2K4</i>	-2.033403888
<i>PLA2G4A</i>	-2.022961449
<i>CCR7</i>	-1.975461962
<i>C4A</i>	-1.77929554
<i>TRAF2</i>	-1.742686734
<i>OXER1</i>	-1.65951614
<i>MAFK</i>	-1.49331069
<i>TCF4</i>	-1.452849745
<i>IL1A</i>	-1.445212836
<i>TNF</i>	-1.433492677
<i>CCL4</i>	-1.379946591
<i>BCL2L1</i>	-1.369081025
<i>BIRC2</i>	-1.363869271
<i>CCL17</i>	-1.362721544
<i>RIPK1</i>	-1.289955882
<i>HRAS</i>	-1.191350109
<i>SHC1</i>	-1.089279385
<i>STAT1</i>	-1.084944227
<i>TNFAIP3</i>	-1.047367283
<i>PPP1R12B</i>	-1.033699962
<i>MAX</i>	-0.966200409
<i>IL12B</i>	-0.932718828
<i>CCR1</i>	-0.901525584
<i>TGFB1</i>	-0.887321389
<i>TREM2</i>	-0.883598153
<i>CCL3</i>	-0.873193115
<i>CXCL3</i>	-0.843755424
<i>TWIST2</i>	-0.830382558
<i>HMGB1</i>	-0.808826214
<i>IRF7</i>	-0.793069876
<i>CREB1</i>	-0.765847083
<i>IL1R1</i>	-0.744521002
<i>MAP3K5</i>	-0.735381496
<i>CCL19</i>	-0.726045691
<i>RAPGEF2</i>	-0.710950932
<i>MYD88</i>	-0.696538117
<i>FXYP2</i>	-0.680591194
<i>C3AR1</i>	-0.673336189

<i>IL18</i>	-0.631318416
<i>CD86</i>	-0.608851128
<i>MAPKAPK2</i>	-0.601598776
<i>ATF2</i>	-0.595549675

Table S5. Fold changes among differentially expressed genes for the 300 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS vs 300 *M. vaccae* NCTC 11659/RPMI 1640 comparison in *Experiment 1* using the NanoString platform.

Gene symbol	log2FoldChange
Upregulated	
<i>TGFB2</i>	6.120263788
<i>CXCR2</i>	6.107778378
<i>RPS6KA5</i>	5.703338822
<i>NOD1</i>	5.661803223
<i>TNFSF14</i>	5.194677406
<i>MAP2K6</i>	4.949104517
<i>MX1</i>	4.49605084
<i>LTB4R2</i>	4.41108765
<i>MX2</i>	4.329610799
<i>C5</i>	4.239846908
<i>IL23A</i>	4.128700691
<i>OAS2</i>	4.004979806
<i>IL1RAP</i>	3.96485466
<i>MAPK8</i>	3.763426708
<i>TLR5</i>	3.537750899
<i>CCL5</i>	3.313953309
<i>LTB4R</i>	3.280034883
<i>CCL22</i>	2.633775154
<i>IL8</i>	2.501388071
<i>STAT1</i>	2.467503503
<i>IL1B</i>	2.436145023
<i>CYSLTR1</i>	2.25625754
<i>MAPK1</i>	2.114514958
<i>C1QA</i>	2.043388814
<i>PLA2G4A</i>	1.964062564
<i>NOD2</i>	1.883765917
<i>CXCL2</i>	1.843106528
<i>CCL3</i>	1.793785343
<i>RELB</i>	1.782622255
<i>MYC</i>	1.768909827
<i>PPP1R12B</i>	1.762143979
<i>RIPK2</i>	1.747898262
<i>PDGFA</i>	1.737370787
<i>TLR6</i>	1.73506275

<i>TLR4</i>	1.725919297
<i>IFI44</i>	1.697092244
<i>CXCL3</i>	1.651744662
<i>MAP2K1</i>	1.572268911
<i>STAT2</i>	1.493993137
<i>TLR8</i>	1.485784135
<i>MYD88</i>	1.434305325
<i>IFIT1</i>	1.411289703
<i>IL1RN</i>	1.396065573
<i>PRKCA</i>	1.296344054
<i>IL10RB</i>	1.260366684
<i>C1QB</i>	1.1416171
<i>OXER1</i>	1.130713266
<i>NFKB1</i>	1.094804731
<i>CCL24</i>	1.076429621
<i>LTB</i>	1.042537016
<i>CXCL1</i>	1.040910047
<i>PTK2</i>	0.995532526
<i>IRF3</i>	0.981334578
<i>ELK1</i>	0.971027671
<i>RAF1</i>	0.964761299
<i>AGER</i>	0.949529562
<i>CEBPB</i>	0.92649671
<i>TLR1</i>	0.832113446
<i>CXCR4</i>	0.779813437
<i>CCL20</i>	0.778011098
<i>NFATC3</i>	0.723543359
<i>MRC1</i>	0.6933714
<i>TLR2</i>	0.685572337
<i>IL23R</i>	0.643337688
<i>CD86</i>	0.596446442
Downregulated	
<i>CCL8</i>	-7.426654069
<i>CCL13</i>	-7.257435442
<i>C1S</i>	-6.581855389
<i>CXCL5</i>	-5.69820227
<i>OASL</i>	-4.721822945
<i>PTGIR</i>	-4.410253909
<i>IFIT3</i>	-4.340959421

<i>TRADD</i>	-4.082988306
<i>TREM2</i>	-4.052520025
<i>GRB2</i>	-3.981070039
<i>CFB</i>	-3.97321765
<i>RAPGEF2</i>	-3.450670393
<i>PTGER2</i>	-3.434476009
<i>DEFA1</i>	-3.100752779
<i>IFIT2</i>	-3.091121102
<i>IL6R</i>	-2.936137512
<i>KEAP1</i>	-2.731145869
<i>TRAF2</i>	-2.658961131
<i>CSF1</i>	-2.655672587
<i>TNF</i>	-2.364319991
<i>BIRC2</i>	-2.295225331
<i>TGFBR1</i>	-2.27154998
<i>CXCL10</i>	-2.220542155
<i>PTGS1</i>	-2.166346112
<i>MAP3K5</i>	-2.159156417
<i>IRF1</i>	-2.033382401
<i>RIPK1</i>	-1.984652105
<i>IRF7</i>	-1.983841175
<i>MAFF</i>	-1.925089041
<i>HLA-DRB1</i>	-1.897946816
<i>BCL2L1</i>	-1.861726507
<i>CREB1</i>	-1.849988742
<i>CCR1</i>	-1.831054792
<i>C4A</i>	-1.77929554
<i>IL15</i>	-1.778732694
<i>LIMK1</i>	-1.776971678
<i>C3</i>	-1.763476573
<i>IL1R1</i>	-1.745736897
<i>IL18</i>	-1.684287109
<i>CD4</i>	-1.640117366
<i>HMGB1</i>	-1.542046711
<i>IL10</i>	-1.487204801
<i>CCL23</i>	-1.468594605
<i>IL1A</i>	-1.445212836
<i>MAFK</i>	-1.426007454
<i>ITGB2</i>	-1.425378067

<i>PRKCB</i>	-1.374451801
<i>CCL17</i>	-1.362721544
<i>NFE2L2</i>	-1.317708723
<i>HSPB1</i>	-1.312101151
<i>SHC1</i>	-1.285676915
<i>MAX</i>	-1.275479399
<i>MAP2K4</i>	-1.247011546
<i>HMGB2</i>	-1.230519584
<i>GNAS</i>	-1.21140752
<i>ALOX5</i>	-1.177598501
<i>CD163</i>	-1.156216443
<i>CSF3</i>	-1.154071013
<i>TGFB1</i>	-1.13997757
<i>C3AR1</i>	-1.107626089
<i>IRF5</i>	-1.086050172
<i>RAC1</i>	-1.050950041
<i>MAPKAPK2</i>	-1.012671347
<i>MEF2C</i>	-1.006319544
<i>GNAQ</i>	-0.995017327
<i>LY96</i>	-0.951152454
<i>IL12B</i>	-0.932718828
<i>PTGER4</i>	-0.919174883
<i>CCL19</i>	-0.898000527
<i>IL11</i>	-0.896658724
<i>MAPK14</i>	-0.876669289
<i>MAPK3</i>	-0.869578113
<i>FXRD2</i>	-0.848908775
<i>MAP3K7</i>	-0.831733933
<i>TWIST2</i>	-0.830382558
<i>CCL2</i>	-0.825029917
<i>RELA</i>	-0.804637744
<i>CFD</i>	-0.783074509
<i>MMP9</i>	-0.763854742
<i>HRAS</i>	-0.684084464
<i>ATF2</i>	-0.683882651
<i>BCL6</i>	-0.606589293
<i>HDAC4</i>	-0.605771718

Table S6. Fold changes among differentially expressed genes for the 30 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 vs. BBS/RPMI 1640 comparison in *Experiment 1* using the NanoString platform.

Gene symbol	log2FoldChange
Upregulated	
<i>CCL8</i>	3.65093055
<i>CCL13</i>	3.149080734
<i>CCR7</i>	3.042399552
<i>IFIT3</i>	2.878938362
<i>MMP9</i>	2.597995121
<i>C1S</i>	2.485042688
<i>CXCL10</i>	2.453873064
<i>CXCL5</i>	2.400323163
<i>CCL22</i>	2.334238711
<i>ELK1</i>	2.299251109
<i>TRADD</i>	2.036206871
<i>CFB</i>	2.00679544
<i>IL8</i>	1.533885836
<i>PTGER2</i>	1.46347844
<i>HLA-DRB1</i>	1.311637521
<i>IL15</i>	1.239788697
<i>ITGB2</i>	1.215136222
<i>IFIT2</i>	1.175723117
<i>MRC1</i>	1.123893462
<i>IL11</i>	1.110389565
<i>CCL5</i>	1.079814026
<i>HMGNI</i>	1.078072869
<i>MAP3K7</i>	1.060341309
<i>PTGIR</i>	1.052475684
<i>NOD2</i>	0.960361151
<i>CD4</i>	0.957328779
<i>NLRP3</i>	0.933533412
<i>IL23A</i>	0.933022695
<i>RAF1</i>	0.912271608
<i>CXCL1</i>	0.87168337
<i>RELB</i>	0.865295586
<i>C1QB</i>	0.843103513
<i>OASL</i>	0.840573093
<i>CSF3</i>	0.832248568

<i>DEFA1</i>	0.827830768
<i>AREG</i>	0.78106527
<i>CCL24</i>	0.760030653
<i>HSPB1</i>	0.752750259
<i>SMAD7</i>	0.750823952
<i>CFL1</i>	0.703655717
<i>TREM2</i>	0.699869662
<i>CCR1</i>	0.685080707
<i>RHOA</i>	0.672560739
<i>MEF2D</i>	0.670231674
<i>CXCL2</i>	0.659513981
Downregulated	
<i>AGER</i>	-5.482472487
<i>OXER1</i>	-3.18713
<i>TLR7</i>	-2.608692744
<i>TNFSF14</i>	-2.447947778
<i>C5</i>	-2.337656428
<i>FXVD2</i>	-2.046789727
<i>PPP1R12B</i>	-1.874183353
<i>PTGS1</i>	-1.644031939
<i>RPS6KA5</i>	-1.501620465
<i>BIRC2</i>	-1.493633999
<i>PDGFA</i>	-1.450070059
<i>LTB4R2</i>	-1.343424763
<i>GRB2</i>	-1.239103301
<i>PTGS2</i>	-1.18047607
<i>IFIT1</i>	-1.070359504
<i>CEBPB</i>	-1.059009382
<i>LTB4R</i>	-1.03310146
<i>TGFB2</i>	-1.004050778
<i>LIMK1</i>	-1.001134201
<i>PRKCA</i>	-0.999303406
<i>IL23R</i>	-0.957511838
<i>CCR2</i>	-0.933749827
<i>FOS</i>	-0.909354375
<i>LTB</i>	-0.89069282
<i>HMGB1</i>	-0.729197953
<i>TYROBP</i>	-0.634158315
<i>PLA2G4A</i>	-0.623782522

<i>GNAS</i>	-0.617431352
<i>NOD1</i>	-0.608089594
<i>PLCB1</i>	-0.590900884

Table S7. Fold changes among differentially expressed genes for the 30 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS vs. BBS/250 ng/mL LPS comparison in *Experiment 1* using the NanoString platform.

Gene symbol	log2FoldChange
Upregulated	
<i>TLR5</i>	2.710084931
<i>C1QA</i>	2.684485845
<i>LTB4R2</i>	2.645940505
<i>CXCR2</i>	2.62672939
<i>MAP2K6</i>	2.453411249
<i>CCR2</i>	2.261744964
<i>NOD1</i>	1.963723256
<i>FXRD2</i>	1.582344947
<i>CCL24</i>	1.563842348
<i>MRC1</i>	1.537153018
<i>TGFB2</i>	1.50602263
<i>C5</i>	1.461106615
<i>PRKCA</i>	1.367938667
<i>MAPK8</i>	1.366182804
<i>TNFSF14</i>	1.34746473
<i>HRAS</i>	1.219384699
<i>LTB4R</i>	1.187643573
<i>RPS6KA5</i>	1.100961863
<i>MAP3K5</i>	1.033791185
<i>CCL23</i>	1.009685291
<i>AREG</i>	0.918382435
<i>PPP1R12B</i>	0.734176045
<i>MAP2K4</i>	0.703026041
<i>NOD2</i>	0.702369056
<i>CCL21</i>	0.667698549
<i>PTGS2</i>	0.624099384
Downregulated	
<i>OASL</i>	-2.784240439
<i>IFIT1</i>	-2.587393775
<i>MX1</i>	-2.33527973
<i>CXCL10</i>	-2.175247988
<i>IFIT3</i>	-2.05367924
<i>CCR7</i>	-1.728967684
<i>CXCL5</i>	-1.273190751

<i>CXCL6</i>	-1.09333728
<i>CCL2</i>	-1.093121135
<i>CCL22</i>	-0.989892313
<i>STAT1</i>	-0.965089457
<i>CCL19</i>	-0.906075234
<i>IL1B</i>	-0.853608949
<i>AGER</i>	-0.825973172
<i>CCL20</i>	-0.799298758
<i>DEFA1</i>	-0.73095191
<i>TNFAIP3</i>	-0.721129743
<i>CCL4</i>	-0.714245346
<i>PTGER2</i>	-0.71408325
<i>PTGIR</i>	-0.687632091
<i>C1S</i>	-0.672161381
<i>CCL8</i>	-0.59167732

Table S8. Fold changes among differentially expressed genes for the 30 µg/mL *M. vaccae* NCTC 11659/250 ng/mL LPS vs. 30 µg/mL *M. vaccae* NCTC 11659/RPMI 1640 comparison in *Experiment 1* using the NanoString platform.

Gene symbol	log2FoldChange
Upregulated	
<i>LTB4R2</i>	4.23281562
<i>CXCR2</i>	4.031971691
<i>AGER</i>	4.016773163
<i>OXER1</i>	4.009490272
<i>FXYP2</i>	4.008614412
<i>C1QA</i>	3.942186977
<i>NOD1</i>	3.811969852
<i>RPS6KA5</i>	3.79423271
<i>TGFB2</i>	3.736054254
<i>TNFSF14</i>	3.674022864
<i>MAP2K6</i>	3.55930419
<i>C5</i>	3.457229883
<i>TLR5</i>	3.456453149
<i>CCR2</i>	2.944770051
<i>IL8</i>	2.521621244
<i>LTB</i>	2.41142563
<i>LTB4R</i>	2.364887827
<i>PRKCA</i>	2.297443796
<i>PPP1R12B</i>	2.172234875
<i>PTGS2</i>	2.134592857
<i>OAS2</i>	2.125492439
<i>MX2</i>	2.111362529
<i>IL1B</i>	2.063350601
<i>STAT1</i>	1.999518899
<i>CCL5</i>	1.995405724
<i>TLR7</i>	1.929568056
<i>CXCL3</i>	1.824985615
<i>CEBPB</i>	1.699492904
<i>MAP3K5</i>	1.638747124
<i>MAPK8</i>	1.593596142
<i>CCL23</i>	1.497632409
<i>MAP2K4</i>	1.448478003
<i>STAT2</i>	1.375884108
<i>CXCL2</i>	1.361997517

<i>PDGFA</i>	1.324831159
<i>CCL4</i>	1.283845327
<i>CCL24</i>	1.138758278
<i>IFIT1</i>	1.089278947
<i>CXCL1</i>	1.007185964
<i>CCL2</i>	0.998759158
<i>IL23R</i>	0.957511838
<i>IRF3</i>	0.955314915
<i>MRC1</i>	0.880993491
<i>CD40</i>	0.839182724
<i>IFI44</i>	0.831107212
<i>RIPK2</i>	0.810193975
<i>GRB2</i>	0.735334921
<i>TLR6</i>	0.71876881
<i>HRAS</i>	0.679538836
<i>CCL3</i>	0.662215323
<i>MX1</i>	0.65700868
<i>IL1RN</i>	0.604535138
<i>TLR8</i>	0.603566607
<i>NFKB1</i>	0.592622323
<i>PLCB1</i>	0.590900884
Downregulated	
<i>CCL13</i>	-3.963713914
<i>CCL8</i>	-3.957226863
<i>CXCL5</i>	-3.510723636
<i>C1S</i>	-3.310503539
<i>IFIT3</i>	-3.03052879
<i>CCR7</i>	-2.538970211
<i>PTGER2</i>	-2.457891183
<i>TREM2</i>	-2.177287723
<i>ELK1</i>	-1.92381998
<i>CFB</i>	-1.888835541
<i>CCL22</i>	-1.887341581
<i>IL1R1</i>	-1.870613946
<i>PTGIR</i>	-1.836531367
<i>OASL</i>	-1.821113402
<i>IL15</i>	-1.766736742
<i>MEF2D</i>	-1.706026107
<i>HMGNI</i>	-1.693181947

<i>CXCL10</i>	-1.681440832
<i>HLA-DRB1</i>	-1.611129159
<i>DEFA1</i>	-1.608033126
<i>IL11</i>	-1.587978562
<i>ITGB2</i>	-1.565214359
<i>CD4</i>	-1.544090696
<i>HSPB1</i>	-1.395500204
<i>MAP3K7</i>	-1.37686946
<i>TRADD</i>	-1.293570771
<i>MAPK14</i>	-1.210057281
<i>NLRP3</i>	-1.202199016
<i>CSF3</i>	-1.197675934
<i>ROCK2</i>	-1.177821221
<i>CFL1</i>	-1.17165777
<i>MAX</i>	-1.033450101
<i>IRF1</i>	-0.971790096
<i>MAPKAPK2</i>	-0.962311663
<i>NR3C1</i>	-0.959382127
<i>TGFB1</i>	-0.940185258
<i>CCR1</i>	-0.92268522
<i>C1QB</i>	-0.843103513
<i>STAT3</i>	-0.832116767
<i>GNAS</i>	-0.791271867
<i>GNAQ</i>	-0.77341131
<i>LY96</i>	-0.771267718
<i>RHOA</i>	-0.76971607
<i>RAF1</i>	-0.769392504
<i>BCL6</i>	-0.767311415
<i>MMP9</i>	-0.762833124
<i>CREB1</i>	-0.73924081
<i>HMGB2</i>	-0.709822123
<i>SMAD7</i>	-0.676374314
<i>TRAF2</i>	-0.6481829
<i>TNF</i>	-0.62012128

Table S9. Sample sizes (*n*) for *Experiment 2* consisting of real time RT-PCR experiments examining the effect of LPS and *M. vaccae* NCTC 11659 on gene expression. Sample size represents 1 experimental replicate. Data came from two independent experiments (*N* = 2).

Figure	Gene	LPS treatment	Bacterial Treatment	Sample Size (<i>n</i>)
S13	<i>IL12A</i>	0 ng/mL	BBS	2
			10 µg/mL <i>M. vaccae</i> NCTC 11659	1
			30 µg/mL <i>M. vaccae</i> NCTC 11659	4
			100 µg/mL <i>M. vaccae</i> NCTC 11659	4
			300 µg/mL <i>M. vaccae</i> NCTC 11659	2
		0.5 ng/mL	BBS	7
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	7
			10 µg/mL <i>M. vaccae</i> NCTC 11659	7
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	7
		250 ng/mL	BBS	4
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	7
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	7
	<i>IL12B</i>	0 ng/mL	BBS	3
			10 µg/mL <i>M. vaccae</i> NCTC 11659	3
			30 µg/mL <i>M. vaccae</i> NCTC 11659	5
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	5
		0.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	7
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8

		250 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
	<i>IL23A</i>	0 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		0.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		250 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
S14	<i>IL10</i>	0 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	7
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		0.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8

		250 ng/mL	300 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			BBS	8	
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8	
	TGFB	0 ng/mL	BBS	8	
			10 µg/mL <i>M. vaccae</i> NCTC 11659	7	
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8	
		0.5 ng/mL	BBS	8	
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8	
		2.5 ng/mL	BBS	7	
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			30 µg/mL <i>M. vaccae</i> NCTC 11659	7	
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8	
		250 ng/mL	BBS	8	
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8	
2		IL10:IL12A	0 ng/mL	BBS	2
				10 µg/mL <i>M. vaccae</i> NCTC 11659	1
				30 µg/mL <i>M. vaccae</i> NCTC 11659	3
				100 µg/mL <i>M. vaccae</i> NCTC 11659	4
	300 µg/mL <i>M. vaccae</i> NCTC 11659			2	
	0.5 ng/mL		BBS	7	
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8	
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8	
	2.5 ng/mL		BBS	7	
			10 µg/mL <i>M. vaccae</i> NCTC 11659	7	
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8	

			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	7
		250 ng/mL	BBS	4
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	7
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	7
	<i>IL10:IL12B</i>	0 ng/mL	BBS	3
			10 µg/mL <i>M. vaccae</i> NCTC 11659	2
			30 µg/mL <i>M. vaccae</i> NCTC 11659	5
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	4
		0.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	7
		250 ng/mL	BBS	7
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
	<i>IL10:IL23A</i>	0 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	7
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		0.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8

S15	TGFB:IL12A		30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		250 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
	TGFB:IL12B	0 ng/mL	BBS	2
			10 µg/mL <i>M. vaccae</i> NCTC 11659	1
			30 µg/mL <i>M. vaccae</i> NCTC 11659	4
			100 µg/mL <i>M. vaccae</i> NCTC 11659	4
			300 µg/mL <i>M. vaccae</i> NCTC 11659	2
		0.5 ng/mL	BBS	7
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	7
			10 µg/mL <i>M. vaccae</i> NCTC 11659	7
			30 µg/mL <i>M. vaccae</i> NCTC 11659	7
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	7
		250 ng/mL	BBS	4
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	7
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	7
		0 ng/mL	BBS	3
			10 µg/mL <i>M. vaccae</i> NCTC 11659	3
			30 µg/mL <i>M. vaccae</i> NCTC 11659	5
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	4
		0.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	6

			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	7
			100 µg/mL <i>M. vaccae</i> NCTC 11659	7
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		250 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
	<i>TGFB:IL23A</i>	0 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		0.5 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		2.5 ng/mL	BBS	7
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	7
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8
		250 ng/mL	BBS	8
			10 µg/mL <i>M. vaccae</i> NCTC 11659	8
			30 µg/mL <i>M. vaccae</i> NCTC 11659	8
			100 µg/mL <i>M. vaccae</i> NCTC 11659	8
			300 µg/mL <i>M. vaccae</i> NCTC 11659	8

Table S10. Post hoc *p* values not specified in main text.

Figure	Gene	LPS condition	Comparison	<i>p</i>
S13	<i>IL12A</i>	Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Within 0.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	0.0688819
		Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	> .1
			BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	> .1
			BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	> .1
		Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1

			10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	0.01458014
		Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
		Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
		Between all LPS conditions within 300 µg/mL <i>M. vaccae</i> NCTC 11659	300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	0.01240536
	<i>IL12B</i>	Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1

			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		Within 0.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	0.0789984
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.09231063
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.01916455
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	< .01
			BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	< .001
			BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	< .001
		Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01

			10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 300 µg/mL <i>M. vaccae</i> NCTC 11659	300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	<i>IL23A</i>	Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .001

		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .001
	Within 0.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
	Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	< .01
		BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	< .001
		BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	< .001
	Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001

		Between all LPS conditions within 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	0.09659867
			30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	< .01
			300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .01
S14	<i>IL10</i>	Within 0 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.03136868
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.0282815
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.03863024
			BBS vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
		Within 0.5 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1

		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.02616086
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
	Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.04470415
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
	Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	0.0232713
		BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	< .01
		BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	> .1
	Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
	Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1

		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1	
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1	
	Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	0.03190491	
		100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1	
		100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1	
	Between all LPS conditions within 300 µg/mL <i>M. vaccae</i> NCTC 11659	300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	< .01	
		300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	0.03972336	
		300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	0.0101786	
	TGFB	Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659			> .1	
BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659			> .1	
Within 0.5 ng/mL		BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1	
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1	
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1	

	BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	0.03918828
	BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.06495136
	BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	0.03227054
Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	> .1
	BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	> .1
	BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	0.0433803
Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	0.01099135
Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	0.01357702

		Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .001
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
		Between all LPS conditions within 300 µg/mL <i>M. vaccae</i> NCTC 11659	300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
		Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Within 0.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.01217065
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	0.0264807
		Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1

		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	0.06869352
		BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	> .1
		BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	> .1
	Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	0.02535678
	Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	0.0625251
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1

		Between all LPS conditions within 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
		Between all LPS conditions within 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	0.01371849
	<i>IL10:IL12B</i>	Within 0 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .001
		Within 0.5 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .001
		Within 2.5 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.03528282
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.01126892
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1

		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	0.06619748
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
	Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	0.04940273
		BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	< .001
		BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	< .001
	Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	0.04720208
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1

			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 300 µg/mL <i>M. vaccae</i> NCTC 11659	300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	<i>IL10:IL23A</i>	Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	0.01920024
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .001
		Within 0.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	0.01299137
		Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1

		BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	0.01408542
		BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	0.01154322
	Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	0.04855252
		BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	< .01
		BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	< .001
	Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	0.07592508

S15	TGFB:IL12A	Between all LPS conditions within 300 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Within 0.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	0.07904917
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.09003819
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1

		BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
	Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	> .1
		BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	> .1
		BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	> .1
	Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	0.02780981
	Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
	Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1

		Between all LPS conditions within 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	> .1
	TGFB:IL12B	Within 0 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.01007759
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .01
		Within 0.5 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.08479317
			BBS vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.01243819
		Within 2.5 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.01583241
			BBS vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	0.0236974
		Within 250 ng/mL	BBS vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	< .01
			BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	0.01706393

	Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	< .01
		BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	< .001
	Between all LPS conditions within 10 µg/mL <i>M. vaccae</i> NCTC 11659	10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01
		10 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	Between all LPS conditions within 30 µg/mL <i>M. vaccae</i> NCTC 11659	30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01
		30 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	Between all LPS conditions within 100 µg/mL <i>M. vaccae</i> NCTC 11659	100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
		100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
		100 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
	Between all LPS conditions within 300 µg/mL <i>M. vaccae</i> NCTC 11659	300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1

			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .01
	<i>TGFB:IL23A</i>	Within 0 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		Within 0.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
		Within 2.5 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.02776241
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	0.03448704
		Within 250 ng/mL	BBS vs. 10 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 30 µg/mL <i>M. vaccae</i> NCTC 11659	> .1
			BBS vs. 100 µg/mL <i>M. vaccae</i> NCTC 11659	0.0724892
			BBS vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659	< .01
		Between all LPS conditions within BBS	BBS + LPS vehicle vs. BBS + 0.5 ng/mL LPS	< .01
			BBS + LPS vehicle vs. BBS + 2.5 ng/mL LPS	< .001
			BBS + LPS vehicle vs. BBS + 250 ng/mL LPS	< .001

		Between all LPS conditions within 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .01
			10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 10 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	< .001
			30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 30 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .001
		Between all LPS conditions within 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1
			100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 100 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .01
		Between all LPS conditions within 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659	300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 0.5 ng/mL LPS	> .1
			300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 $\mu\text{g/mL}$ <i>M. vaccae</i> NCTC 11659 + 2.5 ng/mL LPS	> .1

			300 µg/mL <i>M. vaccae</i> NCTC 11659 + LPS vehicle vs. 300 µg/mL <i>M. vaccae</i> NCTC 11659 + 250 ng/mL LPS	< .01
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Table S11. Primers used for real time RT-PCR listed from 5' to 3'.

Gene	Forward Primer	Reverse Primer	Sequence Name
<i>ACTB</i>	GGACCTGACTGACTACCTCAT	CGTAGCACAGCTTCTCCTTAAT	ACC# NM_001101.3
<i>IL10</i>	GCTGGAGGACTTTAAGGGTTAC	GATGTCTGGGTCTTGGTTCTC	ACC# NM_000572.3
<i>IL12A</i>	CCAGAAGAATGAGAGTTGCCTAA	GGCACAGGGCCATCATAAA	ACC# NM_001354583.2
<i>IL12B</i>	CACATTCTACTTCTCCCTGAC	GTCCGTGAAGACTCTATCTTTCTT	ACC# AF180563.1
<i>IL23A</i>	AGAGAAGAGGGAGATGAAGAGA	CCTTTGCAAGCAGAACTGAC	ACC# NM_016584.3
<i>TGFB1</i>	GTAAGAAGCACGAGCTGTATGT	GCGTTCATGTAGGAGTTCAGAG	ACC# M60316.1

S4. Supplemental References

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