Description of Additional Supplementary Files

File Name: Supplementary Data 1
Description: Genes upregulated in expression in $Nos2^{+/-}$ IMs. Differential gene expression analysis was performed between $NOS2^{+}$ IMs and $NOS2^{-}$ IMs using a two-sided Wilcoxon rank-sum test. P-values were adjusted for multiple comparisons using the Bonferroni correction.

File Name: Supplementary Data 2
Description: List of pathways that are modulated during infection. Generalized additive models (GAMs) were fitted to assess temporal changes in pathway expression levels. An analysis of variance (ANOVA) was performed on these models to derive p-values, which were subsequently adjusted for multiple comparisons using the Benjamini-Hochberg method.

File Name: Supplementary Data 3
Description: Genes upregulated in expression in $CD38^{+/-}$ AMs. Differential gene expression analysis was performed using a two-sided Wilcoxon rank-sum test. P-values were adjusted for multiple comparisons using the Bonferroni correction.

File Name: Supplementary Data 4
Description: Module 2 genes upregulated in BCG-infected macrophages. The module was identified through scWGCNA analysis, which employs an iterative clustering approach to detect co-expression patterns among genes. Modules were determined via hierarchical clustering, utilizing topological overlap matrices generated from pseudocell expression data and dynamic tree cutting, optimizing module stability and biological relevance. Each gene's module membership was assessed and only genes with significant memberships were retained for further analysis. Adjusted p-values for module significance for genes within each module were calculated using the Benjamini-Hochberg method to control the FDR.

File Name: Supplementary Data 5
Description: Cellular pathways enriched in BCG-treated macrophages. Pathway enrichment analysis was conducted using the G::Profiler and the two-sided g:SCS method, as described[118]. Exact adjusted p-values are provided for each pathway. g:SCS threshold is a value pre-calculated for query list sizes up to 1000 genes. Given a fixed input query size, g:SCS analytically approximates a threshold t corresponding to the 5% upper quantile of randomly generated queries of that size. All actual p-values resulting from the query are transformed to corrected p-

values by multiplying these to the ratio of the approximate threshold t and the initial experiment-wide threshold a=0.05