

## Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: **Cluster-specific differentially expressed genes for total scRNASeq dataset (related to Fig1C and FigS1A).**

Defined using the Seurat::FindMarkers function (ref 97). Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction.

File Name: Supplementary Data 2

Description: **Differentially expressed genes between PBS iv+SCV2 and BCG iv+SCV2 experimental conditions for distinct cell types (related to Fig1E).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 3

Description: **Cluster-specific differentially expressed genes for myeloid sub-cluster (related to Fig1F and FigS1D).**

Defined using the Seurat::FindMarkers function (ref 97). Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction.

File Name: Supplementary Data 4

Description: **Differentially expressed genes between alveolar macrophages (enriched in PBS iv+SCV2) and monocyte-derived macrophages (enriched in BCG iv+SCV2) (related to Fig1G and FigS1E).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 5

Description: **Differentially expressed genes between BCG iv+SCV2+isotype and BCG iv+SCV2+anti-IFN $\gamma$  groups for CD45-negative cell types (related to Fig3E).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 6

Description: **Differentially expressed genes between BCG iv+SCV2+isotype and BCG iv+SCV2+anti-IFN $\gamma$  groups myeloid cell types (related to Fig3E).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 7

Description: **Differentially expressed genes between BCG iv+SCV2+isotype and BCG iv+SCV2+anti-IFN $\gamma$  groups lymphoid cell types (related to Fig3E).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 8

Description: **Differentially expressed genes between PBS iv+SCV2+isotype and PBS iv+SCV2+anti-IFN $\gamma$  groups for CD45-negative cell types (related to FigS4A).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 9

Description: **Differentially expressed genes between PBS iv+SCV2+isotype and PBS iv+SCV2+anti-IFN $\gamma$  groups for myeloid cell types (related to FigS4A).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 10

Description: **Differentially expressed genes between PBS iv+SVC2+isotype and PBS iv+SCV2+anti-IFN $\gamma$  groups for lymphoid cell types (related to FigS4A).**

Differentially expressed genes (DEGs) were defined using a Wilcoxon Rank Sum test with Bonferroni correction (p-value < 0.05, log 2 fold change limit of 0.25 and the stipulation that genes must appear in at least 10% of cells in either cluster).

File Name: Supplementary Data 11

Description: **Curated list of genes with validated SARS-CoV-2 restriction properties (related to FigS4B-C).**

Curated from refs 48 and 49.