Figure S1. Representative flow cytometry dot plots (n = 5 mice/group) of the distribution of Cd11b<sup>-</sup>c<sup>-</sup>, CD11b<sup>-</sup>c<sup>+</sup>, and CD11b<sup>+</sup>c<sup>+</sup> cells in lung cells of Mtbi-infected mice.

Figure S2. Quantification of NOS2-expressing cells. Total lung cells from WT and IL4Ra<sup>-/-</sup> (KO) mice were stained for CD11b, CD11c, and NOS-2 protein and analyzed by FACS. The figure presents dot plots of NOS2-expressing cells in CD11b<sup>-</sup>, CD11c<sup>+</sup>, and CD11b<sup>-</sup>c<sup>+</sup> populations from a single representative sample (n = 5 mice/group).
Figure S3. Quantification of Fizz-1–expressing cells. Total lung cells from WT and IL4Rα−/− (KO) mice were stained for CD11b, CD11c, and Fizz-1 protein and analyzed by FACS. The figure presents dot plots of Fizz-1–expressing cells in CD11b+, CD11c+, and CD11b+c+ populations from a single representative sample (n = 5 mice/group).

Figure S4. Enumeration of instilled macrophages. 10 × 10⁶ thioglycollate-elicited peritoneal macrophages (PEM) from WT or IL-4Rα−/− (KO) mice were adoptively transferred via the intratracheal route into IL-4Rα−/− hosts. Lungs were harvested either 10 h after the transfer of peritoneal macrophages and before Nb infection or 5 d after Nb infection (n = 3 for each group at each time point) and single cell suspensions prepared. CFSE-positive cells present in total lung cells were evaluated by flow cytometry and data are presented as the absolute number of cells (mean ± SD). Data are representative of two independent experiments.