Figure S1

(a) PCA of gene expression from WT and Scnn1b-Tg whole lung and purified BAL macrophages at PND 0, 3, 10, and 42 plotted in two-dimensional space for the selected groups of principal components (PCs; shown on the X and Y axis). (b) PCA of gene expression for isolated macrophages from WT and Scnn1b-Tg mice for PCAs as indicated on the axis. Squares = WT. Triangles = Scnn1b-Tg. Age is designated by color: PND0 (red), PND 3 (green), PND 10 (blue), and PND42 (purple). PND 42 macrophages from germ-free (GF) mice are orange. Each symbol represents the results of a single microarray, which for whole lung represents pools of individual mice as described in the methods.
Figure S3

RAW: Pre-Column
Ly6G Negative Fraction: Purified Macrophages
Ly6G Positive Fraction

Red and blue arrows indicate representative polymorphonuclear cells [neutrophils; only seen in (a and c)] and macrophages, respectively.
Figure S4

Macrophage WT vs. Tg

PND 0 3 10 42

- T-cell mediated cytotoxicity
- Antigen processing and presentation
- Positive regulation of reproductive process
- Single organism membrane organization
- Protein activation cascade
- Positive regulation of biological process
- Cell killing
- Regulation of response to stimulus
- Modification of morphology or physiology of other organism
- Rhythmic behavior
- Multi-organism cellular process
- Response to stress
- Immune system development
- Cell proliferation
- Death
- Immune effector process
- Response to biotic stimulus
- Response to other organism
- Negative regulation of immune system process
- Regulation of multi-organism process
- Leukocyte homeostasis
- Rhythmic process
- Movement in environment of other organism involved in symbiotic interaction
- Interspecies interaction between organisms
- Production of molecular mediator of immune response
- Multi-organism process
- Negative regulation of multi-organism process
- Behavior
- Growth involved in symbiotic interaction
- Regulation of growth
- Growth
- Regulation of developmental process
- Ovulation cycle
- Ovulation cycle process
- Negative regulation of response to stimulus
- Myeloid cell homeostasis
- Negative regulation of locomotion
- Positive regulation of developmental process
- Anatomical structure morphogenesis
- Anatomical structure formation involved in morphogenesis

Macrophage WT vs. Tg

PND 0 3 10 42

- Muscle adaptation
- Response to abiotic stimulus
- Regulation of biological quality
- Developmental pigmentation
- Response to endogenous stimulus
- Developmental process
- Multicellular organismal development
- Cellular developmental process
- Developmental process involved in reproduction
- Single-organism developmental process
- Anatomical structure development
- Innervation
- Stem cell maintenance
- Organ growth
- Cardiac muscle tissue growth
- Pattern specification process
- Negative regulation of developmental process
- Hormone metabolic process
- Developmental growth
- Response to chemical stimulus
- Positive regulation of response to stimulus
- Leukocyte activation
- Immune system process
- Regulation of immune system process
- Positive regulation of growth
- Tolerance induction
- Immune response
- Leukocyte migration
- Activation of immune response
- Positive regulation of immune system process
- Cell growth
- Biological adhesion
- Cell adhesion
- Response to external stimulus
- Regulation of localization
- Taxis
- Cell motility
- Localization of cell
- Regulation of locomotion
- Positive regulation of locomotion
- Locomotion
Figure S5

The graph shows the densitometric quantification of the western data. ** = p < 0.01; *** = p < 0.001.
Figure S7

Heat-maps from normalized expression values of M1 and M2 macrophage-activation-related genes (see gene list in Additional file 6: Results file S3 under headings "Macrophage M1 Activation" and "Macrophage M2 Activation"). Higher and lower expression is represented by red and blue, respectively; with each individual heat-map produced separately (each heat-map has its own unique range of values indicated by dark blue to bright red). The corresponding data can be found in Additional file 7: Results file S4. Each column represents data from one array (n = 3 for GF macrophages and lung; n = 4 for SPF macrophage groups for each genotype), with WT or Scn1b-Tg (Tg) status listed above the columns. Each row represents a single gene.