

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: A list of differentially expressed genes ($P < 0.05$) in 13 clusters of myeloid cells from the aortas of *ApoE*^{-/-} mice by single cell RNA sequencing (related to Figure 1). Differentially expressed genes were identified using the two-sided Wilcoxon Rank Sum test with Bonferroni's correction for multiple hypothesis testing.

File name: Supplementary Data 2

Description: A list of inflammatory genes related to Supplementary Figure 2c.

File name: Supplementary Data 3

Description: A list of differentially expressed genes ($P < 0.05$) in *Clec4a2*-deficient BMDMs relative to WT cells by RNA sequencing (related to Figure 5). Differential expression was assessed using the two-sided Robinson and Smyth exact test with Bonferroni's correction for multiple hypothesis testing.

File name: Supplementary Data 4

Description: A list of differentially expressed genes ($P < 0.05$) in 13 clusters of myeloid cells from the aortas of *ApoE*^{-/-} and *ApoE*^{-/-} *Clec4a2*^{-/-} littermate mice by single cell RNA sequencing (related to Figure 7). Differentially expressed genes were identified using the two-sided Wilcoxon Rank Sum test with Bonferroni's correction for multiple hypothesis testing.

File name: Supplementary Data 5

Description: A list of differentially expressed genes ($P < 0.05$) in vascular resident macrophages (Cluster 1) of *ApoE*^{-/-} *Clec4a2*^{-/-} mice relative to *ApoE*^{-/-} mice by single cell RNA sequencing (related to Figure 7). Differentially expressed genes were identified using the two-sided Wilcoxon Rank Sum test with Bonferroni's correction for multiple hypothesis testing.