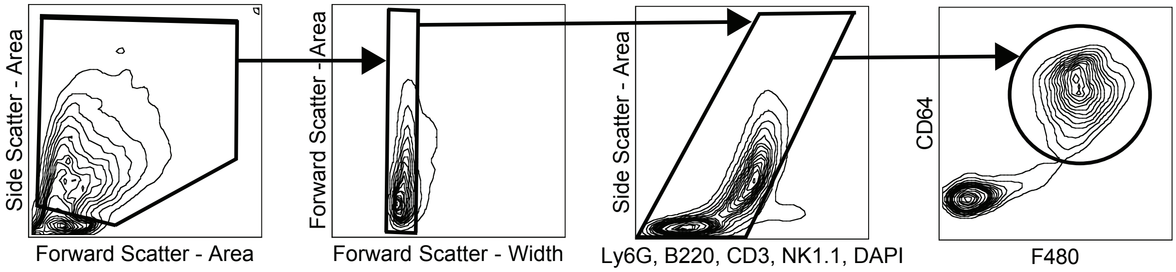
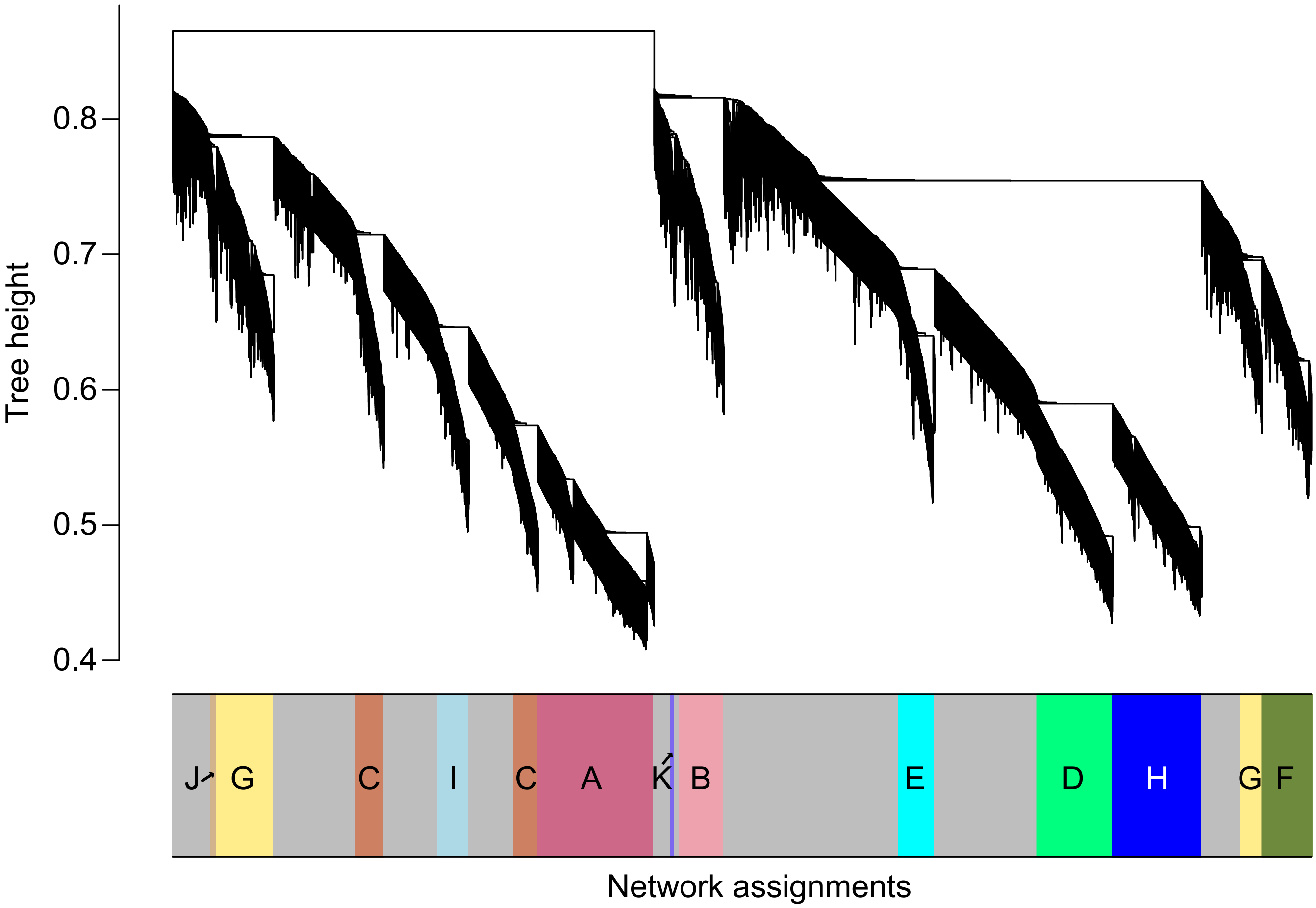
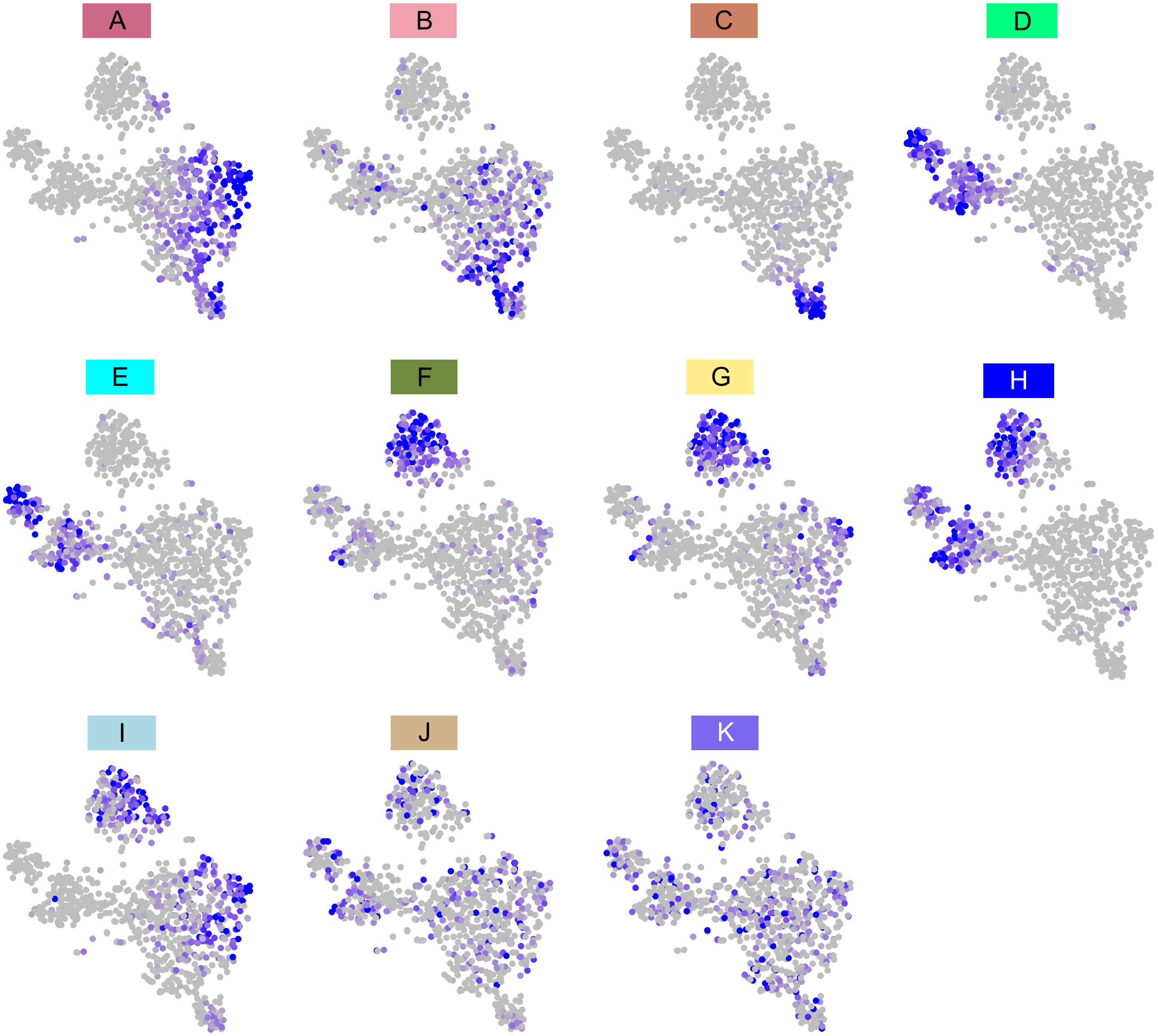
Supplemental Information



Supplemental Figure 1. **Sort strategy.** Macrophages were isolated from bronchoalveolar lavage of mice treated with intratracheal LPS using FACS. Forward scatter and side scatter were used to exclude lymphocytes and monocytes. Doublets were excluded using the pulse width. Dead and contaminating cells were further eliminated using DAPI, NK1.1, CD3, B220, and Ly6g. Airspace macrophages were identified by high expression of CD64 and F480.



Supplemental Figure 2. WGCNA dendrogram and network assignments. Gene dendrogram based on hierarchical clustering of topological overlap values (which measure interconnectedness of genes) calculated with WGCNA using previously published “bulk” RNA-seq data from purified resident and recruited AMs. Genes are assigned to 1 of 11 networks (A through K). Gray color indicates unassigned genes.



Supplemental Figure 3. Overlay of WGCNA-derived gene networks from ‘bulk’ RNA-seq onto single cell clusters. Summary (eigengene) expression of genes from each of 11 WGCNA networks overlaid on the single cell tSNE plot.

Supplemental Tables are located in Excel File in the following tabs:

Supplemental Table 1: Pathway Enrichment for cluster 1 versus RecAMs

Supplemental Table 2: Pathway Enrichment for cluster 2 versus RecAMs

Supplemental Table 3: Pathway Enrichment for cluster 2 versus cluster 1

Supplemental Table 4: Pathway Enrichment for cluster 1, day 0 versus cluster 1, days 3 and 6

Supplemental Table 5: Pathway Enrichment for cluster 1, day 3 versus cluster 1, days 0 and 6

Supplemental Table 6: Pathway Enrichment for cluster 1, day 6 versus cluster 1, days 0 and 3

Supplemental Table 7: Pathway Enrichment for clusters 3 and 4 versus clusters 1, 2, and 5

Supplemental Table 8: Pathway Enrichment for cluster 3 versus cluster 4

Supplemental Table 9: Pathway Enrichment for cluster 4 versus cluster 3

Supplemental Table 10: Pathway Enrichment for cluster 5 versus clusters 1, 2, 3, and 4

Supplemental Table 11: Genes comprising Figure 6

Supplemental Table 12: Pathway Enrichment for WGCNA modules