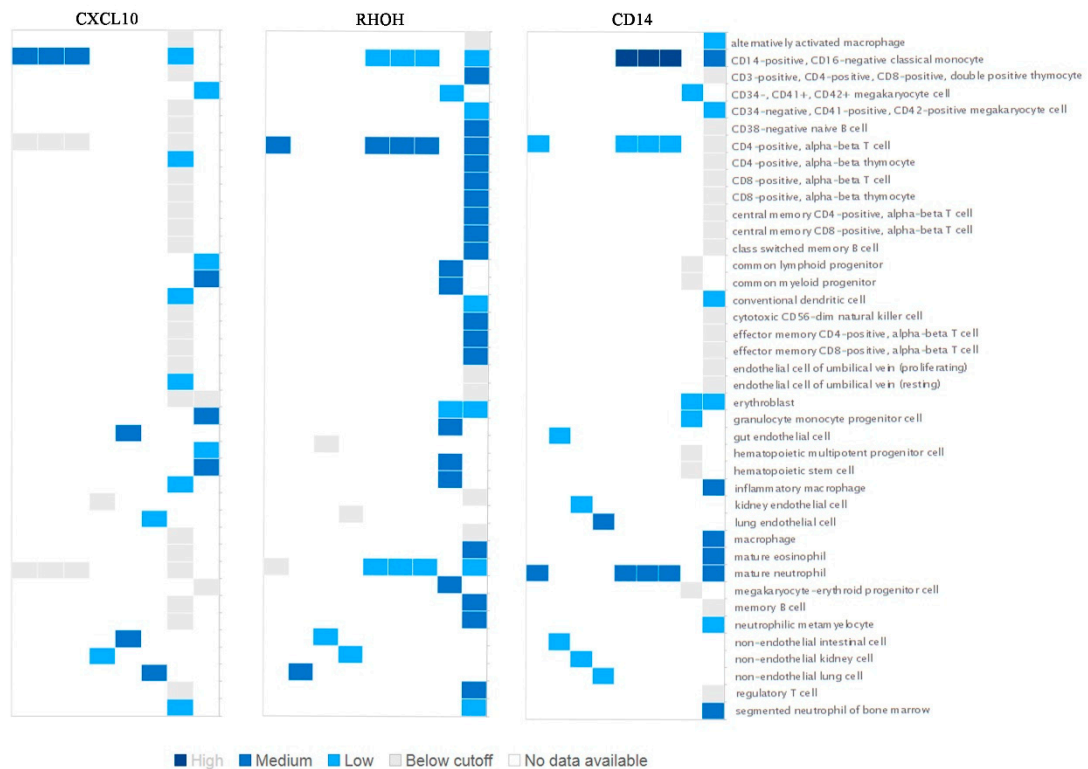


**Figure S1. A synergistic analysis of Hub genes in the blood of three diseases.** A-C, Heatmaps of the expression profiles of 10 hub genes in the blood of RSV infection, asthma, and COPD. Each column showed a single sample, each row represented a marker gene, and its expression value is normalized among 50 genes. D, the barplot display of the differential analysis of the expression of 10 hub genes in the lung of RSV infection, asthma, and COPD (\* $p < 0.05$ , \*\* $p < 0.01$ , and \*\*\* $p < 0.001$  vs. Healthy). E, detection of mRNA levels of hub genes in blood of RSV-induced model using qRT-PCR (n = 6) (\* $p < 0.05$ , \*\* $p < 0.01$  and \*\*\* $p < 0.001$  vs. Control).



**Figure S2. Expression distribution of CXCL10, RHOH, and CD14 in cell types.** Using the Expression Atlas database (<http://www.ebi.ac.uk/gxa/home>) to analyze the expression distribution of hub genes CXCL10, RHOH, and CD14 in cell lines.

**Table S1.** Primers for the quantitative RT-PCR.

| Genes                  | Sequences   |
|------------------------|---|
| LCP1-F (Mouse)         | TCTGTGCCAGACACGATTGACG                                  |
| LCP1-R (Mouse)         | GAGGCAGAGTTCAGAGCCAAGT                                  |
| CCR1-F (Mouse)         | GCCAAAAGACTGCTGTAAGAGCC                                 |
| CCR1-R (Mouse)         | GCTTTGAAGCCTCCTATGCTGC                                  |
| CXCL10-F (Mouse)       | ATCATCCCTGCGAGCCTATCCT                                  |
| CXCL10-R(Mouse)        | GACCTTTTTTTGGCTAAACGCTTTC                               |
| CD14-F (Mouse)         | TTGAACCTCCGCAACGTGTCGT                                  |
| CD14-R (Mouse)         | CGCAGGAAAAGTTGAGCGAGTG                                  |
| ZEB1-F (Mouse)         | ATTCAGCTACTGTGAGCCCTGC                                  |
| ZEB1-R (Mouse)         | CATTCTGGTCCTCCACAGTGGA                                  |
| PRKCB-F (Mouse)        | CCAAGATGACGATGTGGAGTGC                                  |
| PRKCB-R (Mouse)        | CTCCATCACAAAGTACAGGCGG                                  |
| PZRY14-F (Mouse)       | ACCTCCGTCAAGAGGAAGTCCA                                  |
| PZRY14-R (Mouse)       | GCTGTAGTGACCTTCCGTCTGA                                  |
| IRAK2-F (Mouse)        | GGACAGATTCCTACAGGCAGAG                                  |
| IRAK2-R (Mouse)        | GGTAGATGAGGCTGTGGAAGT                                   |
| RHOH-F (Mouse)         | TGGATGGCATCCAGATCAGCCT                                  |
| RHOH-R (Mouse)         | GTAGCACATCAGTACCACGTCTG                                 |
| GAPDH-F (Mouse)        | CATCACTGCCACCCAGAAGACTG                                 |
| GAPDH-R (Mouse)        | ATGCCAGTGAGCTTCCCGTTCAG                                 |
| CXCL10-F (Human)       | GGTGAGAAGAGATGTCTGAATCC                                 |
| CXCL10-R (Human)       | GTCCATCCTTGGAAAGCACTGCA                                 |
| CD14-F (Human)         | CTGGAACAGGTGCCTAAAGGAC                                  |
| CD14-R (Human)         | GTCCAGTGTGAGGTTATCCACC                                  |
| RHOH-F (Human)         | TGGATGGCATCCAGATCAGCCT                                  |
| RHOH-R (Human)         | GCCACAGAGTAGCACATCAGCA                                  |
| GAPDH-F (Human)        | GTCTCCTCTGACTTCAACAGCG                                  |
| GAPDH-R(Human)         | ACCACCCTGTTGCTGTAGCCAA                                  |
| miR-34b-5p-F           | CGCGTAGGCAGTGTCAATTAGC                                  |
| miR-34b-5p-R           | AGTGCAGGGTCCGAGGTATT                                    |
| miR-34b-5p(RT Primer)  | GTCGTATCCAGTGCAGGGTCCGAGGTATTCG-<br>CACTGGATACGACCAATCA |
| miR-34c-5p-F           | CGCGAGGCAGTGTAGTTAGCT                                   |
| miR-34c-5p-R           | AGTGCAGGGTCCGAGGTATT                                    |
| miR-34c-5p (RT Primer) | GTCGTATCCAGTGCAGGGTCCGAGGTATTCG-<br>CACTGGATACGACGCAATC |
| RSVF-F                 | CACCTTGTTGGAAACTGCACACATC                               |
| RSVF-R                 | CAGTACCATCCTCTGTCGGTTCTTG                               |
| U6-F                   | CTCGCTTCGGCAGCACA                                       |
| U6-R                   | AACGCTTCACGAATTTGCGT                                    |

**Table S2.** Expression changes of miR34b/c-5p in the datasets.

| DataSets  | miRNA          | logFC    | p-Value  |
|-----------|----------------|----------|----------|
| GSE62306  | hsa-miR-34c-5p | -3.10729 | 0.000101 |
|           | hsa-miR-34b-5p | -2.33405 | 0.002036 |
| GSE33336  | hsa-miR-34c-5p | -1.79645 | 0.030761 |
|           | hsa-miR-34b-5p | -1.41812 | 0.025615 |
| GSE142237 | hsa-miR-34c-5p | -1.05808 | 0.011845 |
|           | hsa-miR-34b-5p | -1.89674 | 0.013616 |

**Table S3.** Ontological analysis of common DEGs.

| GO                 | Term  | p-value               | Genes                               |
|--------------------|---|-----------------------|-------------------------------------|
| Biological Process | cytokine-mediated signaling pathway (GO:0019221)                                      | $6.25 \times 10^{-5}$ | CCR1;CXCL10;ZEB1;TNFSF14;IRAK2;LCP1 |
|                    | cellular response to molecule of bacterial origin (GO:0071219)                        | $1.19 \times 10^{-4}$ | CXCL10;PDE4B;CD14                   |
|                    | T cell activation (GO:0042110)  | $1.37 \times 10^{-4}$ | TNFSF14;RHOH;LCP1                   |
|                    | cellular response to lipopolysaccharide (GO:0071222)                                  | $1.51 \times 10^{-4}$ | CXCL10;PDE4B;CD14                   |
|                    | positive regulation of monocyte chemotaxis (GO:0090026)                               | $1.70 \times 10^{-4}$ | CCR1;CXCL10                         |
|                    | positive regulation of mononuclear cell migration (GO:0071677)                        | $2.14 \times 10^{-4}$ | CCR1;CXCL10                         |
|                    | regulation of monocyte chemotaxis (GO:0090025)  | $2.88 \times 10^{-4}$ | CCR1;CXCL10                         |
|                    | MyD88-dependent toll-like receptor signaling pathway (GO:0002755)                     | $5.04 \times 10^{-4}$ | IRAK2;CD14                          |
|                    | response to lipopolysaccharide (GO:0032496)   | $7.21 \times 10^{-4}$ | CXCL10;PDE4B;CD14                   |
|                    | negative regulation of transport (GO:0051051)   | $9.61 \times 10^{-4}$ | MCTP1;PRKCB                         |
| Molecular Function | histone threonine kinase activity (GO:0035184)  | 0.00802               | PRKCB                               |
|                    | cAMP-dependent protein kinase regulator activity (GO:0008603)                         | 0.00802               | CXCL10                              |
|                    | G-protein coupled nucleotide receptor activity (GO:0001608)                           | 0.00916               | P2RY14                              |
|                    | C-C chemokine binding (GO:0019957)  | 0.00916               | CCR1                                |
|                    | G-protein coupled purinergic nucleotide receptor activity (GO:0045028)                | 0.00916               | P2RY14                              |
|                    | protein kinase C activity (GO:0004697)  | 0.01144               | PRKCB                               |
|                    | long-chain fatty acid-CoA ligase activity (GO:0004467)                                | 0.01144               | ACSL1                               |
|                    | calcium-dependent protein serine/threonine kinase activity (GO:0009931)               | 0.01258               | PRKCB                               |
|                    | metal ion binding (GO:0046872)  | 0.01367               | MCTP1;PHACTR1;LCP1                  |
|                    | racemase and epimerase activity, acting on carbohydrates and derivatives (GO:0016857) | 0.01372               | PHACTR1                             |
| Cellular Component | recycling endosome (GO:0055037)   | 0.00819               | MCTP1;RAB8B                         |
|                    | trans-Golgi network transport vesicle (GO:0030140)                                    | 0.01712               | RAB8B                               |
|                    | anchored component of external side of plasma membrane (GO:0031362)                   | 0.02051               | CD14                                |
|                    | intrinsic component of external side of plasma membrane (GO:0031233)                  | 0.02501               | CD14                                |
|                    | lytic vacuole membrane (GO:0098852)   | 0.02911               | AP1S2;LITAF                         |
|                    | lysosomal membrane (GO:0005765)   | 0.04367               | AP1S2;LITAF                         |
|                    | contractile actin filament bundle (GO:0097517)  | 0.04503               | LCP1                                |
|                    | stress fiber (GO:0001725)   | 0.04503               | LCP1                                |

|  |         |       |
|--|---------|-------|
| peroxisomal membrane (GO:0005778)                  | 0.04503 | RAB8B |
| anchored component of plasma membrane (GO:0046658) | 0.04503 | CD14  |

**Table S4.** Pathway enrichment analysis of common DEGs.

| <b>Term</b>   | <b><i>p</i>-value</b> | <b>Genes</b>        |
|---|-----------------------|---------------------|
| NF-kappa B signaling pathway                        | $1.72 \times 10^{-4}$ | TNFSF14;PRKCB;CD14  |
| Chemokine signaling pathway                         | 0.001299              | CCR1;CXCL10;PRKCB   |
| Cytokine-cytokine receptor interaction              | 0.004478              | CCR1;CXCL10;TNFSF14 |
| MAPK signaling pathway                              | 0.004521              | PRKCB;CD14;CACNA1E  |
| Morphine addiction                                  | 0.004868              | PRKCB;PDE4B         |
| Amoebiasis  | 0.005402              | PRKCB;CD14          |
| Toll-like receptor signaling pathway                | 0.00631               | CXCL10;CD14         |
| Parathyroid hormone synthesis, secretion and action | 0.006547              | PRKCB;PDE4B         |
| Leukocyte transendothelial migration                | 0.007282              | PRKCB;RHOH          |
| Lysosome  | 0.008723              | AP1S2;LITAF         |