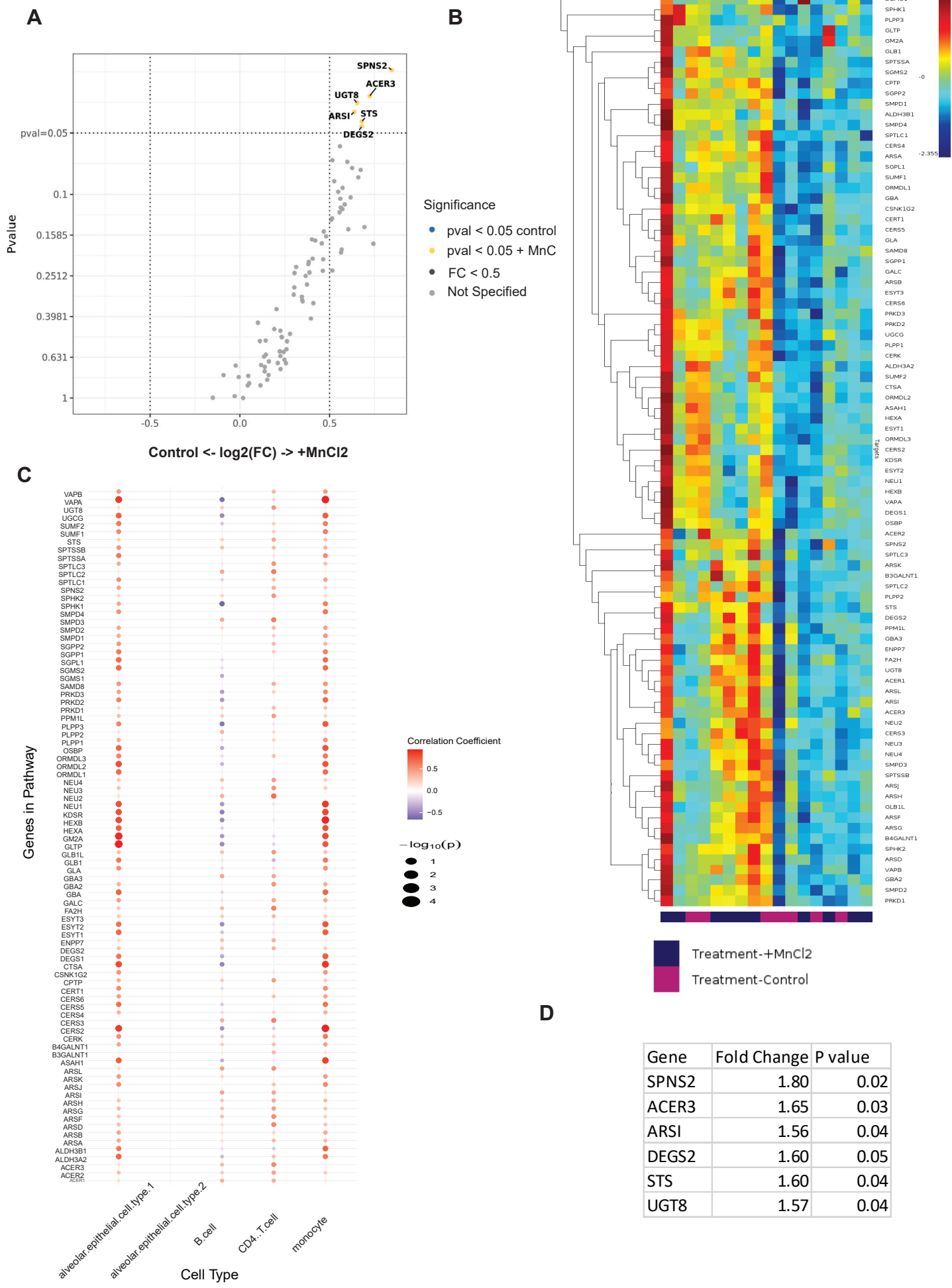
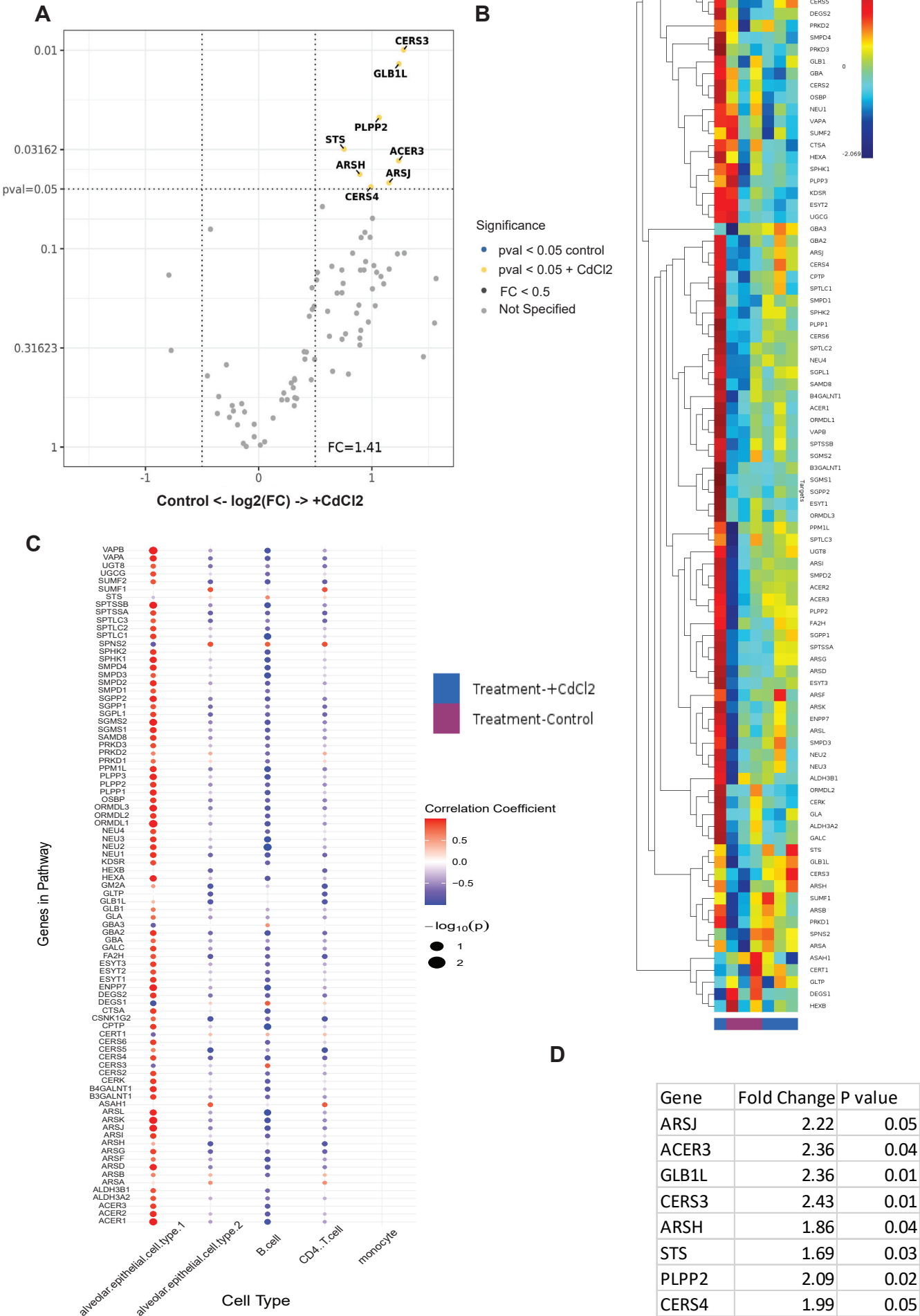


Supplemental Figure 1



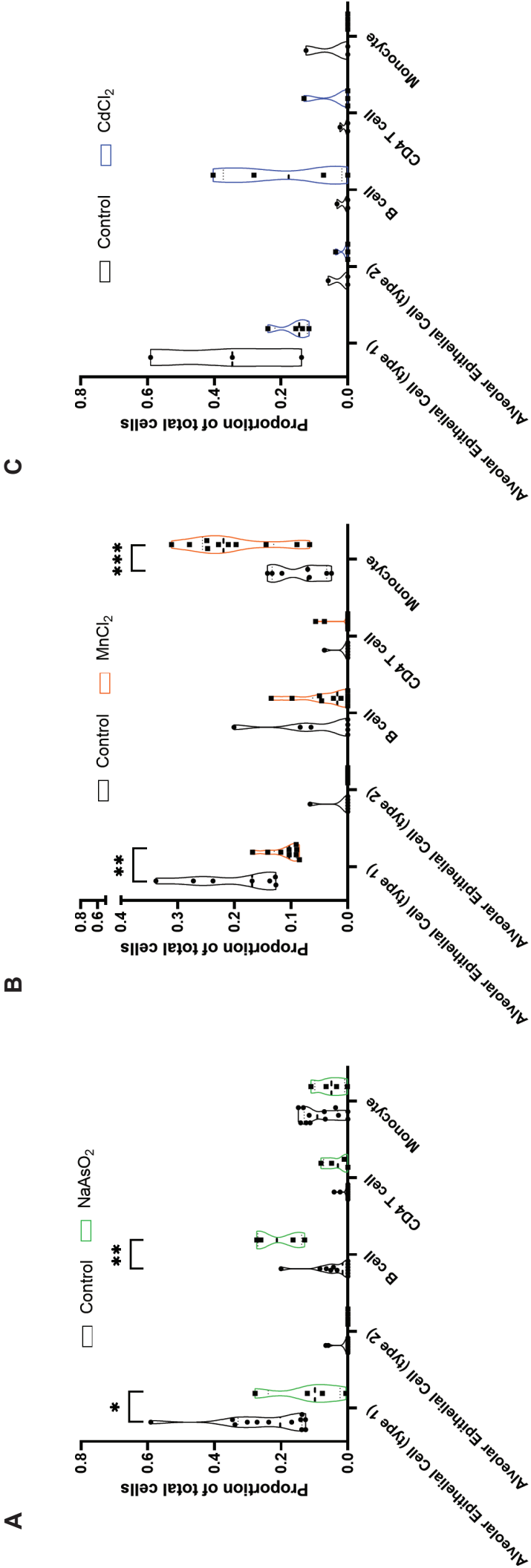
Supplemental Figure 1. Gene expression changes in the sphingolipid pathway in HM-exposed lung tissues following MnCl₂ exposure. **A.** Volcano plot displaying differential gene expression between MnCl₂-exposed and unexposed (control) lung tissues. **B,D.** Heatmap (**B**) and table (**D**) highlighting significantly altered genes with MnCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of sphingolipid pathway with scaled abundance of specific cell populations in the lung tissue following MnCl₂ exposure.

Supplemental Figure 2



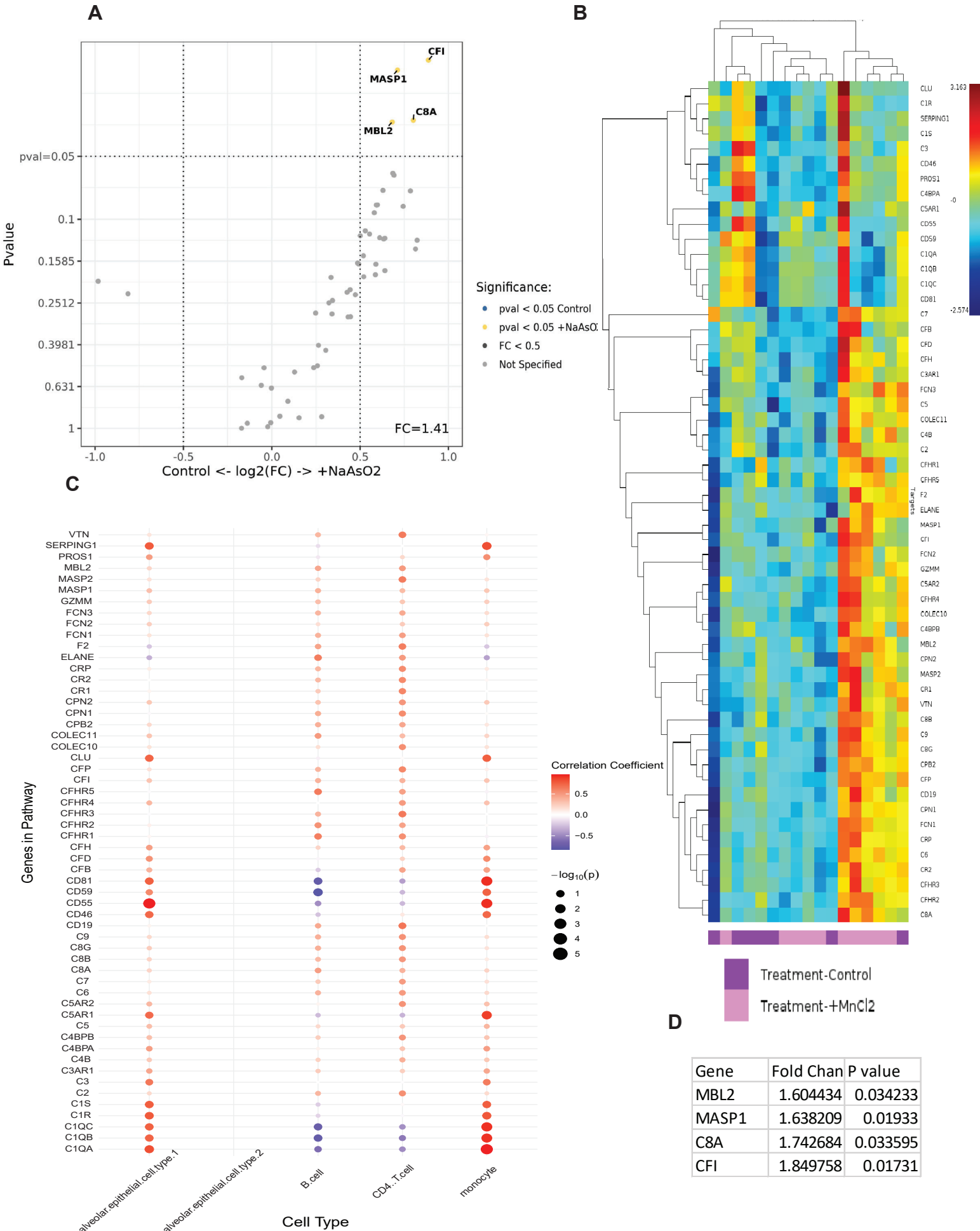
Supplemental Figure 2. Gene expression changes in the sphingolipid pathway in HM-exposed lung tissues following CdCl₂ exposure. **A.** Volcano plot displaying differential gene expression between CdCl₂-exposed and unexposed (control) lung tissues. **B,D.** Heatmap (**B**) and table (**D**) highlighting significantly altered genes with CdCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of sphingolipid pathway with scaled abundance of specific cell populations in the lung tissue following CdCl₂ exposure.

Supplemental Figure 3



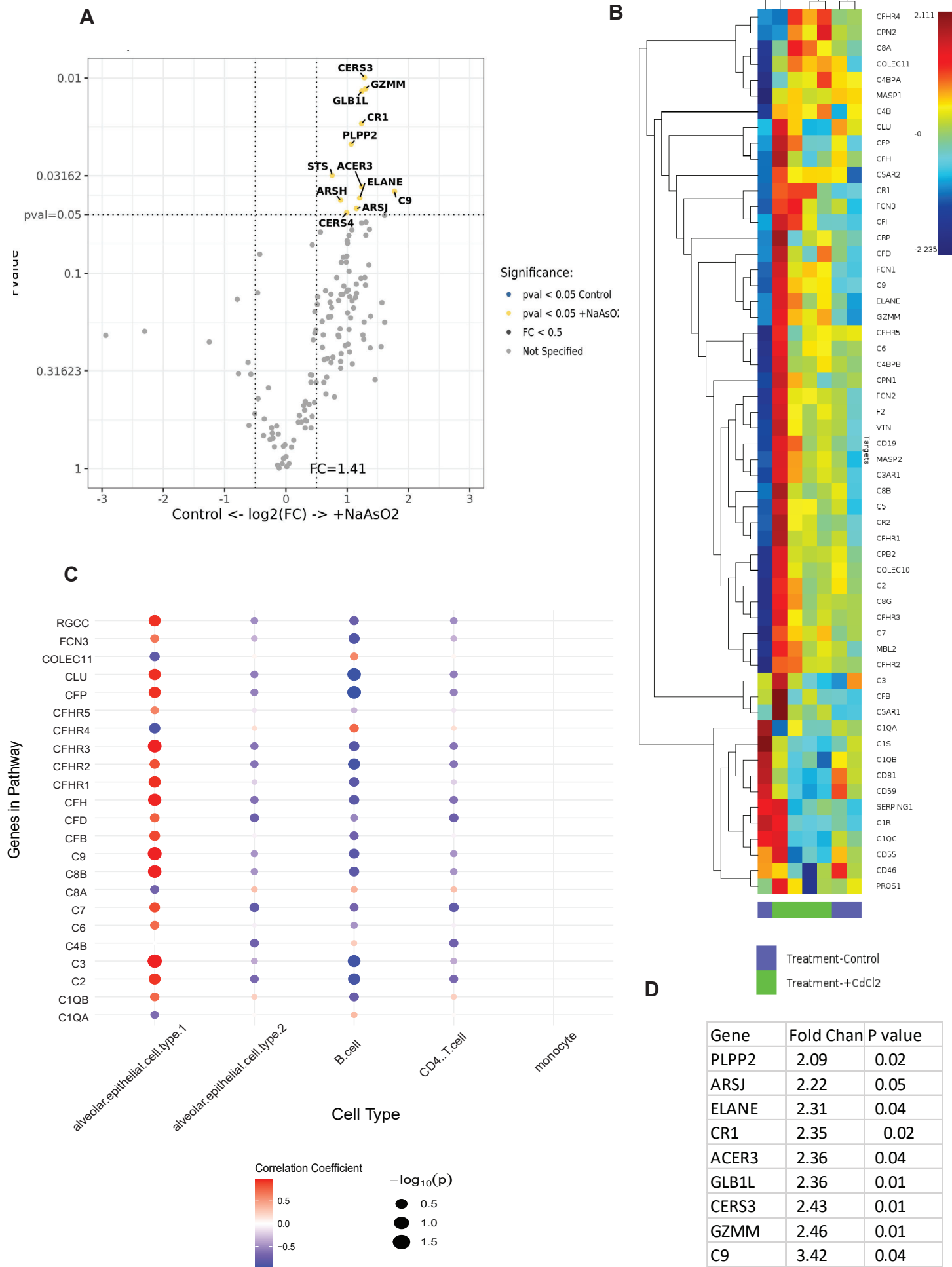
Supplemental Figure 3. Cell abundance changes following heavy metal exposure. A. Cell abundance plot showing differential cell abundance between NaAsO₂-exposed and unexposed (control) lung tissues. **B.** Cell abundance plot showing differential cell abundance between MnCl₂-exposed and unexposed (control) lung tissues. **C.** Cell abundance plot showing differential cell abundance between CdCl₂-exposed and unexposed (control) lung tissues.

Supplemental Figure 4



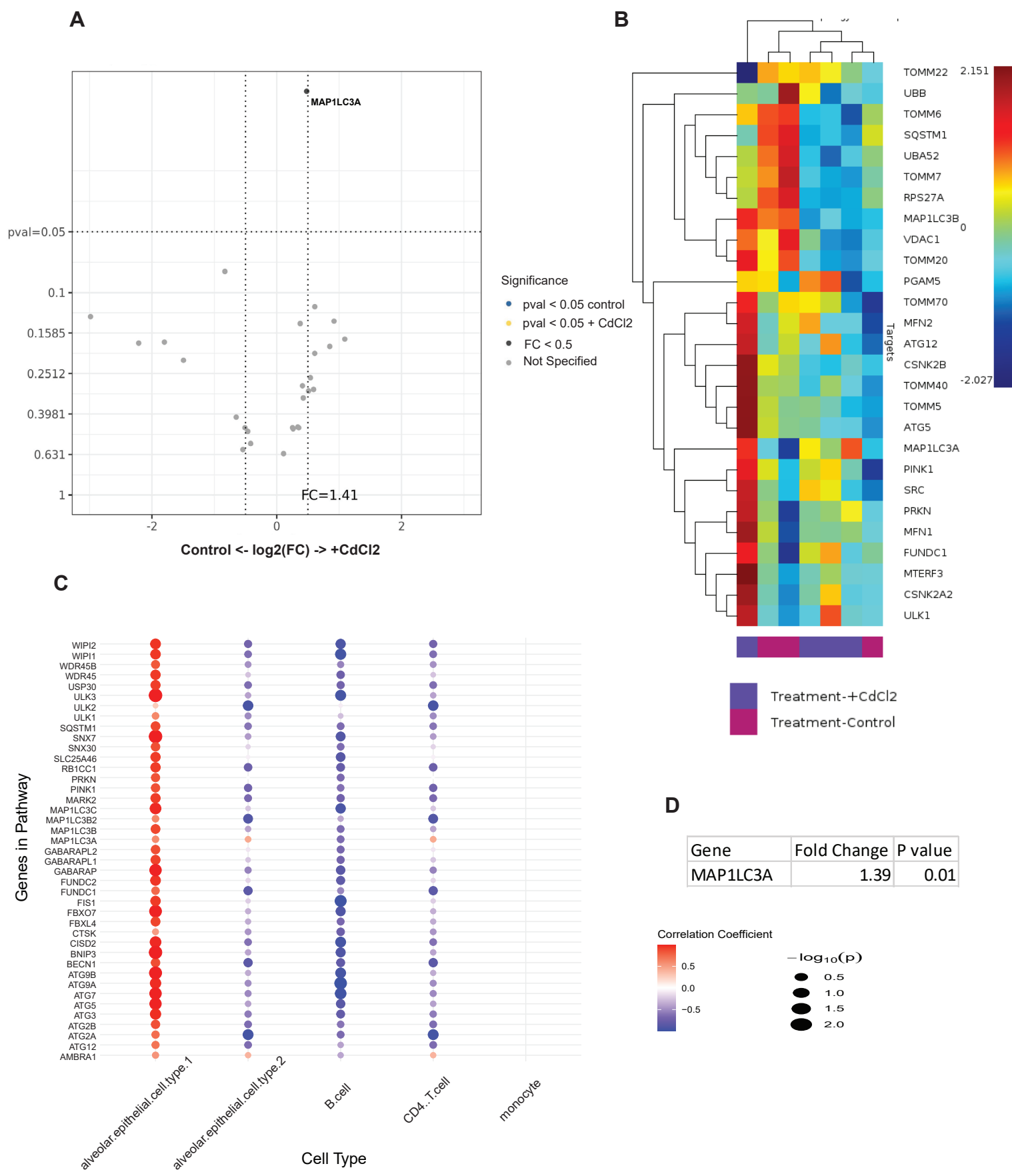
Supplemental Figure 4. Gene expression changes in the complement pathway in HM-exposed lung tissues following MnCl₂ exposure. **A.** Volcano plot displaying differential gene expression between MnCl₂-exposed and unexposed (control) lung tissues. **B,D.** Heatmap (**B**) and table (**D**) highlighting significantly altered genes with MnCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of complement pathway with scaled abundance of specific cell populations in the lung tissue following MnCl₂ exposure.

Supplemental Figure 5



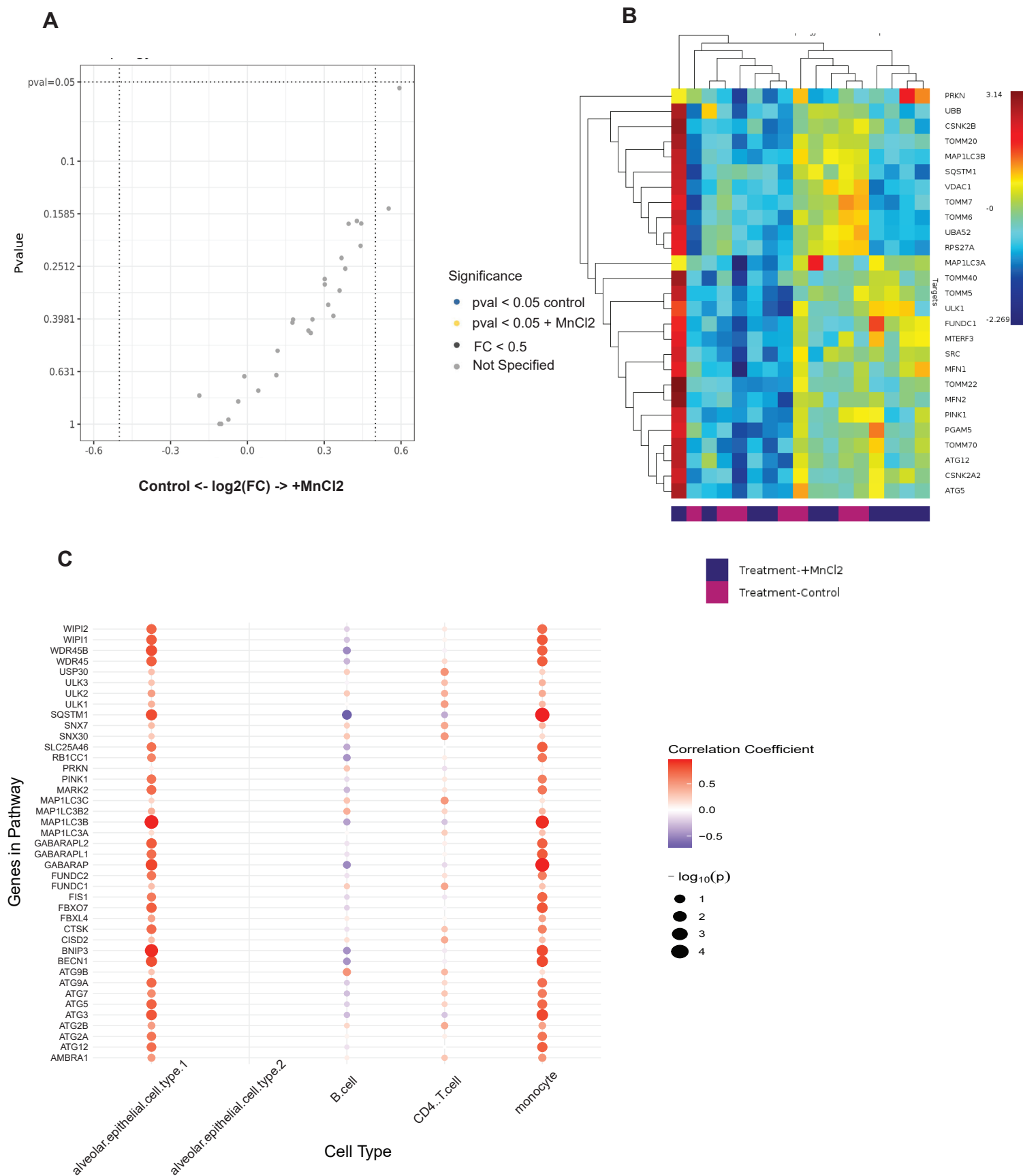
Supplemental Figure 5. Gene expression changes in the complement pathway in HM-exposed lung tissues following CdCl₂ exposure. **A.** Volcano plot displaying differential gene expression between CdCl₂-exposed and unexposed (control) lung tissues. **B,D.** Heatmap (**B**) and table (**D**) highlighting significantly altered genes with CdCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of complement pathway with scaled abundance of specific cell populations in the lung tissue following CdCl₂ exposure.

Supplemental Figure 6



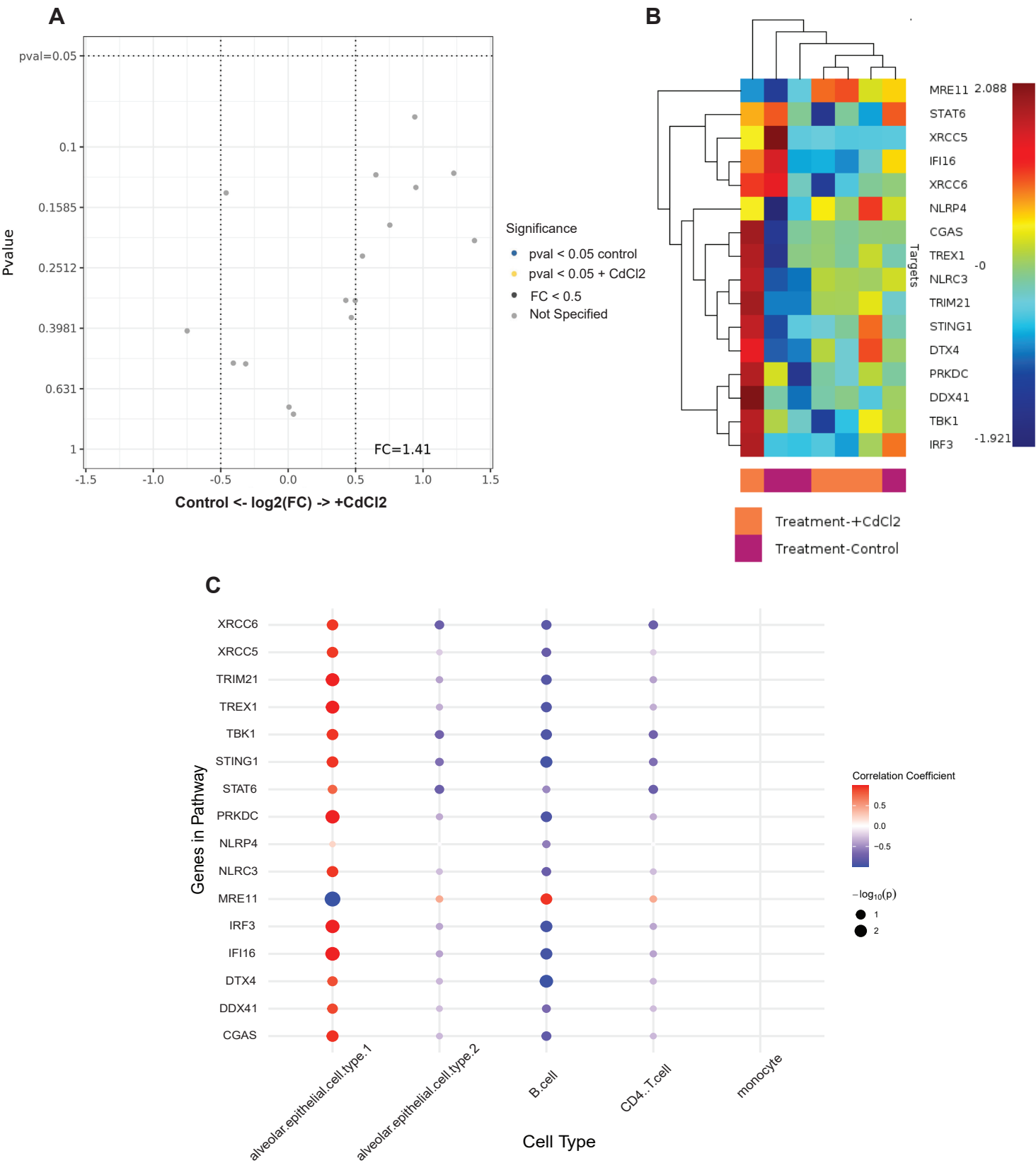
Supplemental Figure 6. Gene expression changes in the mitophagy pathway in HM-exposed lung tissues following CdCl₂ exposure. **A.** Volcano plot displaying differential gene expression between CdCl₂-exposed and unexposed (control) lung tissues. **B,D.** Heatmap (**B**) and table (**D**) highlighting significantly altered genes with CdCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of mitophagy pathway with scaled abundance of specific cell populations in the lung tissue following CdCl₂ exposure.

Supplemental Figure 7



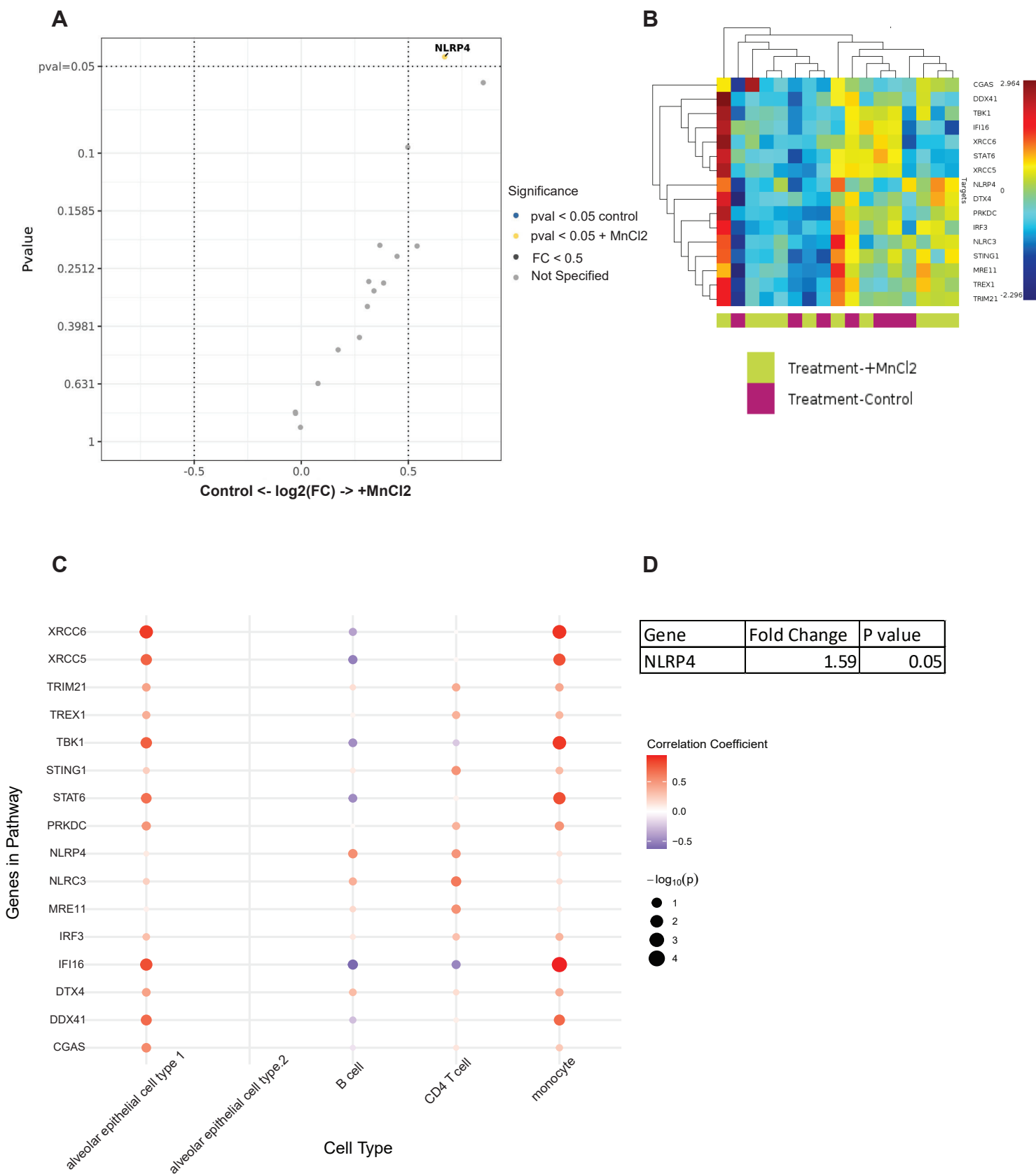
Supplemental Figure 7. Gene expression changes in the mitophagy pathway in HM-exposed lung tissues following MnCl₂ exposure. **A.** Volcano plot displaying differential gene expression between MnCl₂-exposed and unexposed (control) lung tissues. **B.** Heatmap highlighting significantly altered genes with MnCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of mitophagy pathway with scaled abundance of specific cell populations in the lung tissue following MnCl₂ exposure.

Supplemental Figure 8



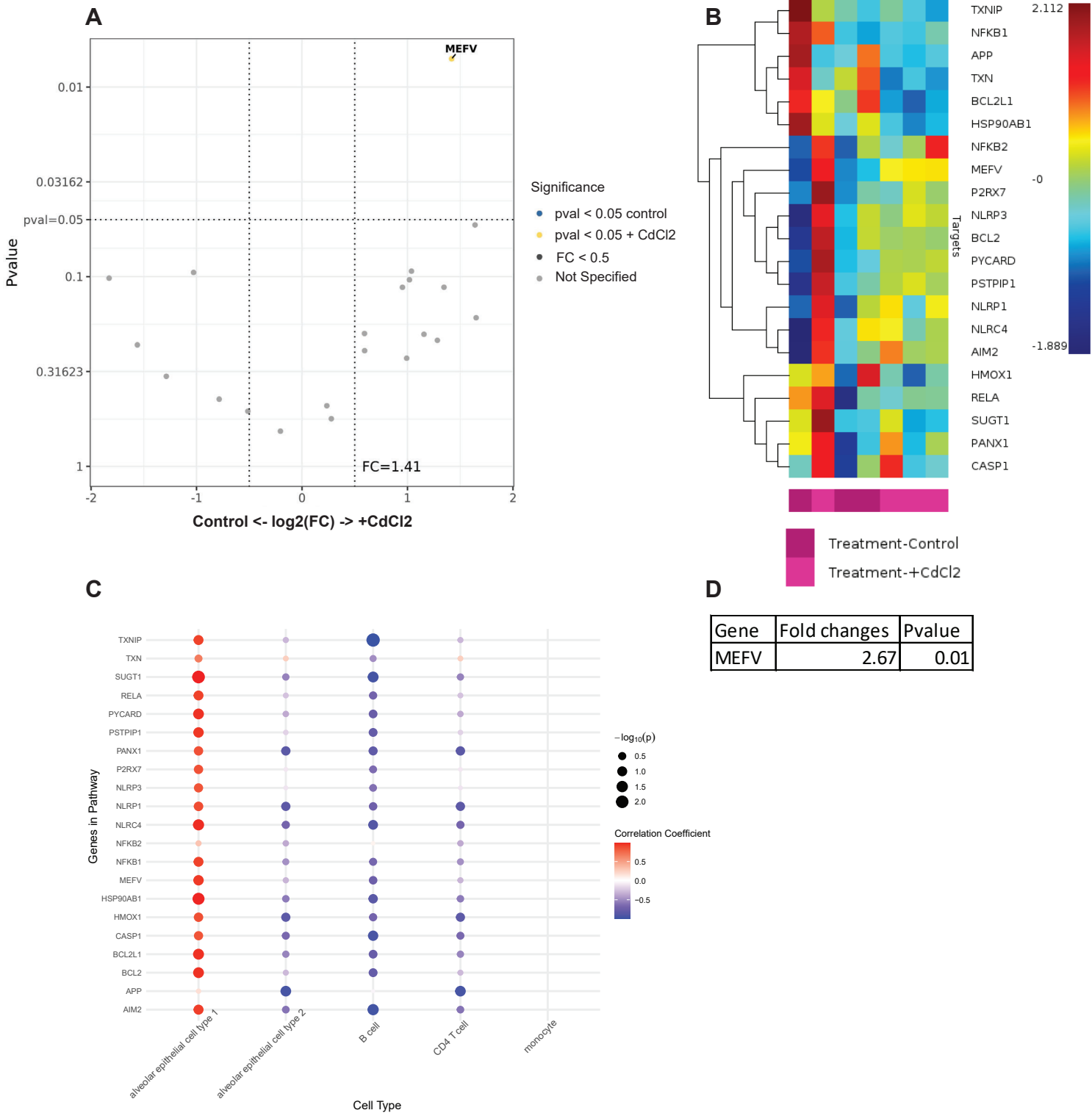
Supplemental Figure 8. Gene expression changes in the STING pathway in HM-exposed lung tissues following CdCl₂ exposure. **A.** Volcano plot displaying differential gene expression between CdCl₂-exposed and unexposed (control) lung tissues. **B.** Heatmap highlighting significantly altered genes with CdCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of STING pathway with scaled abundance of specific cell populations in the lung tissue following CdCl₂ exposure.

Supplemental Figure 9



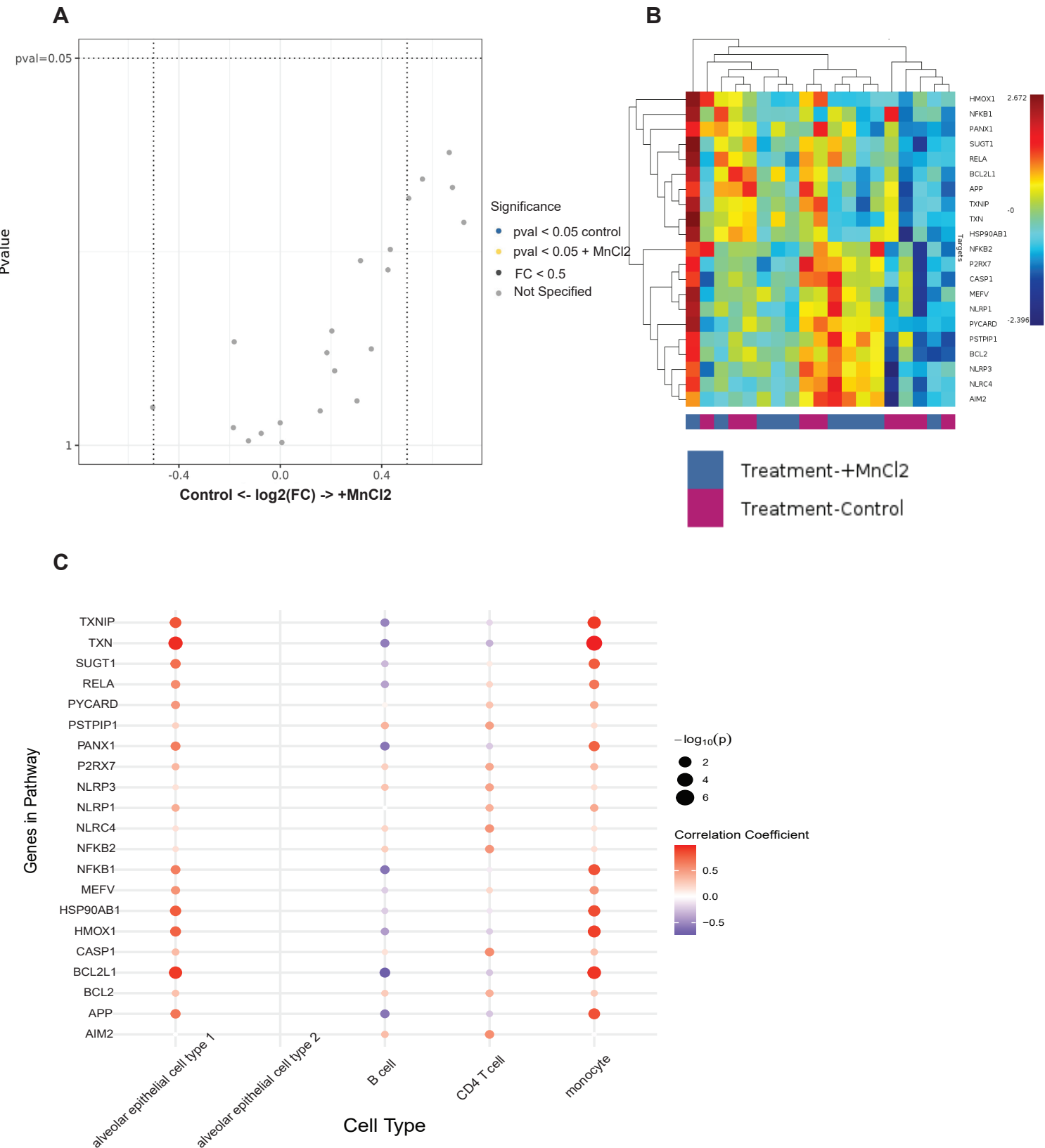
Supplemental Figure 9. Gene expression changes in the STING pathway in HM-exposed lung tissues following MnCl₂ exposure. **A.** Volcano plot displaying differential gene expression between MnCl₂-exposed and unexposed (control) lung tissues. **B,D.** Heatmap (**B**) and table (**D**) highlighting significantly altered genes with MnCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of STING pathway with scaled abundance of specific cell populations in the lung tissue following MnCl₂ exposure.

Supplemental Figure 10



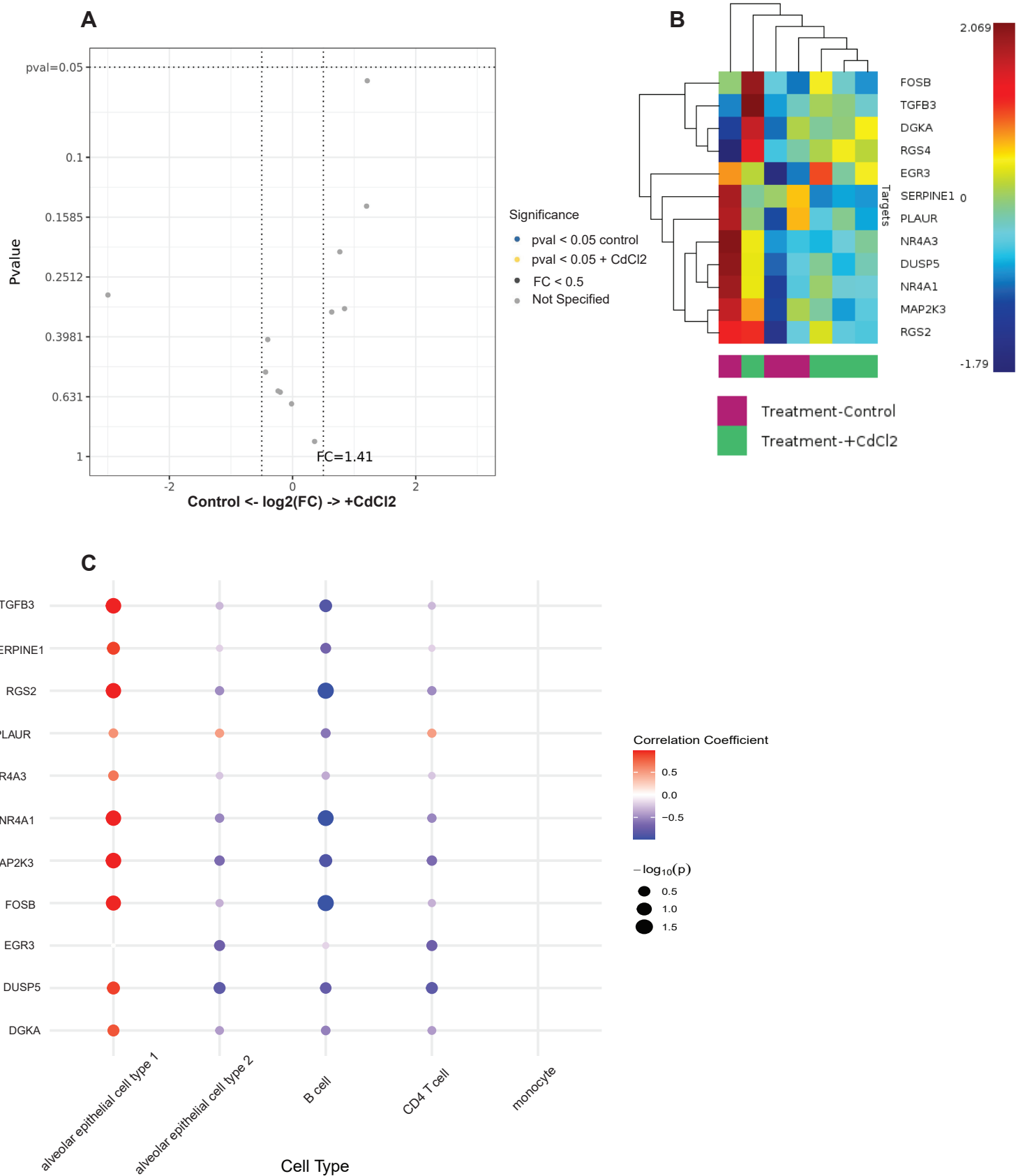
Supplemental Figure 10. Gene expression changes in the inflammasome pathway in HM-exposed lung tissues following CdCl₂ exposure. **A.** Volcano plot displaying differential gene expression between CdCl₂-exposed and unexposed (control) lung tissues. **B,D.** Heatmap (**B**) and table (**D**) highlighting significantly altered genes with CdCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of inflammasome pathway with scaled abundance of specific cell populations in the lung tissue following CdCl₂ exposure.

Supplemental Figure 11



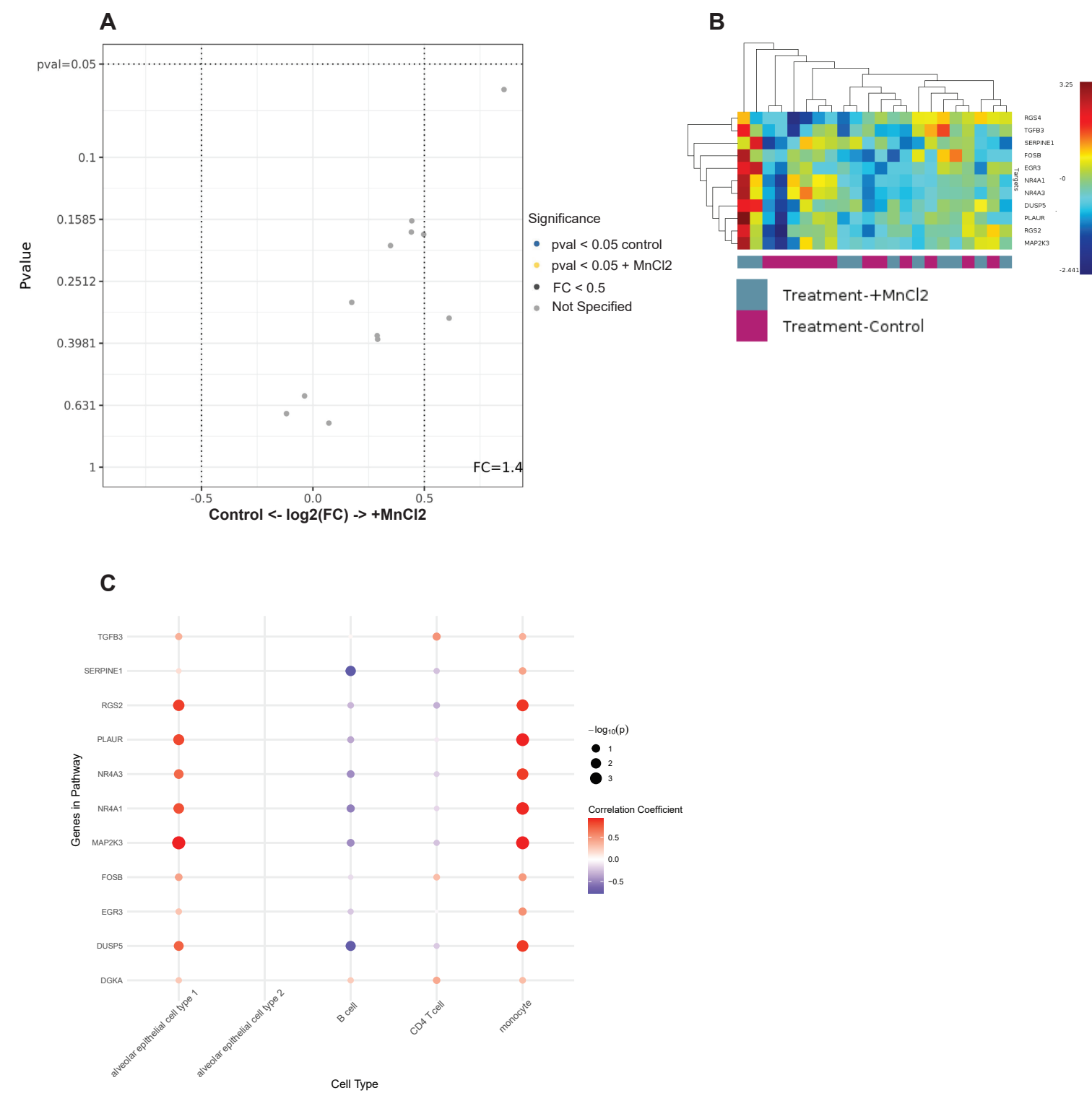
Supplemental Figure 11. Gene expression changes in the inflammasome pathway in HM-exposed lung tissues following MnCl₂ exposure. **A.** Volcano plot displaying differential gene expression between MnCl₂-exposed and unexposed (control) lung tissues. **B.** Heatmap highlighting significantly altered genes with MnCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of inflammasome pathway with scaled abundance of specific cell populations in the lung tissue following MnCl₂ exposure.

Supplemental Figure 12



Supplemental Figure 12. Gene expression changes in the airway remodeling pathway in HM-exposed lung tissues following CdCl₂ exposure. **A.** Volcano plot displaying differential gene expression between CdCl₂-exposed and unexposed (control) lung tissues. **B.** Heatmap highlighting significantly altered genes with CdCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of airway remodeling pathway with scaled abundance of specific cell populations in the lung tissue following CdCl₂ exposure.

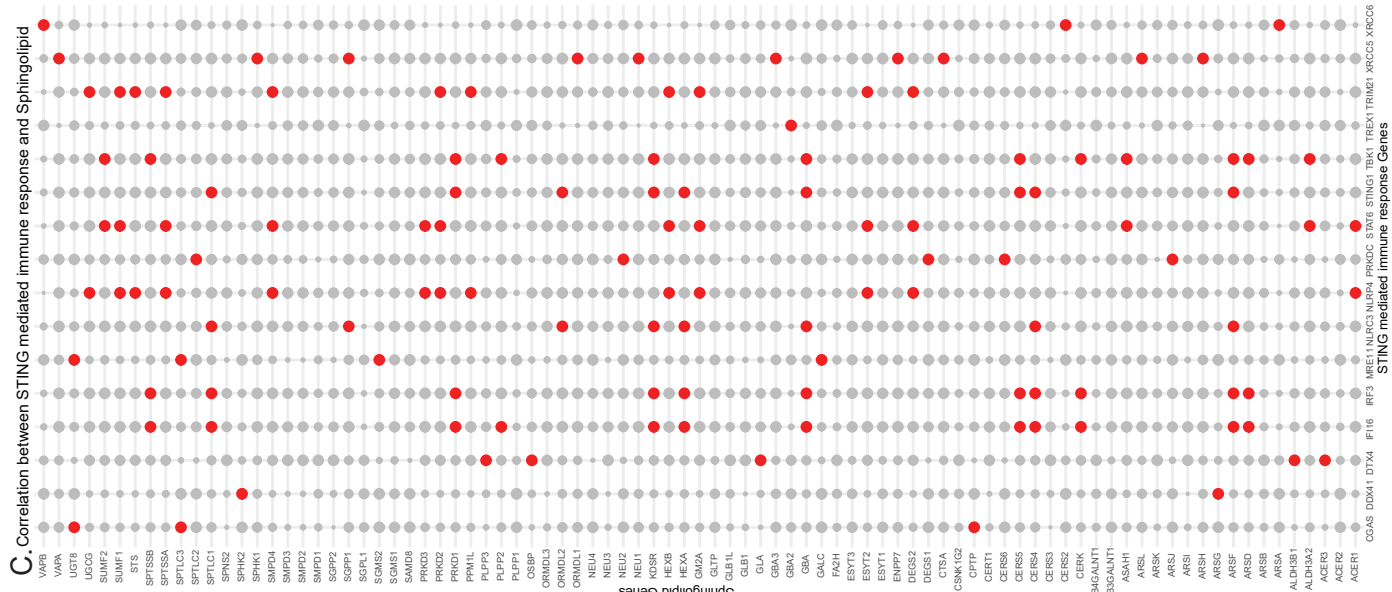
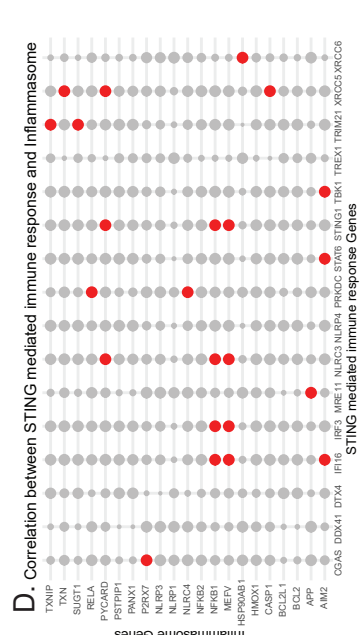
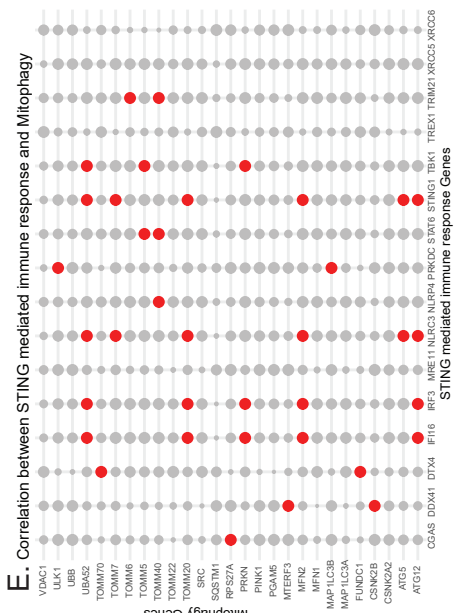
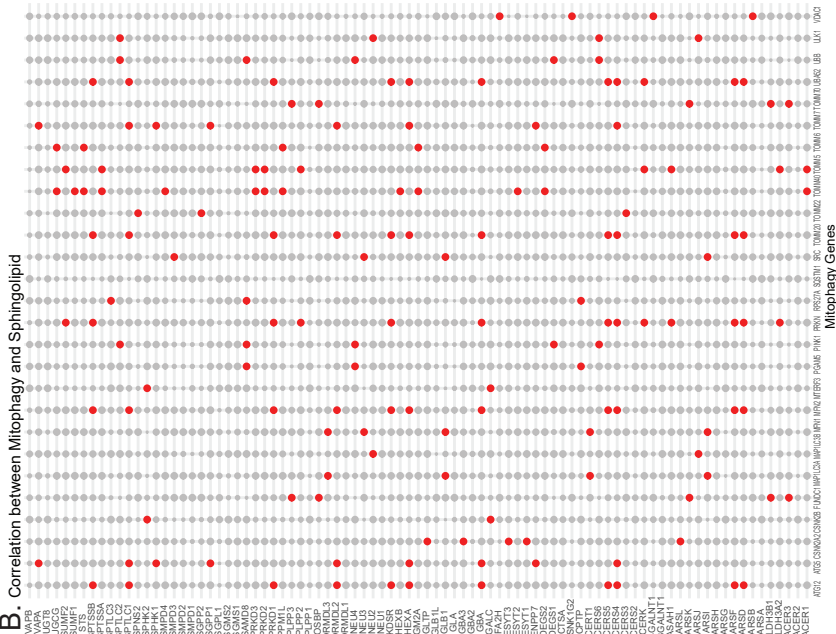
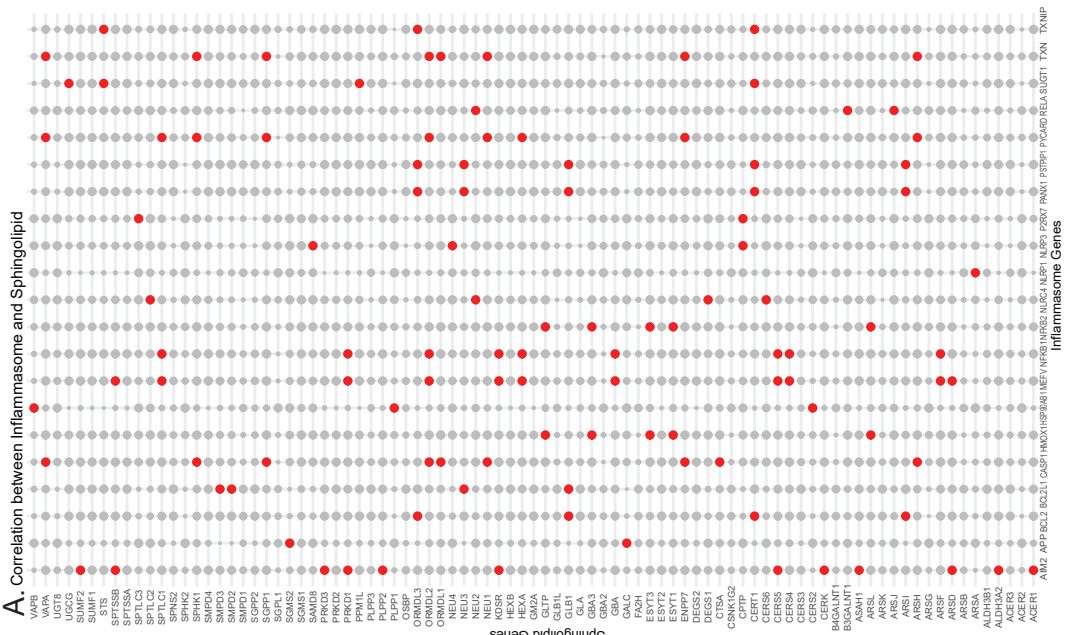
Supplemental Figure 13



Supplemental Figure 13. Gene expression changes in the airway remodeling pathway in HM-exposed lung tissues following MnCl₂ exposure. **A.** Volcano plot displaying differential gene expression between MnCl₂-exposed and unexposed (control) lung tissues. **B.** Heatmap highlighting significantly altered genes with MnCl₂ exposure. **C.** Cell deconvolution analysis correlating gene expression of airway remodeling pathway with scaled abundance of specific cell populations in the lung tissue following MnCl₂ exposure

Supplemental Figure 14

Supplemental Figure 14. Correlation of gene expression between complement and sphingolipid pathways following NaAsO₂ exposure. Dot plot correlating expression of sphingolipid metabolism genes (y-axis) with expression of complement genes (x-axis) following NaAsO₂ exposure.

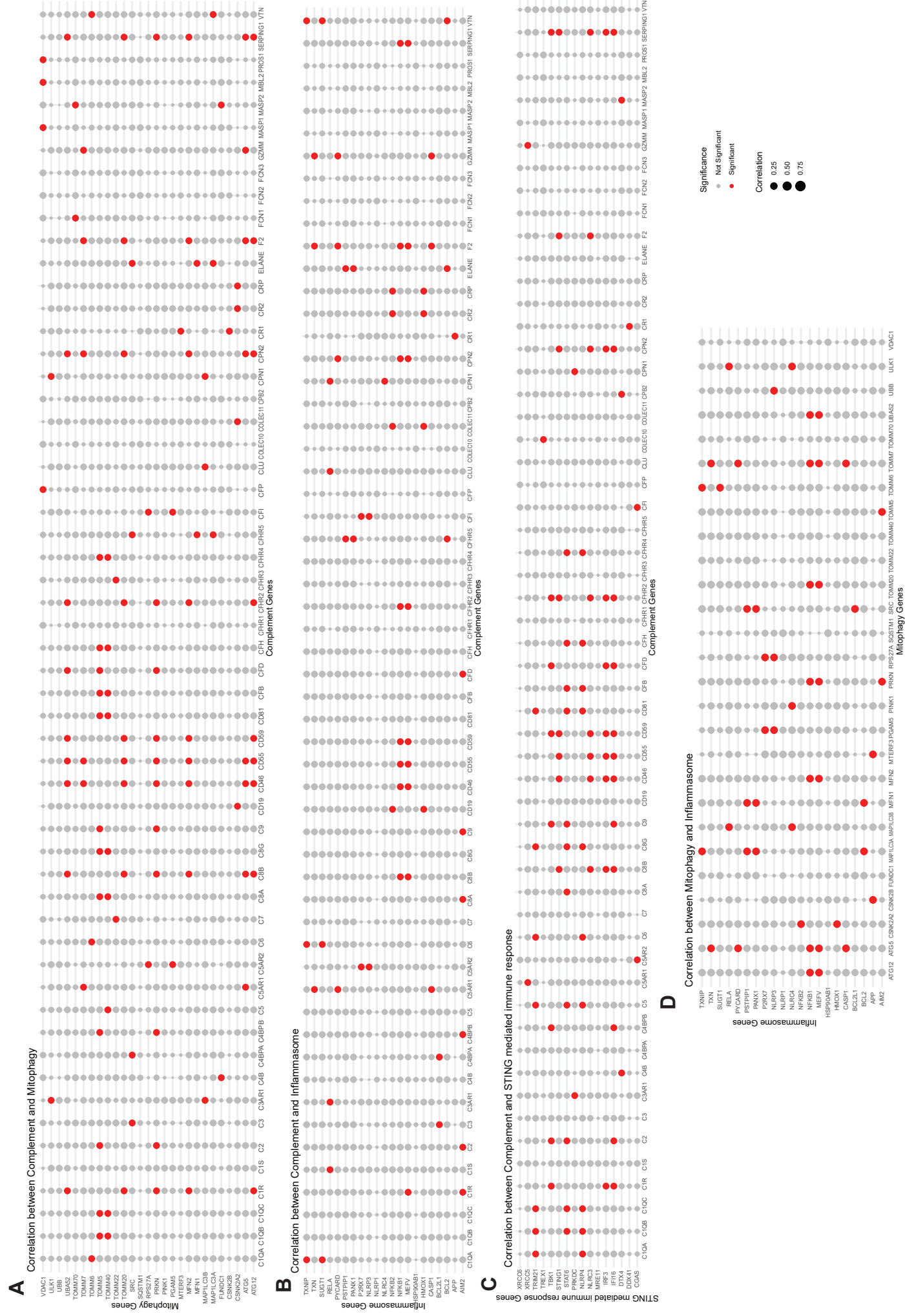


STING mediated immune response Genes

Supplemental Figure 15. Correlation of gene expression between sphingolipid, inflammasome, STING, and mitophagy pathways following NaAsO₂ exposure

A. Dot plot correlating expression of sphingolipid genes (y-axis) with expression of inflammasome genes (x-axis) following NaAsO₂ exposure. **B.** Dot plot correlating expression of sphingolipid genes (y-axis) with expression of mitophagy genes (x-axis) following NaAsO₂ exposure. **C.** Dot plot correlating expression of sphingolipid genes (y-axis) with expression of STING genes (x-axis) following NaAsO₂ exposure. **D.** Dot plot correlating expression of inflammasome genes (y-axis) with expression of STING genes (x-axis) following NaAsO₂ exposure. **E.** Dot plot correlating expression of mitophagy genes (y-axis) with expression of STING genes (x-axis) following NaAsO₂ exposure.

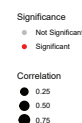
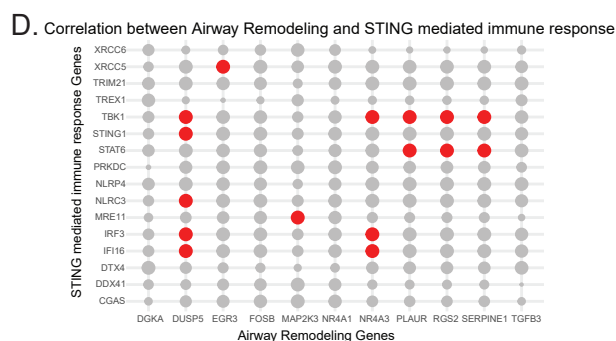
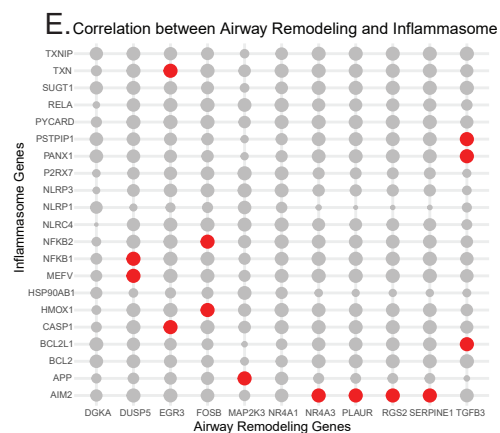
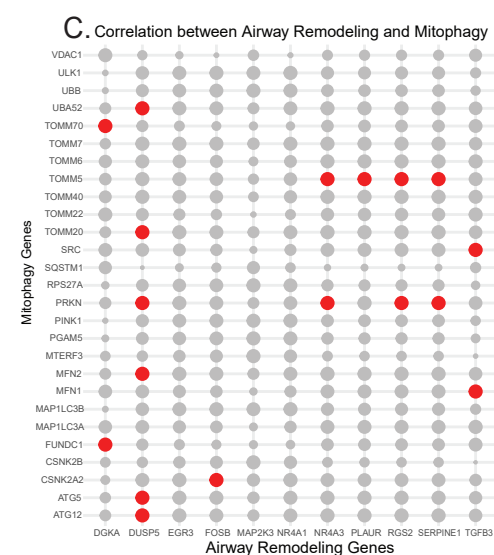
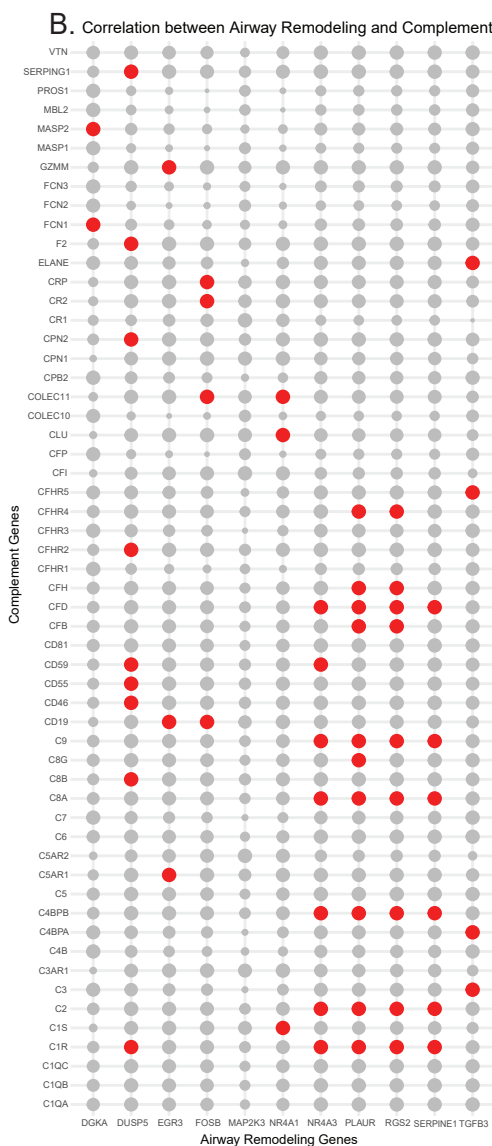
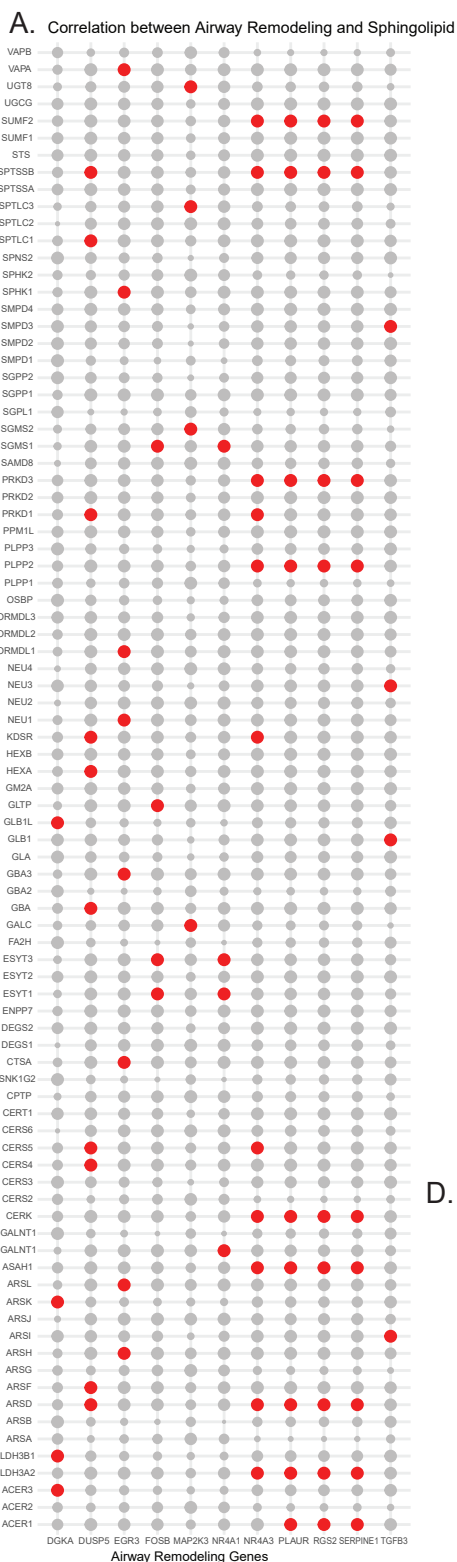
Supplemental Figure 16



Supplemental Figure 16. Correlation of gene expression between complement, mitophagy, inflammasome, and STING pathways following NaAsO₂ exposure

A. Dot plot correlating expression of mitophagy genes (y-axis) with expression of complement genes (x-axis) following NaAsO₂ exposure. **B.** Dot plot correlating expression of inflammasome genes (y-axis) with expression of complement genes (x-axis) following NaAsO₂ exposure. **C.** Dot plot correlating expression of STING genes (y-axis) with expression of complement genes (x-axis) following NaAsO₂ exposure. **D.** Dot plot correlating expression of inflammasome genes (y-axis) with expression of mitophagy genes (x-axis) following NaAsO₂ exposure.

Supplemental Figure 17



Supplemental Figure 17. Correlation of gene expression between airway remodeling pathway and sphingolipid, complement, mitophagy, STING, or inflammasome pathways following NaAsO₂ exposure

A. Dot plot correlating expression of sphingolipid genes (y-axis) with expression of airway remodeling genes (x-axis) following NaAsO₂ exposure. **B.** Dot plot correlating expression of complement genes (y-axis) with expression of airway remodeling genes (x-axis) following NaAsO₂ exposure. **C.** Dot plot correlating expression of mitophagy genes (y-axis) with expression of airway remodeling genes (x-axis) following NaAsO₂ exposure. **D.** Dot plot correlating expression of STING genes (y-axis) with expression of airway remodeling genes (x-axis) following NaAsO₂ exposure. **E.** Dot plot correlating expression of inflammasome genes (y-axis) with expression of airway remodeling genes (x-axis) following NaAsO₂ exposure.