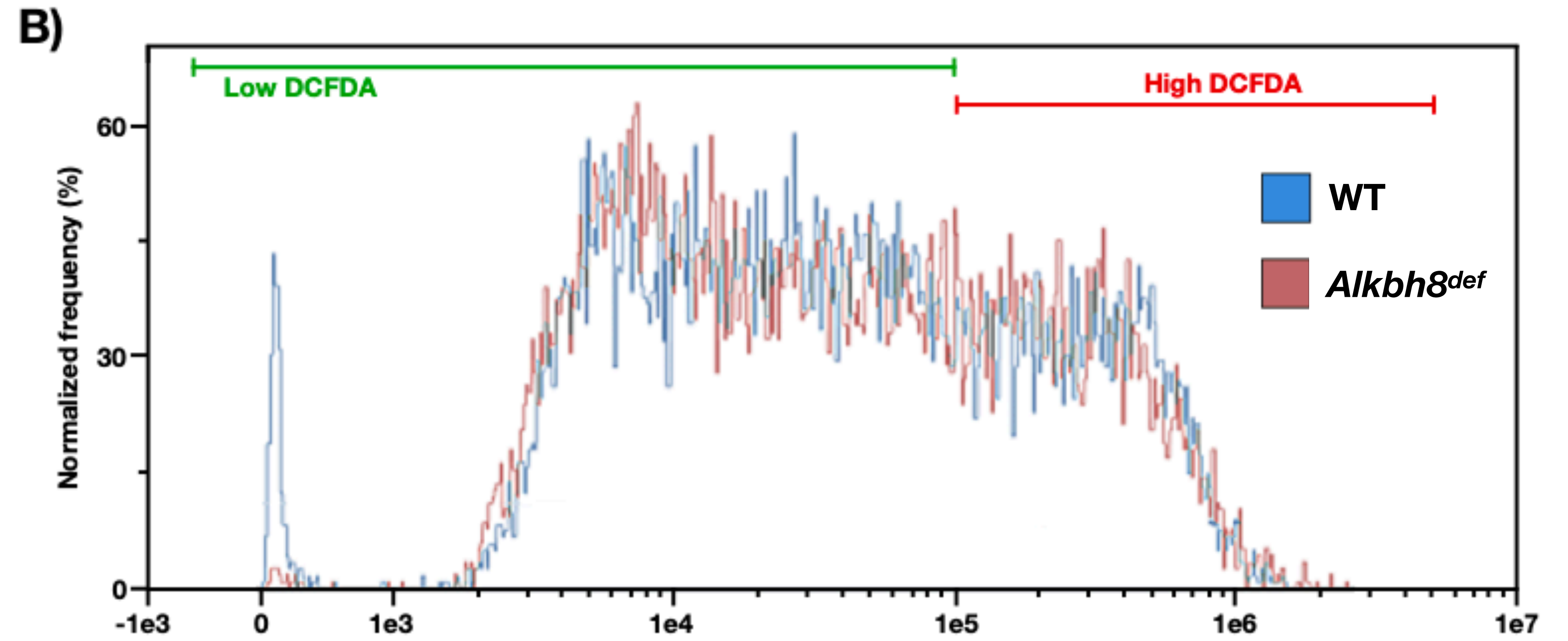
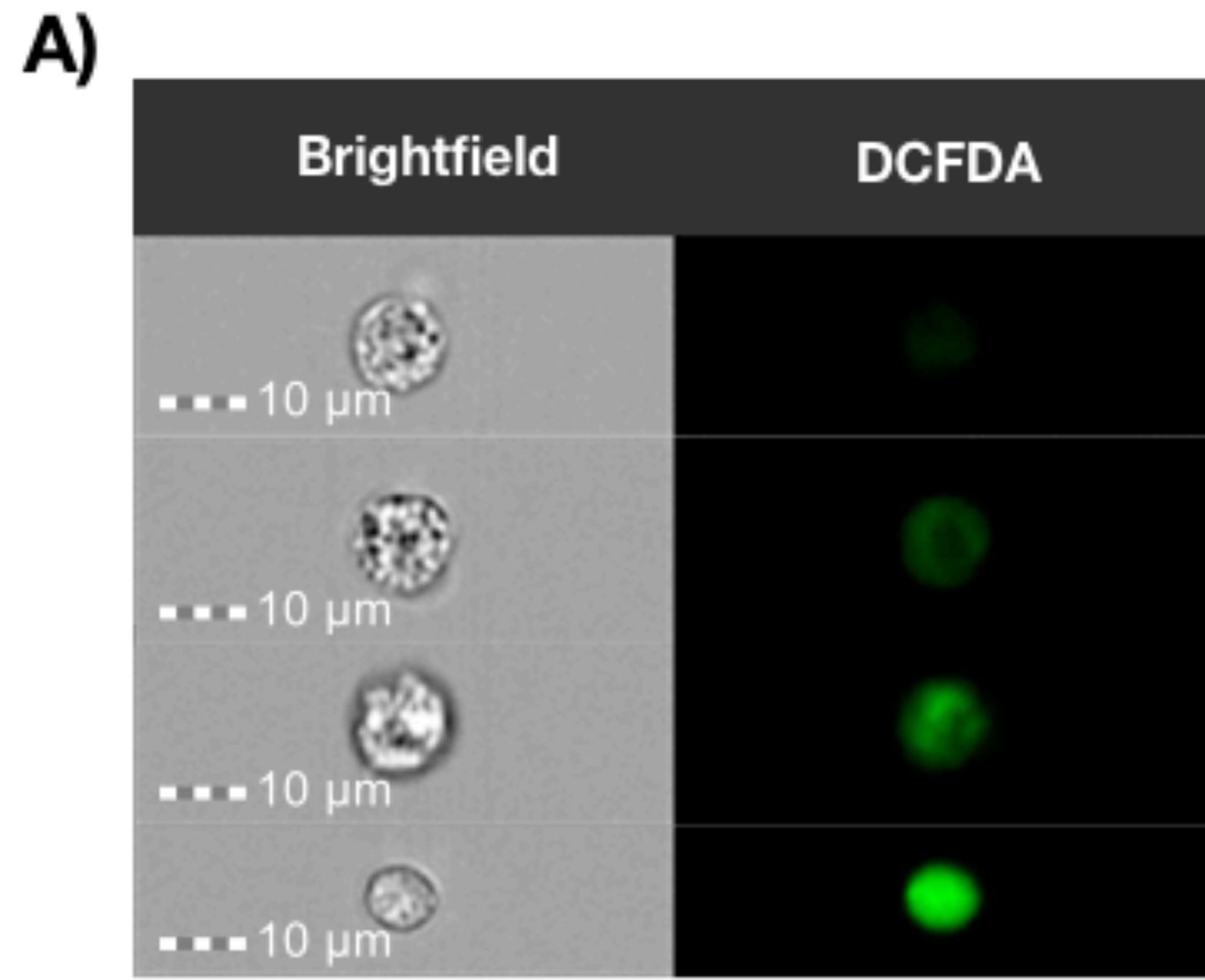
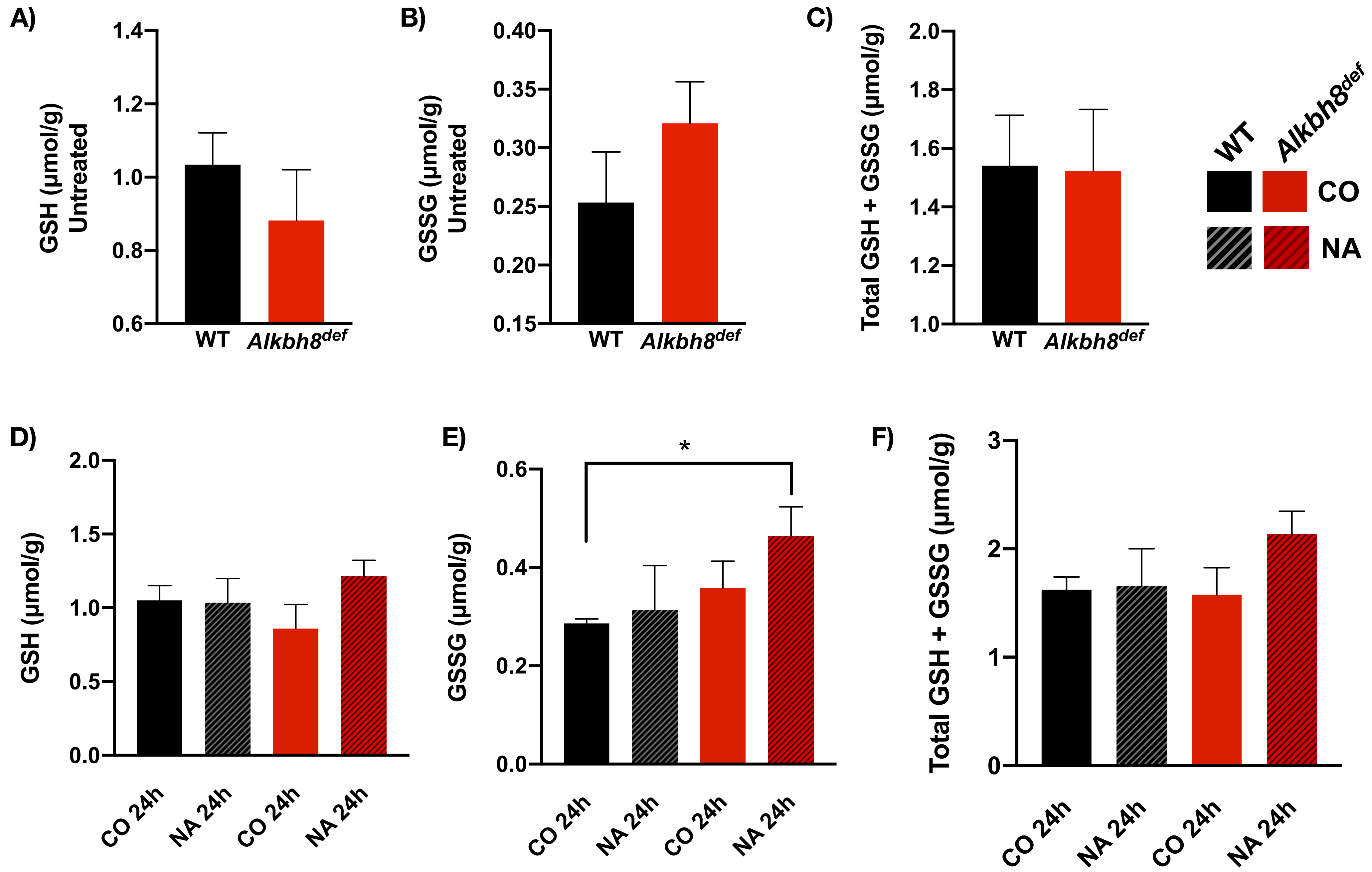


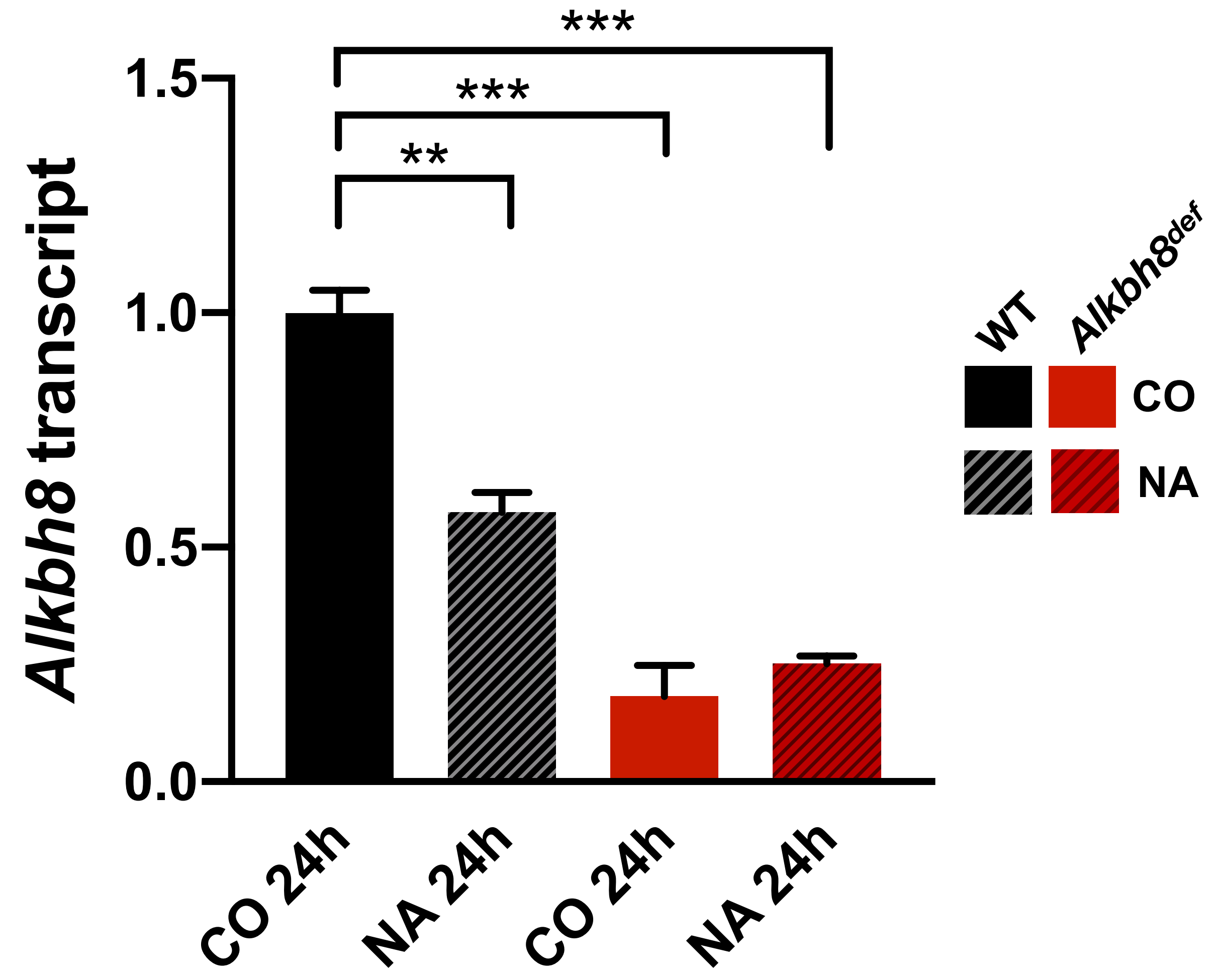
Supplemental Figure 2.



Supplemental Figure 3.



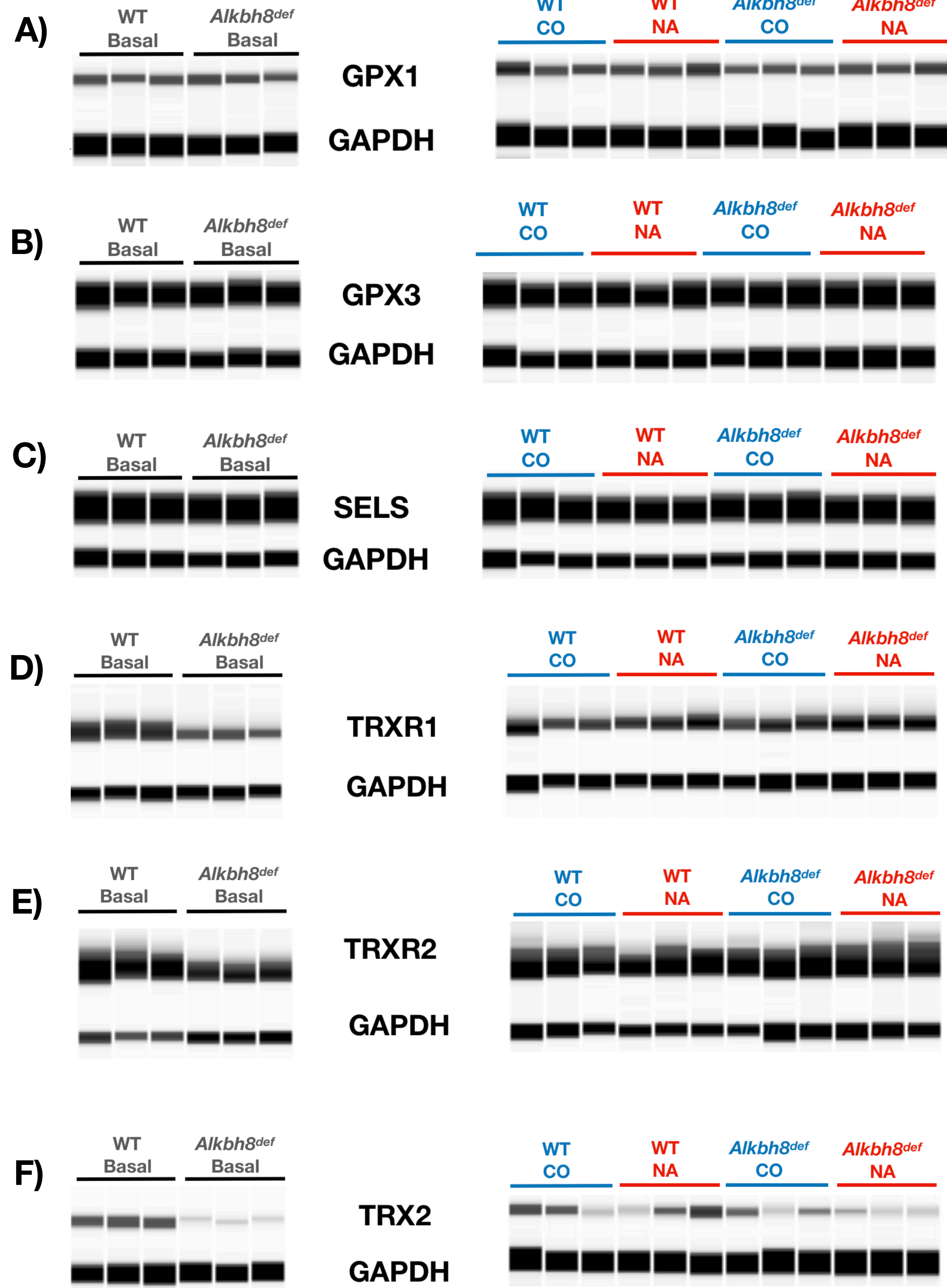
Supplemental Figure 4.



Supplemental Figure 5.

Untreated

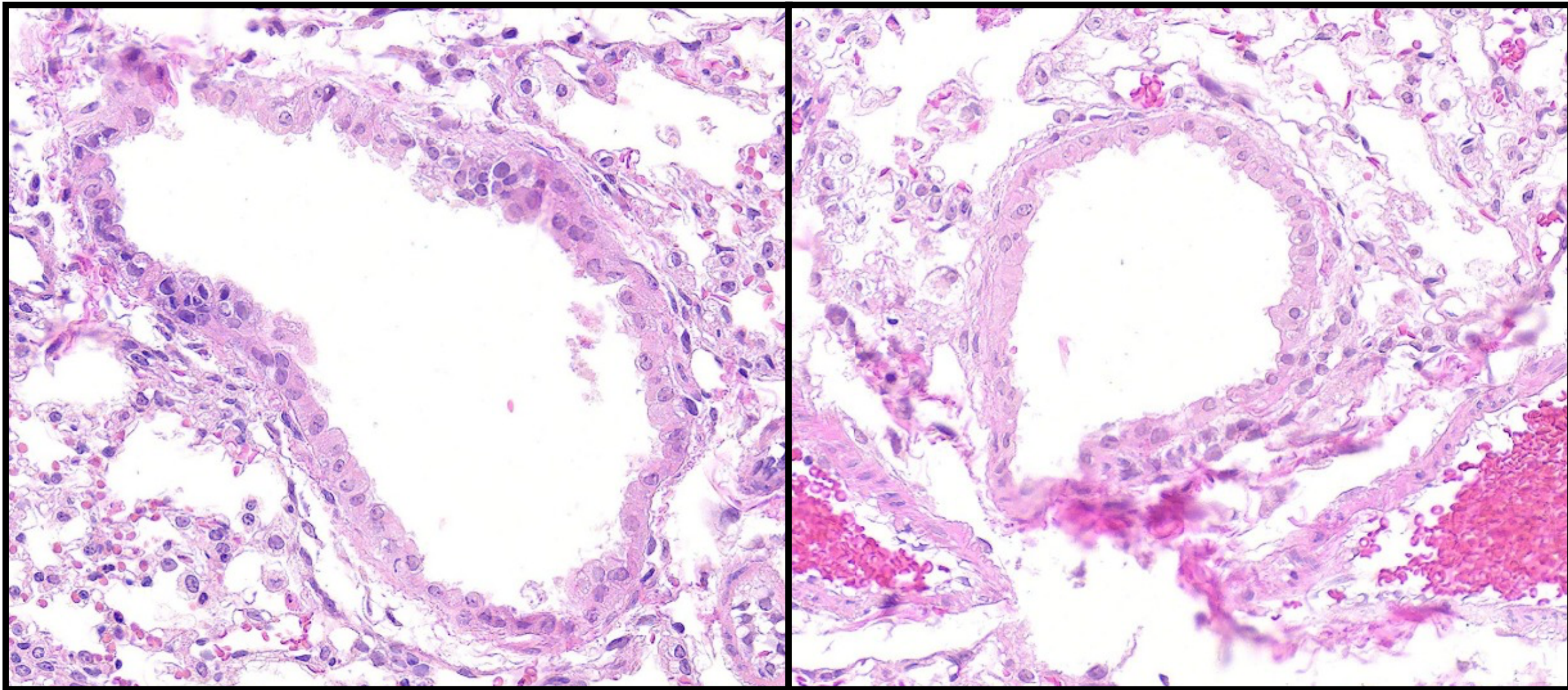
NA/CO Challenged



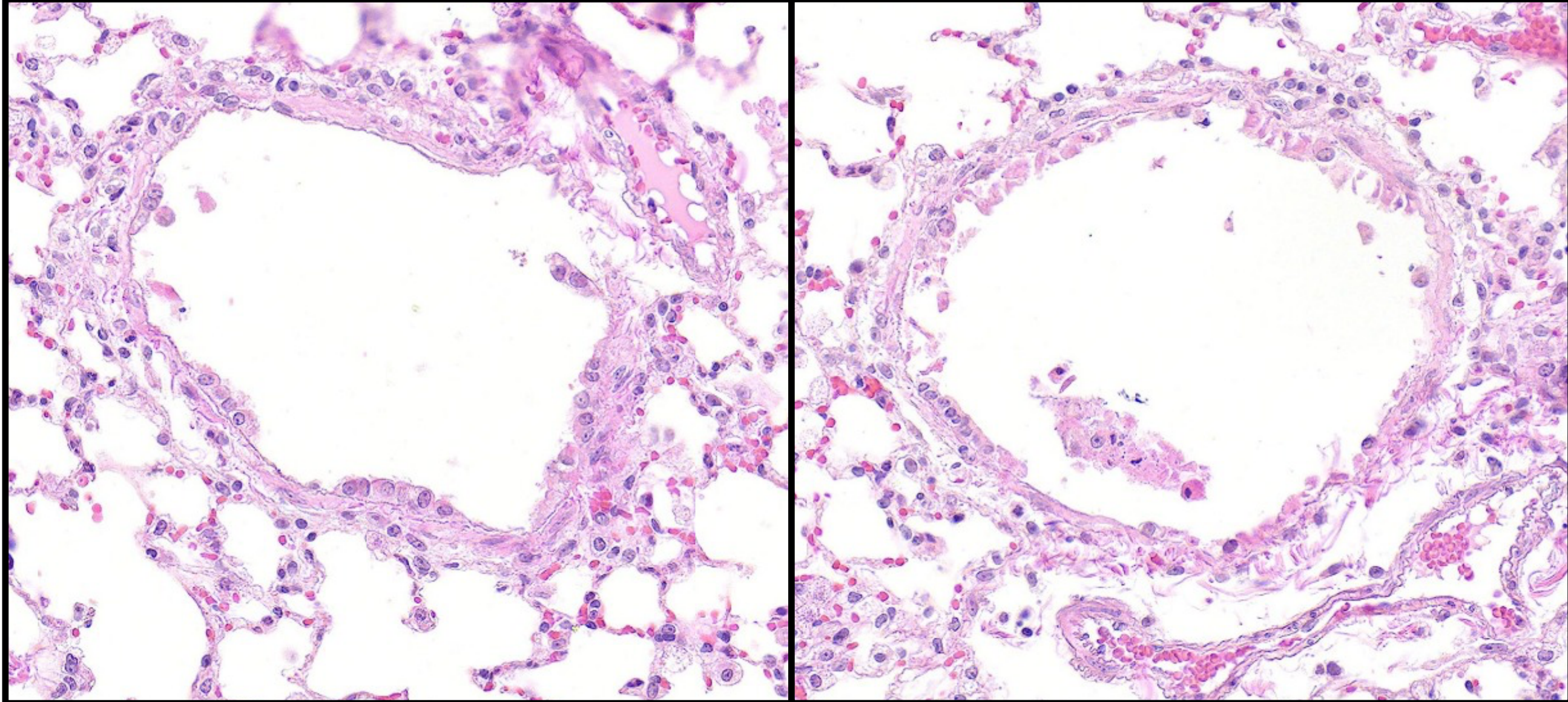
Supplemental Figure 6.

NA 200mg/kg, 3 days

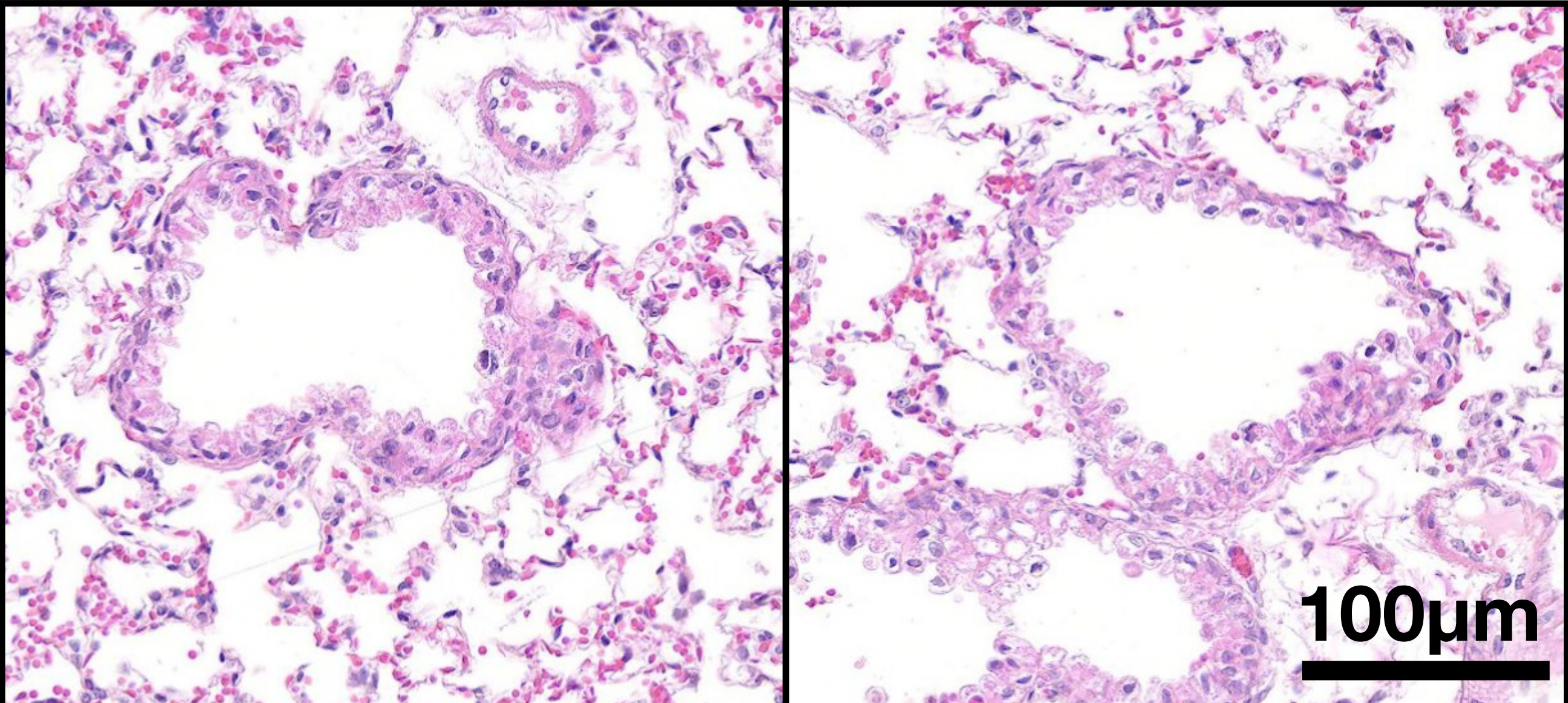
WT



Alkbh8^{def}



Cyp2abfgs-null



Supplemental Table 1: Targeted RNAseq Gene Panel

Genes on panel:	Ensembl ID:
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<i>Aimp1</i>	ENSMUSG00000028029
<i>Alb</i>	ENSMUSG00000029368
<i>Als2</i>	ENSMUSG00000026024
<i>Aox1</i>	ENSMUSG00000063558
<i>Apc</i>	ENSMUSG00000005871
<i>Apex1</i>	ENSMUSG00000035960
<i>ApoE</i>	ENSMUSG00000002985
<i>Atf4</i>	ENSMUSG00000042406
<i>Atf6</i>	ENSMUSG00000026663
<i>Atf6b</i>	ENSMUSG00000015461
<i>Atm</i>	ENSMUSG00000034218
<i>Atr</i>	ENSMUSG00000032409
<i>Atrx</i>	ENSMUSG00000031229
<i>Atxn3</i>	ENSMUSG00000021189
<i>Bax</i>	ENSMUSG00000003873
<i>Blm</i>	ENSMUSG00000030528
<i>Bmp2</i>	ENSMUSG00000027358
<i>Brca1</i>	ENSMUSG00000017146
<i>Brca2</i>	ENSMUSG00000041147
<i>Brip1</i>	ENSMUSG00000034329
<i>Calr</i>	ENSMUSG00000003814
<i>Canx</i>	ENSMUSG00000020368
<i>Casp1</i>	ENSMUSG00000025888
<i>Cat</i>	ENSMUSG00000027187
<i>Ccl1</i>	ENSMUSG00000020702
<i>Ccl11</i>	ENSMUSG00000020676
<i>Ccl12</i>	ENSMUSG00000035352
<i>Ccl17</i>	ENSMUSG00000031780
<i>Ccl19</i>	ENSMUSG00000071005
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<i>Ccl22</i>	ENSMUSG00000031779
<i>Ccl24</i>	ENSMUSG00000004814
<i>Ccl3</i>	ENSMUSG00000000982
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<i>Ccl6</i>	ENSMUSG00000018927
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<i>Ccl8</i>	ENSMUSG00000009185
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<i>Ccr1</i>	ENSMUSG00000025804
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<i>Cyp2e1</i>	ENSMUSG00000025479
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<i>Vegfa</i>	ENSMUSG00000023951
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<i>Xbp1</i>	ENSMUSG00000020484
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Supplemental Tables and Figure Legends

Supplemental Table 1. Complete gene panel for targeted RNA sequencing

Gene names are shown on the left and Ensembl ID on the right.

Supplemental Figure 1. Expression of 350 stress response transcripts obtained via targeted RNA sequencing.

Heat map showing differences in quantitated gene expression of 350 stress response genes. **A)** Basal *Alkbh8^{def}* lung transcripts relative to WT **B)** Corn Oil and 24 hour, 200mg/kg NA-treated WT and *Alkbh8^{def}* lungs. N = 2 mice per condition.

Supplemental Figure 2. Amnis Imagestream experimental data showing DCFDA results and γ H2AX examples.

Intracellular ROS was measured in mouse lungs by DCFDA staining. Untreated 8-12 week old WT and *Alkbh8^{def}* mice were sacrificed, lungs removed and enzymatically and mechanically dissociated into a single-cell suspension as described in methods. The live cells were then incubated with DCFDA dye and imaged with an Amnis Imagestream ISX100 flow cytometer. **A)** Representative images showing range of DCFDA fluorescence in the mixed population of lung cells. **B)** The frequency of WT (blue) and *Alkbh8^{def}* (red) cells exhibiting specific DCFDA intensities is plotted for a population of 12,160 and 11,726, respectively. An arbitrary cutoff of 1×10^5 RFU was used to separate low and high DCFDA intensity. 30.6% of WT cells fall into the high DCFDA category,

compared to 30.9% of *Alkbh8*^{def} ($P = 0.946$). γ H2AX staining was performed using the Amnis Imagestream ISX100 flow cytometer. **C)** shows representative images of a low spot count ≤ 1 and **D)** high spot count ≥ 2 .

Supplemental Figure 3. *Alkbh8*^{def} mice have less GSH and more GSSG under basal conditions, and more GSSG under NA-challenged conditions.

LC-MS/MS was employed to measure GSH and GSSG in WT and *Alkbh8*^{def} mice. **A)** GSH in untreated lungs **B)** GSSG in untreated lungs **C)** Total GSH + GSSG in untreated lungs **D)** GSH in CO and NA-challenged lungs and **E)** GSSG in CO and NA-challenged lungs **F)** Total GSH + GSSG in NA-challenged lungs. (N = 3 mice per condition, * $P \leq 0.05$).

Supplemental Figure 4. *Alkbh8*^{def} mice have less *Alkbh8* transcript after CO and NA challenge.

Quantitative RT-PCR (qRT-PCR) was used to measure *Alkbh8* transcript in 24h CO and 24h, 200 mg/kg NA-treated mouse lungs as described in the methods. (N = 3 lungs per condition, ** $P \leq 0.01$, *** $P \leq 0.001$).

Supplemental Figure 5. Wes blots for selenoproteins GPX1, GPX3, SELS, TRXR1 and TRXR2 and non-selenoprotein TRX2.

Wes capillaries showing full protein expression results for **A)** GPX1 **B)** GPX3, **C)** SELS **D)** TRXR1, **E)** TRXR2, and **F)** TRX2. Loading control (GAPDH) was multiplexed in each

capillary and is shown on the bottom in each data set. Each capillary blot represents one mouse.

Supplemental Figure 6. *Alkbh8*^{def} mice show increased lung injury after 3-day NA exposure.

Two examples from lungs of WT (top row), *Alkbh8*^{def} (middle row) and *Cyp2abfgs-null* (bottom row) mouse lungs after 3-day NA exposure, 200 mg/kg.