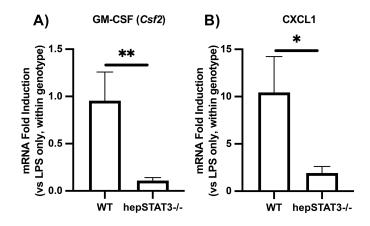
Supplemental Table I. Top upregulated Molecules	q-Value	Fold Change
Altered in WT BALF only		
SERPINA1	0.005	45.6
A2M	0.0002	24.15
H2AZ2	0.012	20.37
SAA2-SAA4	0.011	14.49
A1BG	0.045	14.16
GNA14	0.004	-15.35
COPS4	0.007	-14.19
WBP2	0.010	-9.33
RENBP	0.006	-7.43
CADM1	0.006	-7.19
Altered in hepSTAT3-/- BALF only		
FBP1	0.048	20.99
RHOG	0.029	3.45
Ighg	0.049	3.37
PLEK	0.040	2.94
TUBB	0.026	2.88
Bpifb9a/Bpifb9b	0.017	-24.60
COL6A1	0.003	-9.16
ALDOB	0.011	-4.74
AMDHD2	0.010	-3.25
Gm21596/Hmgb1	0.006	-3.14
Altered in both with WT values shown		
CAMP	0.0006	53.21
F13B	0.005	44.36
ITGAM	0.001	42.46
IL4I1	0.001	28.05
IL1R2	0.0007	27.23
OXCT1	0.005	-47.64
FMO2	0.005	-40.74
PON3	0.007	-38.90
RTKN2	0.004	-37.33
GM14743 (includes others)	0.012	-30.69
Altered in both with hepSTAT3-/- values		2516
IL4I1	0.005	35.16
CAMP	0.000056	33.04
ITGAM	0.002	23.07
Apoc3	0.004	19.05
IL1R2	0.001	18.20
GM14743 (includes others)	0.024	-33.42
ACOT7	0.001	-27.10
SCGB3A2	0.002	-25.12
FMO2	0.013	-21.98
Mup1 (includes others)	0.049	-19.63

Supplemental Table I. Top upregulated and downregulated pneumonia-induced molecules

WT and hepSTAT3^{-/-} mice were given 18h i.p. LPS with or without an additional 24h challenge with i.t. *E. coli*. Bronchoalveolar lavage fluid (BALF) was collected and analyzed via mass spectrometry. Significant protein changes occurring within each genotype between LPS only and LPS with 24h *E. coli* were compared to each other as shown in **Figure 7**. The top 5 upregulated and downregulated pneumonia-induced protein differences (FDR<0.05) are listed above as altered in WT only BALF, altered in hepSTAT3^{-/-} only, or altered in both genotypes with each genotype values shown separately. Molecules are ranked by fold change, and protein IDs are indicated as mapped in Ingenuity Pathway Analysis. (n=4/group from 2 independent experiments)



Supplemental Figure 1: During endotoxemia, pneumonia-induced cytokine induction is diminished in lungs of hepSTAT3^{-/-} mice compared to that observed in WT counterparts following an intratracheal challenge with *Staphylococcus aureus*. Lung mRNA induction was determined for (A) GM-CSF and (B) CXCL1 in specimens collected from mice treated for 18h with i.p. LPS and a subsequent i.t. instillation with *S. aureus* (10⁷ CFU) for 6h. Fold induction was calculated versus gene expression values detected in uninfected mice of the same genotype given 18h i.p. LPS alone. Data are represented as means with standard error of mean (SEM), and significance was determined using an unpaired t-test. (*p<0.05, **p<0.01) (n=4-6/group from one independent experiment)