

543 **Tables**

544 **Table S1. Cytokine analysis at 4 h, 2 d, and 7 d post-intranasal infection with G636.**

Cytokine ^{a,b}	WT			<i>tlr4</i> mutant		
	10 ⁵ G636	10 ⁸ G636	Mock	10 ⁵ G636	10 ⁸ G636	Mock
4 h						
IL-23	23.26 (10.14)	38.53 (6.36)	10.67 (7.09)	22.57 (13.26)	32.61 (3.61)	15.90 (15.90)
IL-1α	58.57 (18.27)	323.11 (75.42) ^{#,\$}	2.5 (0.43)	2.77 (0.47)	429.19 (90.22) ^{#,\$}	1.49 (0.13)
IFN-γ	0.77 (0.36)	5.13 (1.30) ^{#,\$}	0.00 (0.00)	0.23 (0.23)	4.34 (0.39) ^{#,\$}	0.00 (0.00)
TNF-α	2219.55 (214.72)	14888.73 (311.27) ^{#,\$}	108.38 (66.66)	49.51 (6.47)	12802.47 (3073.56) ^{#,\$}	12.82 (3.58)
MCP-1	0.00 (0.00)	65.73 (15.07) ^{#,\$}	0.00 (0.00)	0.00 (0.00)	65.57 (8.23) ^{#,\$}	0.00 (0.00)
IL-12p70	0.00 (0.00)	1.43 (1.43)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-1β	9.50 (1.95)	46.26 (10.54) ^{#,\$}	0.00 (0.00)	0.00 (0.00)	56.58 (12.58) ^{#,\$}	0.00 (0.00)
IL-10	0.00 (0.00)	4.18 (4.18)	0.00 (0.00)	0.00 (0.00)	2.04 (2.04)	0.00 (0.00)
IL-6	910.41 (172.71)	7885.57 (1645.56) ^{#,\$}	18.19 (5.67)	8.09 (2.69)	6334.72 (1218.67) ^{#,\$}	2.70 (2.70)
IL-27	0.00 (0.00)	85.90 (13.54) ^{#,\$}	0.00 (0.00)	0.00 (0.00)	42.77 (24.83) ^{\$}	0.00 (0.00)
IL-17A	1.05 (0.74)	8.36 (2.46) ^{#,\$}	0.00 (0.00)	0.00 (0.00)	4.66 (0.39) ^{#,\$}	0.00 (0.00)
IFN-β	0.00 (0.00)	29.75 (17.23) ^{*,#,\$}	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
GM-CSF	96.65 (13.37) ^{*,#}	55.42 (7.19) ^{#,\$}	0.00 (0.00)	0.00 (0.00)	47.41 (6.96) ^{#,\$}	0.00 (0.00)
2 d						
IL-23	19.93 (9.61)	27.05 (8.76)	44.09 (21.87)	26.04 (11.37)	11.35 (5.56)	72.50 (36.30)
IL-1α	1.14 (0.19)	157.28 (58.45) ^{*,#,\$}	1.13 (0.20)	2.00 (0.50)	25.68 (6.15)	19.64 (18.02)
IFN-γ	2.20 (0.98)	212.26 (54.96) ^{*,#,\$}	0.00 (0.00)	3.70 (2.48)	4.96 (2.48)	0.00 (0.00)
TNF-α	1.85 (0.82)	592.26 (154.11) ^{*,#,\$}	1.03 (0.60)	19.79 (6.79)	52.20 (8.86)	5.76 (4.31)
MCP-1	0.00 (0.00)	160.30 (14.27) ^{*,#,\$}	0.00 (0.00)	0.00 (0.00)	33.52 (6.37) ^{#,\$}	0.00 (0.00)
IL-12p70	0.00 (0.00)	46.17 (17.63) ^{*,#,\$}	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-1β	1.06 (1.06)	12.35 (2.80) ^{*,#,\$}	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-10	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-6	0.00 (0.00)	1179.63 (323.29) ^{*,#,\$}	0.00 (0.00)	0.00 (0.00)	20.45 (3.83)	4.29 (4.29)
IL-27	0.00 (0.00)	137.76 (81.43) ^{*,#,\$}	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-17A	0.42 (0.42)	25.31 (10.22) ^{*,#,\$}	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IFN-β	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
GM-CSF	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
7 d						
IL-23	41.43 (14.43)	30.14 (19.51)	20.66 (20.66)	9.07 (5.32)	29.77 (12.87)	12.69 (12.69)
IL-1α	1.05 (0.18)	41.50 (23.66)	1.62 (0.92)	5.54 (4.27)	4.60 (2.50)	1.79 (0.85)
IFN-γ	0.00 (0.00)	53.36 (40.45) ^{\$}	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
TNF-α	0.00 (0.00)	93.32 (36.14) ^{*,#,\$}	0.00 (0.00)	3.17 (3.17)	2.41 (1.54)	0.00 (0.00)
MCP-1	0.00 (0.00)	14.83 (14.83)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-12p70	0.00 (0.00)	1.54 (1.54)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-1β	0.00 (0.00)	1.43 (1.43)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-10	0.00 (0.00)	6.84 (6.84)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-6	0.00 (0.00)	232.41 (182.45)	0.00 (0.00)	5.19 (5.19)	16.72 (16.72)	0.00 (0.00)
IL-27	0.00 (0.00)	26.87 (26.87)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IL-17A	0.00 (0.00)	13.67 (11.48)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
IFN-β	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
GM-CSF	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)

545 ^aMean pg/ml (SEM) from two independent experiments at each timepoint is displayed.

546 ^b**P* < 0.05 relative to *tlr4* mutant at same inoculum; #*P* < 0.05 relative to mock in same mouse
547 strain. \$*P* < 0.05 relative to 10⁵ inoculum in same mouse strain. Two-way ANOVA, Tukey's test
548 for multiple comparisons. Significant differences are also highlighted in green.

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550 **Table S2. MICs for *A. baumannii* strains G636 and G654.**

Antibiotic	G636 (Resistant/Sensitive)	G654 (Resistant/Sensitive)	Clinical Breakpoint^a
Imipenem	>256 µg/ml (Resistant)	>256 µg/ml (Resistant)	2 µg/ml
Ampicillin	>256 µg/ml (N/A)	>256 µg/ml (N/A)	N/A ^c
Ciprofloxacin	>256 µg/ml (Resistant)	>256 µg/ml (Resistant)	1 µg/ml
Levofloxacin	32 µg/ml (Resistant)	128 µg/ml (Resistant)	2 µg/ml
Colistin	1 µg/ml (Intermediate) ^b	8 µg/ml (Resistant)	2 µg/ml ^b
Polymyxin B	2 µg/ml (Intermediate) ^b	4 µg/ml (Resistant)	2 µg/ml ^b
Tigecycline	2 µg/ml (N/A) ^c	1 µg/ml (N/A) ^c	N/A ^c
Gentamicin	>256 µg/ml (Resistant)	2-4 µg/ml (Sensitive)	4 µg/ml
Apramycin	16 µg/ml (N/A) ^c	16 µg/ml (N/A) ^c	N/A ^c

551 ^aClinical breakpoints are according to the Clinical and Laboratory Standard Institute (CLSI) M100
552 Performance Standards for Antimicrobial Susceptibility Testing 30th Edition (122).

553 ^b A “sensitive” breakpoint is not available for colistin or polymyxin B from the CLSI. Strains with
554 MICs of less than or equal to 2 µg/ml are considered to have “intermediate resistance.”

555 ^cThe clinical breakpoint has not been defined for ampicillin, tigecycline, and apramycin by the
556 CLSI.

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558 **Table S3. Plasmids and strains used in this study.**

Plasmid or Strain	Description ^a	Source ^b
Plasmids		
pEX18Tc	Precursor plasmid used for generation of pEX18Ap; Tet ^r	(114)
pKD4-Apr	Source for apramycin cassette for mutant generation; Apr ^r	(115)
pEX18Ap	Plasmid background used for generation of <i>A. baumannii</i> mutants; Apr ^r	This study
pEX18Ap::G636 <i>invLKO</i>	Plasmid used for mutation of <i>invL</i> in G636; Apr ^r	This study
pUC18T-miniTn7T-Apr	Vector used for genetic complementation at the mTn7 site; Apr ^r	(116)
pUC18T-miniTn7T-Apr::G636 <i>invLKO</i> comp	Plasmid used for complementation of the Δ <i>invL</i> mutant; Apr ^r	This study
PB-FLuc+GFPd2	Plasmid source for <i>gfp</i> cassette; Amp ^r	^b
pUC18T-miniTn7T-Apr::gfpd2	Expression vector; Apr ^r	This study
pRK2013	Helper plasmid for mobilization of non-self-transmissible plasmids; Kan ^r	(123)
pTNS2	T7 transposase expression vector; Amp ^r	(124)
Strains		
<i>E. coli</i>		
Stellar	<i>mrr-hsdRMS-mcrBC</i> and <i>mcrA</i> ; Host strain for cloning	TaKaRa
HB101	F- <i>mcrB mrr hsdS20</i> (rB- mB-) <i>recA13 leuB6 ara-14 proA2 lacY1 galK2 xyl-5 mtl-1 rpsL20 glnV44</i> λ -; Host strain for pRK2013	Promega
EC100D	F - <i>mcrA</i> Δ (<i>mrr-hsdRMS-mcrBC</i>) ϕ 80 <i>dlacZ</i> Δ M15 Δ <i>lacX74 recA1 endA1 araD139</i> Δ (<i>ara, leu</i>)7697 <i>galU galK</i> λ - <i>rpsL nupG pir</i> +(DHFR); Host strain for pTNS2	Fisher
<i>A. baumannii</i>		
G636	2018 <i>A. baumannii</i> respiratory isolate (Strain 3689)	^c
G636 Δ <i>invL</i>	G636 <i>invL</i> mutant	This study
G636 <i>invL</i> ⁺	G636 <i>invL</i> mutant complemented	This study
G636 Δ <i>bap</i>	G636 <i>bap</i> mutant	This study
G636 Δ <i>ata</i>	G636 <i>ata</i> mutant	This study
G636 Δ <i>fhaBC</i>	G636 <i>fhaBC</i> mutant	This study
G636- <i>gfp</i>	G636 expressing <i>gfpd2</i>	This study
G654	2020 <i>A. baumannii</i> respiratory isolate (Strain 6919)	^c
Ab19606	1948 <i>A. baumannii</i> urinary isolate	(125)
<i>S. aureus</i>		
Newman	1952 osteomyelitis isolate	(126)
<i>K. pneumoniae</i>		
TOP52	2006 cystitis isolate	(127)

559 ^aTet, tetracycline; Apr, apramycin; Amp, ampicillin; Kan, kanamycin.

560 ^bPB-FLuc+GFPd2 was a gift from Jordan Green (Addgene plasmid # 127190;
561 <http://n2t.net/addgene:127190>; RRID: Addgene_127190).

562 ^cStrains G636 and G654 were collected by the CDC-funded Georgia Emerging Infections
563 Program's (EIP) Multi-site Gram-Negative Surveillance Initiative (MuGSI) and kindly provided by
564 Sarah Satola.

565

566

567 **Table S4. Primers used in this study.**

Primer	Sequence
5' pEX18 marker swap	ACACGGTGCCTGACTGCGTTAGC
3' pEX18 marker swap	ATGGAAGCCGGCGGCACC
5' Apr for pEX18Ap	GAGGTGCCGCCGGCTTCCATGATCCTCAGCCAATCGACTGGC
3' Apr for pEX18Ap	AACGCAGTCAGGCACCGTGTGATTCCCTTTGTCAACAGCAATGG
5' pEX18Tc	ATGCCTGCAGGTGCGACTCTAGAGG
3' pEX18Tc	GCAAGCTTGGCACTGGCCGT
5' F1 G636 <i>invLKO</i>	ACGGCCAGTGCCAAGCTTGCGGCAATGTCTCAAATAAAAAATTTAACTC
3' F1 G636 <i>invLKO</i>	TGAGATCCGCTATTACTTCCAG
5' F2 G636 <i>invLKO</i>	AGTAATAATAGCGGATCTCATGCTTCTTTTTTTAGAGTTGTGTTCC
3' F2 G636 <i>invLKO</i>	TAGAGTCGACCTGCAGGCATAAAATAACCGCATAGCCAGCTTGAGC
5' G636 <i>fdeCKO</i> Comp	GCATGAGCTCACTAGTGGATCCGAGATTAAGACTTTACTTGGCATAACACC
5' F1 G636 <i>bapKO</i>	ACGGCCAGTGCCAAGCTTGCAGAAGCGGCTGGCAATGTCACG
3' F1 G636 <i>bapKO</i>	TCAAGCACCGGTGCATACTGACC
5' F2 G636 <i>bapKO</i>	CAGTATGCACCGGTGCTTGAGGTGGTAACACTACAATTCAGATTGACC
3' F2 G636 <i>bapKO</i>	TAGAGTCGACCTGCAGGCATTCCATAAATGAATTTGCCATTTTCTTGAACTCTG
5' F1 G636 <i>ataKO</i>	ACGGCCAGTGCCAAGCTTGTCTAAGTCGGTCTGGCTATTTCGCC
3' F1 G636 <i>ataKO</i>	TGATGACGTTGAGAAAAAAGCTAATGCAGG
5' F2 G636 <i>ataKO</i>	CTTTTTTCTCAACGTCATCAAAAACCTTCTCAGACAAATACCGAACTCAACG
3' F2 G636 <i>ataKO</i>	TAGAGTCGACCTGCAGGCATCGTGATCAATTTCTTCTGTAAGCGAATCTTTTTGC
5' F1 G636 <i>fhaBCKO</i>	ACGGCCAGTGCCAAGCTTGTCTAAAATTTTAAAGCAGTTTGATGAGCC
3' F1 G636 <i>fhaBCKO</i>	CAGAATTGTACGTATAAGAACTTTATTTTACAC
5' F2 G636 <i>fhaBCKO</i>	TTCTTATACGTACAATTCTGTAACAATGAAAAATGCACATGCGG
3' F2 G636 <i>fhaBCKO</i>	TAGAGTCGACCTGCAGGCATCTTTATTGGTACCCTGATTGCG
3' G636 <i>fdeCKO</i> Comp-His6 v2	TCAGTGGTGATGGTGATGATGATTACCATTTGAACAGTTTGGATCTATTCC
Tn7 linear Fwd-His6	CATCATCACCATCACCCTGAAAGCTTGGGCCCGGTACCTC
Tn7 linear Rev	GGATCCACTAGTGAGCTCATGC

5' d2EGFP for pUC18T-mTn7	AGAAAGAGGAGAAATACTAGATGGTGAGCAAGGGCGAGG
3' d2EGFP for pUC18T-mTn7	GAGGTACCGGGCCCAAGCTTCTACACATTGATCCTAGCAGAAGC
5' pUC18T-mTn7 for d2EGFP	AAGCTTGGGCCCCGGTACCTCG
3' pUC18T-mTn7 for d2EGFP	CTAGTATTTCTCCTCTTTCTCTAGTAATTGTTATCC

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622 **Figure S1.** Intracellular *A. baumannii* are detectable in BALF at early timepoints in the chronic
623 respiratory infection model. Groups of C3H/HeJ (*tlr4* mutant) mice were intranasally inoculated
624 with 10^5 G636, and BALF was collected at 4 hpi (A), 2 dpi (B), and 7 dpi (C) and either treated
625 with 50 μ g/ml colistin or mock-treated. Following, bacterial CFU in the treated (intracellular; IC)
626 and mock treated (total) BALF, as well as in the remaining lungs following BALF collection, were
627 enumerated by serial dilution plating. The horizontal line represents the mean, and the SEM is
628 indicated by error bars. Shown are the results from at least two independent experiments.
629 C3H/HeJ (*tlr4* mutant) mice were infected with G636 expressing *gfp*, and, at these same
630 timepoints, BALF was collected, and host cells were isolated and stained with DAPI (blue) and
631 phalloidin (red). Intracellular bacteria were identified by microscopy at 4 hpi (D) and 2 dpi (E).
632 Shown are representative images from independent samples from at least two biological
633 replicates. Scale bar = 5 μ m.

634 **Figure S2.** The chronic respiratory infection model results in lung pathology during infection.
635 Groups of C3H/HeJ (*tlr4* mutant) mice were inoculated with 10^5 G636 or mock-inoculated with
636 PBS, and at 4 hpi (A), 2 dpi (B), 7 dpi (C), 14 dpi (D), and 21 dpi (E), lungs slices were prepared
637 and H&E stained. Shown are representative images from each timepoint. Lung slice scale bar:
638 1000 μ m; Inset scale bar: 100 μ m.

639 **Figure S3.** The chronic respiratory infection model does not cause goblet cell hyperplasia or
640 fibrosis. Groups of C3H/HeJ (*tlr4* mutant) mice were inoculated with 10^5 G636 or mock-inoculated
641 with PBS, and at 4 hpi, 2 dpi, 7 dpi, 14 dpi, and 21 dpi, lungs slices were prepared, H&E stained,
642 and scored for goblet cell hyperplasia (A) and fibrosis (B). The mean is shown on the graph, and
643 the SEM is indicated by error bars. Unpaired Student's *t*-test.

644 **Figure S4.** Testing of G636 adhesin mutants in the chronic respiratory infection model reveals a
645 potential role for InvL in bacterial persistence. Groups of C3H/HeJ (*tlr4* mutant) mice were
646 intranasally inoculated with 10^5 G636, G636 Δ *bap*, G636 Δ *ata*, G636 Δ *fhaBC*, and G636 Δ *invL*.
647 1 (A) and 14 (B) dpi, mice were sacrificed, and CFU in the lungs were quantified. Each data point
648 represents an individual mouse, the horizontal line represents the mean, and the SEM is indicated
649 by error bars. Shown are results from single experiments for each strain.

650 **Figure S5.** The chronic respiratory infection model can be used to study outcomes of antibiotic
651 treatment. Groups of C3H/HeJ (*tlr4* mutant) mice were infected with 10^5 G636 (A, C) or 10^5 G654
652 (B, D) and sacrificed at 1, 3, and 5 dpi (long-term). Additionally, groups of C57Bl/6 mice were
653 infected with 10^9 G636 (A, C) or 10^9 G654 (B, D) and sacrificed at 24 hpi (acute). Mice in both
654 infection models were treated intraperitoneally treated with PBS or 5 mg/kg *colistin* (col) every 8
655 h (A, B) or PBS or 100 mg/kg *imipenem* (im) every 12 h (C, D) with all treatments beginning 4 hpi.
656 At each timepoint, CFU were quantified in the lungs. Shown are the results from at least two

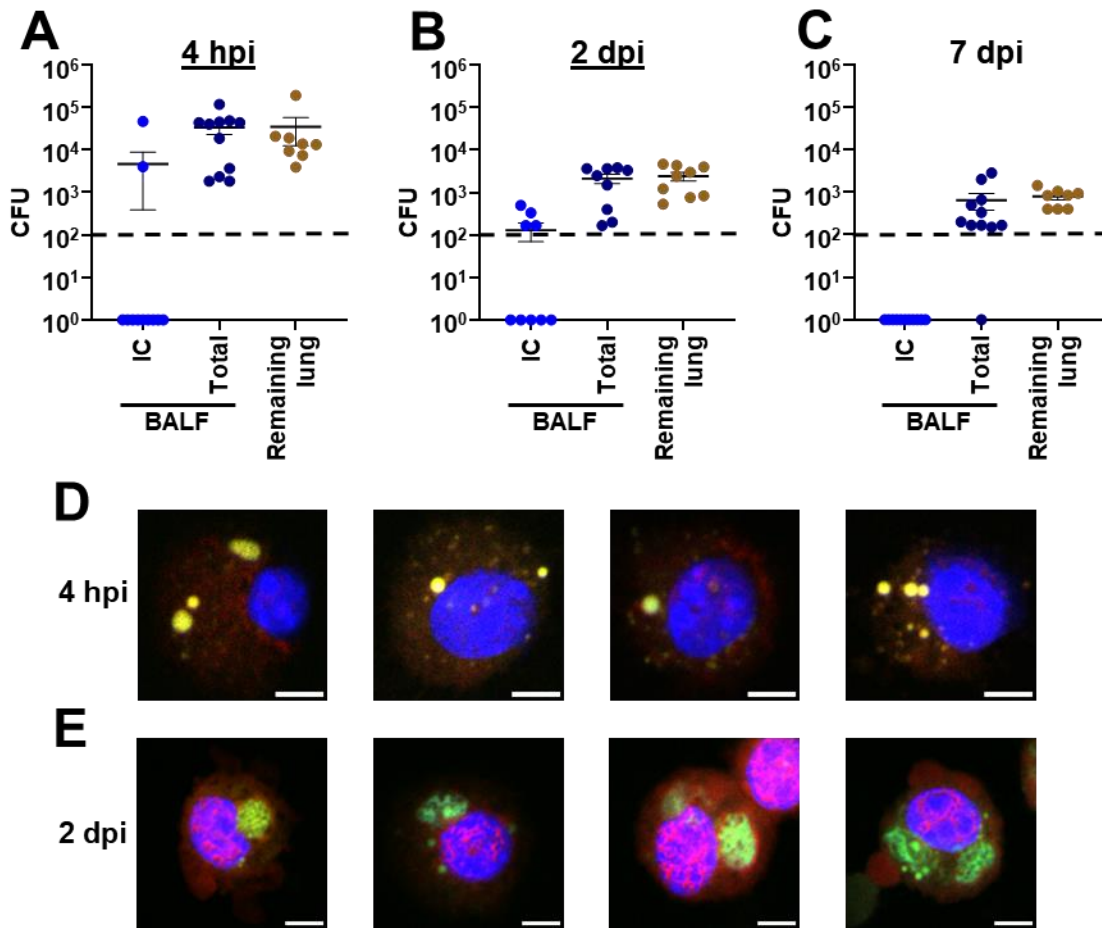
657 independent experiments, each data point represents an individual mouse, the horizontal line
658 represents the mean, and the SEM is represented by error bars. * $P < 0.05$; Mann-Whitney U test.

659 **Figure S6.** *S. aureus* secondary infection sometimes causes *A. baumannii* dissemination to the
660 spleen and kidneys in the chronic respiratory infection model. C3H/HeJ (*tlr4* mutant) mice were
661 intranasally inoculated with 10^5 G636. At 14 days post-*A. baumannii* infection, groups of mice
662 were either not inoculated (untreated), inoculated with PBS (mock-infected), infected with *S.*
663 *aureus*, or infected with *K. pneumoniae*. Subsequently, on days 15 (A and B) and 16 (C and D)
664 post-*A. baumannii* infection (1 and 2 days post-secondary infection), groups of mice were
665 sacrificed, and *A. baumannii* CFU were quantified in the spleen (A and C), and kidneys (C and
666 D). Each data point represents an individual mouse, the horizontal line represents the mean, and
667 the SEM is indicated by error bars. Shown are results from at least 2 independent experiments.
668 Significant differences were not detected; Kruskal-Wallis H test with Dunn's test for multiple
669 comparisons.

670 **Figure S7.** Ongoing *A. baumannii* pneumonia alters bacterial numbers following secondary
671 infection with *S. aureus* and *K. pneumoniae*. C3H/HeJ (*tlr4* mutant) mice were either intranasally
672 inoculated with 10^5 G636 14 days prior to infection with *S. aureus* or *K. pneumoniae* (+Ab) or not
673 infected prior to *S. aureus* or *K. pneumoniae* infection (-Ab). At 14 days post-*A. baumannii*
674 infection, groups of mice were infected with *S. aureus* or *K. pneumoniae*. 1 and 2 dpi with *S.*
675 *aureus* (A, B, and C) or *K. pneumoniae* (D, E, and F), mice were sacrificed, and these bacteria
676 were quantified in the lung (A and D), spleen (B and E), and kidneys (C and F). Each data point
677 represents an individual mouse, the horizontal line represents the mean, and the SEM is indicated
678 by error bars. Shown are results from at least 2 independent experiments. * $P < 0.05$; Mann-
679 Whitney U test.

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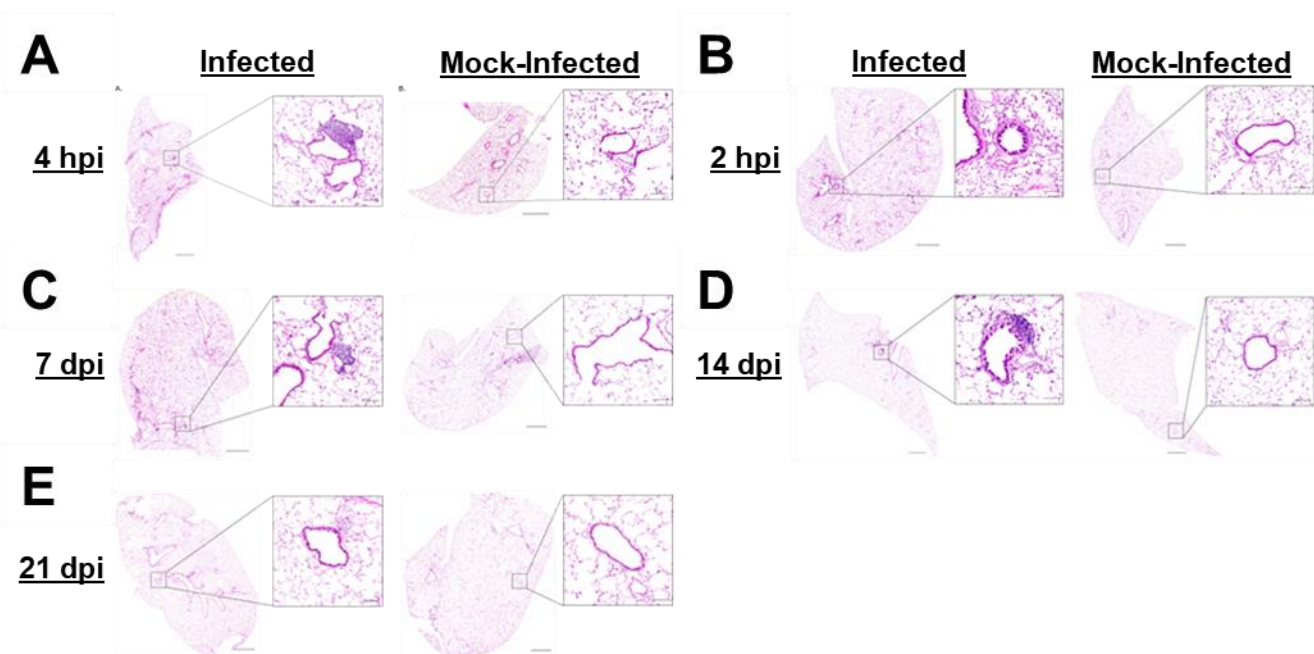
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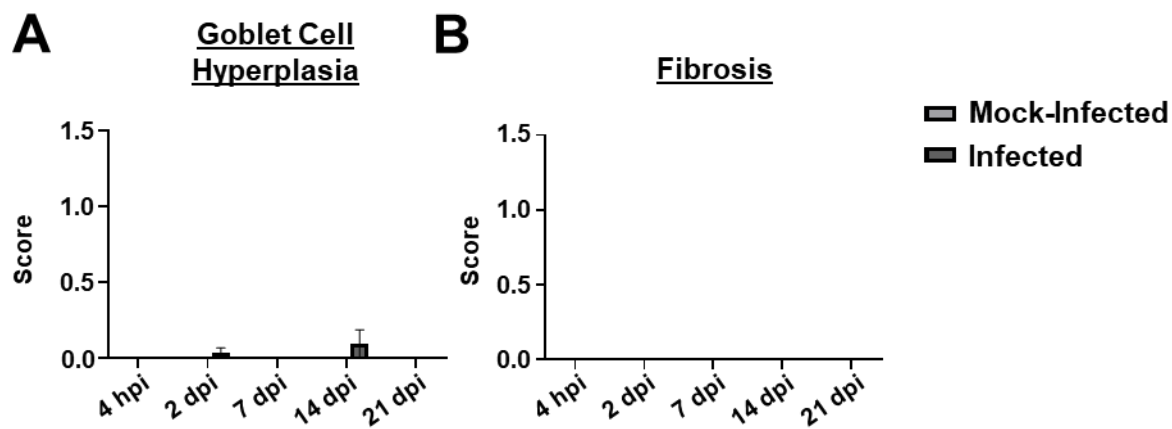
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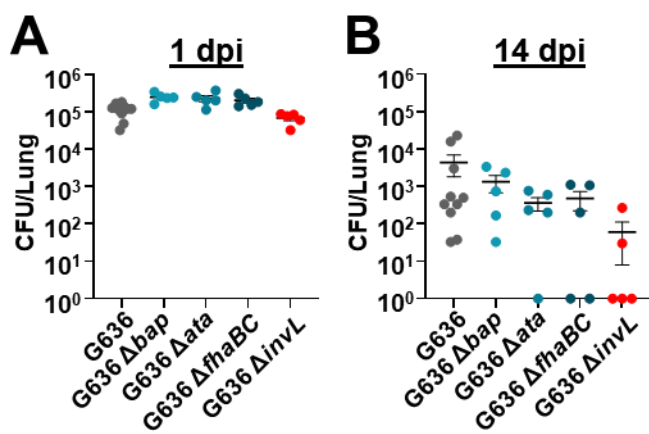
705 Figure S3



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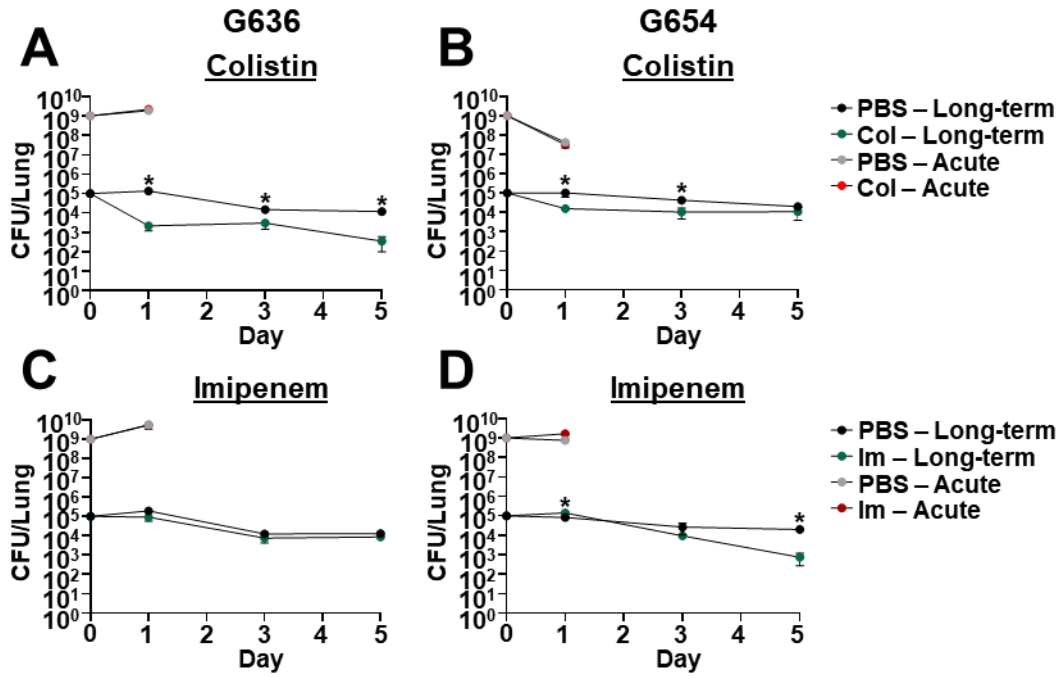
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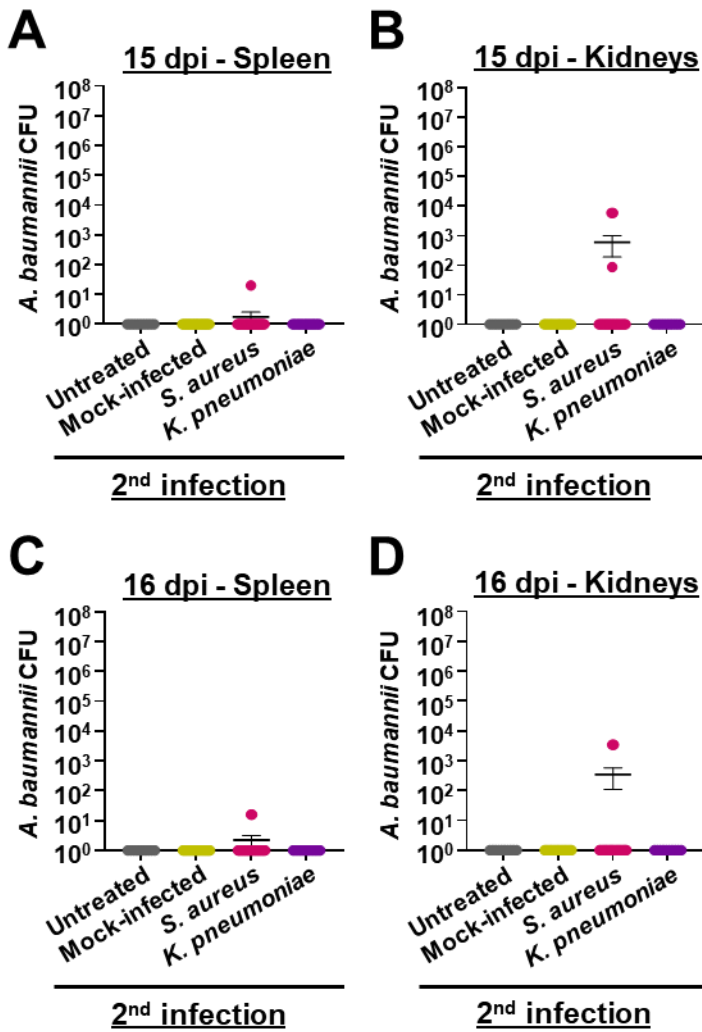
711 Figure S5



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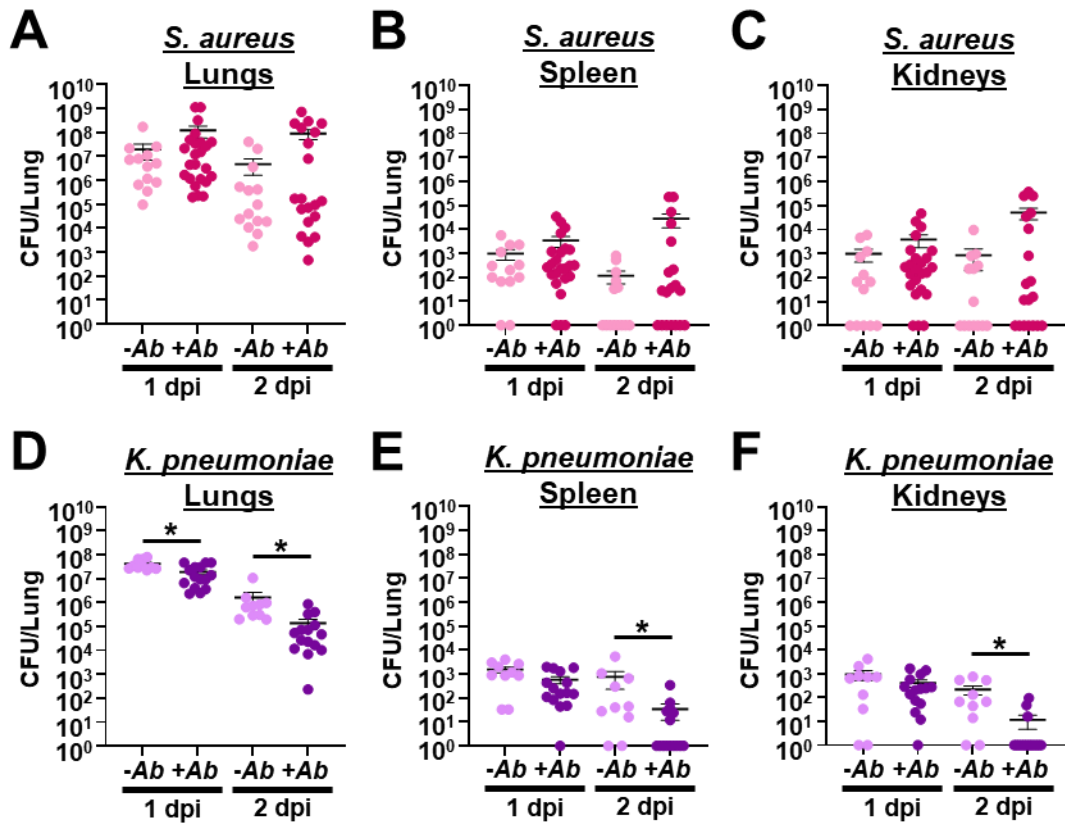
714 Figure S6



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717 Figure S7



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