

Α



В









A







Hours

Hours







	USA300			USA100		
Gene	Ref.	TI1	TI3	Ref.	TI2	
bbp						
clfA						
clfB						
ebpS						
fbpA						
fnbA						
fnbB						
icaA						
icaB						
icaC						
sdrC						
sdrE						
srtA						
adsA						

	Immune eva	sion				
)		U	ISA30	USA100		
2	Gene	Ref.	TI1	TI3	Ref.	TI2
	aur					
	capA					
	capB					
	capC					
	capD					
	capE					
	capF					
	capG					
	capH					
	capl					
	capJ					
	capK					
	capL					
	capM					
	capN					
	capO					
	capP					
	chp					
	coa					
	eap/map				*	*
	ebhA					
	ebhB					
	ebh					
	efb					
	higA					
	hlgB					
	hlgC					
	lukD					

lukE lukF-PV lukG lukH lukS-PV MprF oatA sbi scn scpA spa ssl11nm ssl6nm ssl7nm vwbp

Pr	σ	te	
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Protease							
	l	USA300			USA100		
Gene	Ref.	TI1	TI3	Ref.	TI2		
sak							
splA							
splB							
spIC							
spID							
splF							
sspA							
sspB							

	U	USA300			USA100		
Gene	Ref.	TI1	TI3	Ref.	TI2		
essC							
agrA							
agrB							
agrC							
arcA							
arcB							
arcC							
arcD							
arcR							
clpC							
clpP							
clpX							
codY							
cshA							
saeQ							
saeR							
saeS							
sarH1/sarS							
sarH2/sarU							
car7							

srrA srrB

	U	ISA30	USA	100	
Gene	Ref.	TI1	TI3	Ref.	TI2
ear					
eta					
hla					
sec3					
seg					
sei					
sek					
sel					
sem					
sen					
seo					
sep					
seq					
set6					
set7					
set8					
set9					
set10					
set11					
set12					
set13					
set14					
set15					
tst					

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Unici	ι	JSA30	0	USA	100
Gene	Ref.	TI1	TI3	Ref.	TI2
blaz					
ccra					
ditA					
ermA					
ileS					
ant(9)					
eniB					
eniC					
aeh					
puc					
nholl					
sceD					
speG					
siaB					
ariB				*	*
arlS					
arsB					
atl					
cadD					
fhuB					
fhuD					
fmt					
araR					
graS					
htrA					
hvsA					
IsaA					
IsdA					
lip					
ipi1					
ipi2					
ipl3					
lpl4					
lpl5					
lpl6					
lpl7					
lpl8					
lpl9					
lytR					
lytS					
putP					
rot					
rsbU					
scrA					
ahpC					
katA					
ksgA					
plc					
argR					
citB/acnA					
citZ/gltA					
frIA					
hemB					
hsdM					
menD					
mutL					
mutS					
rplF					
sucC					
sucD					
tcaB					
thyA					

## **1** Supplemental Figure Legends

2

## 3 Figure S1

4 Percentage of mouse survival by week after injection with either NRS384 or LAC. Mice were

- 5 sacrificed early (3 or 4 weeks post-injection) if lameness or hind-limb paralysis was observed.
- 6

## 7 Figure S2

Explanation of BLI signal measurements. Regions of interest (ROIs) used to measure the BLI signal from each hind limb are shown. (A) An example of a mouse with one BLI+ (left) leg and one BLI-(right) leg. BLI+ designation relies upon a discrete BLI signal focus originating from the left leg exceeding a signal of 70,000 photons/second. (B) An example of a mouse with one BLI+ (left) leg and one BLI- (right) leg. The right leg of this mouse is designated as BLI- even though it has a BLI signal of 1.6054x10<sup>5</sup> because there is no clear focus of signal originating from the leg and high BLI signal originating from the bladder at the edge of the leg ROI.

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### 16 Figure S3

Effects of HOM on different bone compartments. (A) Representative microCT reconstructions of cortical (upper panels) and trabecular (lower panels) bone of femurs from control (Non-injected) mice or BLI- and BLI+ femurs after NRS384 injection. (B) Representative microCT reconstructions of trabecular bone of BLI- and BLI+ femurs and tibias from LAC injected mice measured at 2- or 5weeks post injection. Scale bars 1 mm for cortical scans and 100 µm for trabecular scans.

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In vitro CFU and BLI correlation with *lux* operon in clinical isolates. (A) BLI image of serially diluted
 TI1, TI2, and TI3. Bacteria were grown overnight in TSB at 1:200 shaking at 220 rpm overnight and
 subcultured 1:100 for 2 hours before dilutions. (B) Correlation of the BLI signal from 10<sup>-4</sup>, 10<sup>-5</sup>, and 10<sup>-6</sup>
 <sup>6</sup> dilutions (A and B) from each isolate and the CFU count for these dilutions. CFUs enumerated from
 sampling of each dilution grown overnight on TSA. Blue triangle, TI1; brown squares, TI2; black dots,
 TI3.

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### 31 Figure S5

Bacterial growth assay. (A) The OD<sub>600</sub> of each *lux* strain and isolate was measured every 30 minutes for 5 hours to determine growth curves. \*p=0.0011, Tl2 and Tl5 compared to all other strains by repeated measures two-way ANOVA with Geisser-Greenhouse correction and Tukey's post-hoc test, n=2 repeats. (B) The OD<sub>600</sub> of each parental strain or isolate was measured every 30 minutes for 5 hours and compared to its respective *lux* transformed strain or isolate by repeated measures ANOVA, n=2 repeats.

#### 38

#### 39 Figure S6

Characterization of additional clinical isolates of *S. aureus*. (A) *In vivo* bioluminescent imaging (BLI) of
three representative mice for each isolate at 5 weeks post-injection. (B) The quantification of BLI
signal measured in the hind limb of each injected mouse over the 5 weeks post-injection (n=20/strain;
BLI Threshold 70,000 photons/second). (C) Percentage of mouse survival after injection with each
clinical isolate. TI2, TI4, and TI5 injected mice all had 100% survival.

45

Unusual histological formations with HOM infections. (A) Abscess formed along the periosteum of the
distal tibia with robust periosteal bone formation encompassing the abscess from a TI3-injected
mouse. (B-D) Inflammation with reactive bone formation on the periosteal surface of two tibias of
LAC-injected mice (D is higher magnification of black boxed area in C). (E,F) Fibrosis and new bone
formation directly under the growth plate of a tibia from a TI2 injected mouse.

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#### 53 Figure S8

Osteoclast intracellular proliferation assay. (A) Confirmation of equivalent input CFU for each strain from the bacteria-containing media used to infect osteoclast cultures. (B) Intracellular CFU measured from lysed osteoclasts 1.5 or 18 hours post infection. Each dot represents a biological replicate (cells cultured from a different mouse on a different day). There is no difference in phagocytosis of bacteria (1.5 hour timepoint) in any strain. \*\*\*\*p<0.0001, 1.5 hour vs 18 hour timepoints, and #p≤0.0003, 18 hour TI2 vs all other groups, by Two-way ANOVA with Tukey's post-hoc test.

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## 61 Figure S9

Clinical isolate polymorphisms by gene. 173 virulence associated genes (modified from (<u>31</u>)) and their presence, absence, and sequence relative to the reference strain. USA300\_FPR3757 is the USA300 reference genome, and N315 is the USA100 reference genome. Grey = present in reference genome, White = absent in reference genome, Blue = present and identical sequence to reference genome, Red = present with at least one SNP, and Red/White stripped = absent in isolate but present in reference genome. \* denotes a truncated gene. Genes are organized by function, which is listed above each table.

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