

Figure S1: Real-time PCR of *nos* expression in wildtype and *srrAB* mutant low-oxygen cultures. Wild-type and *srrAB* mutant low-oxygen TSB+G cultures were grown for 6 hours, and RNA was extracted from cell pellets. Expression of *nos* was measured in cDNA synthesized from each RNA sample by real-time PCR. Relative fold expression was calculated using the Livak method ($2^{-\Delta\Delta Ct}$) and normalized to the reference housekeeping gene *sigA*. Data represent the average from n=3 biological samples, error bars = SEM. *P<0.001 Mann-Whitney Rank Sum Test.

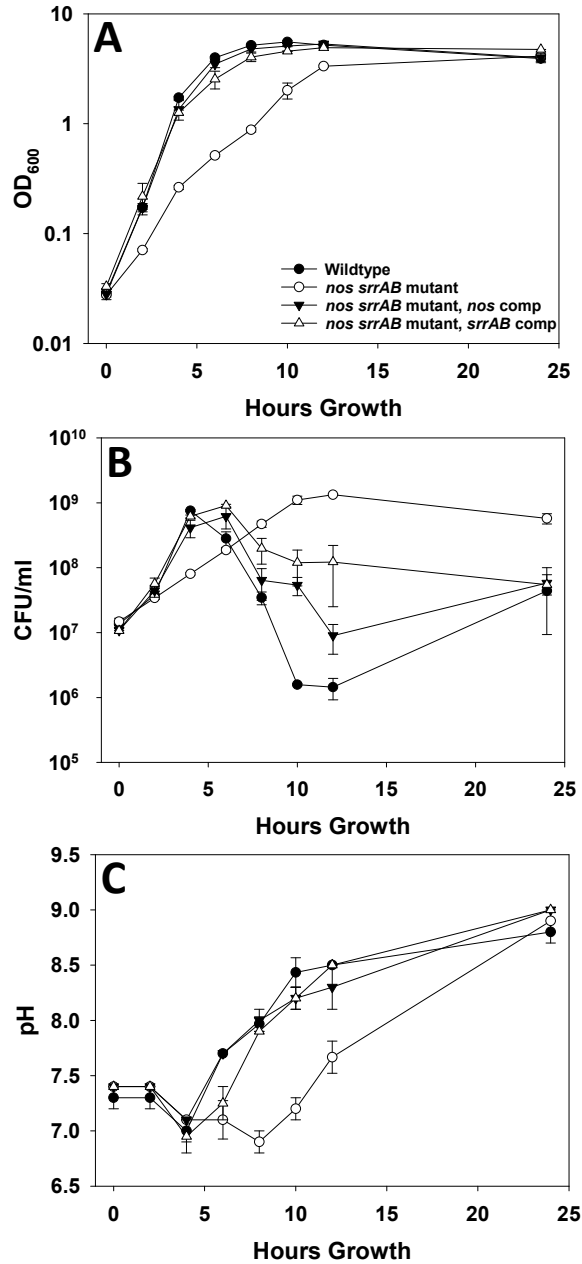


Figure S2: Growth analysis of UAMS-1 (wildtype), *nos srrAB* mutant, and *nos srrAB* complement strains. Aerobic TSB-G cultures were inoculated to an $OD_{600} = 0.025$ in TSB-G media and grown at 37°C with aeration (250 RPM; 1:12.5 volume to flask ratio). Growth over a 24-hour period was monitored by tracking OD_{600} measurements (A), CFU/ml by serial dilution plating (B), and pH measurement (C). Data points represent the average of 3 independent experiments and error bars = SEM.

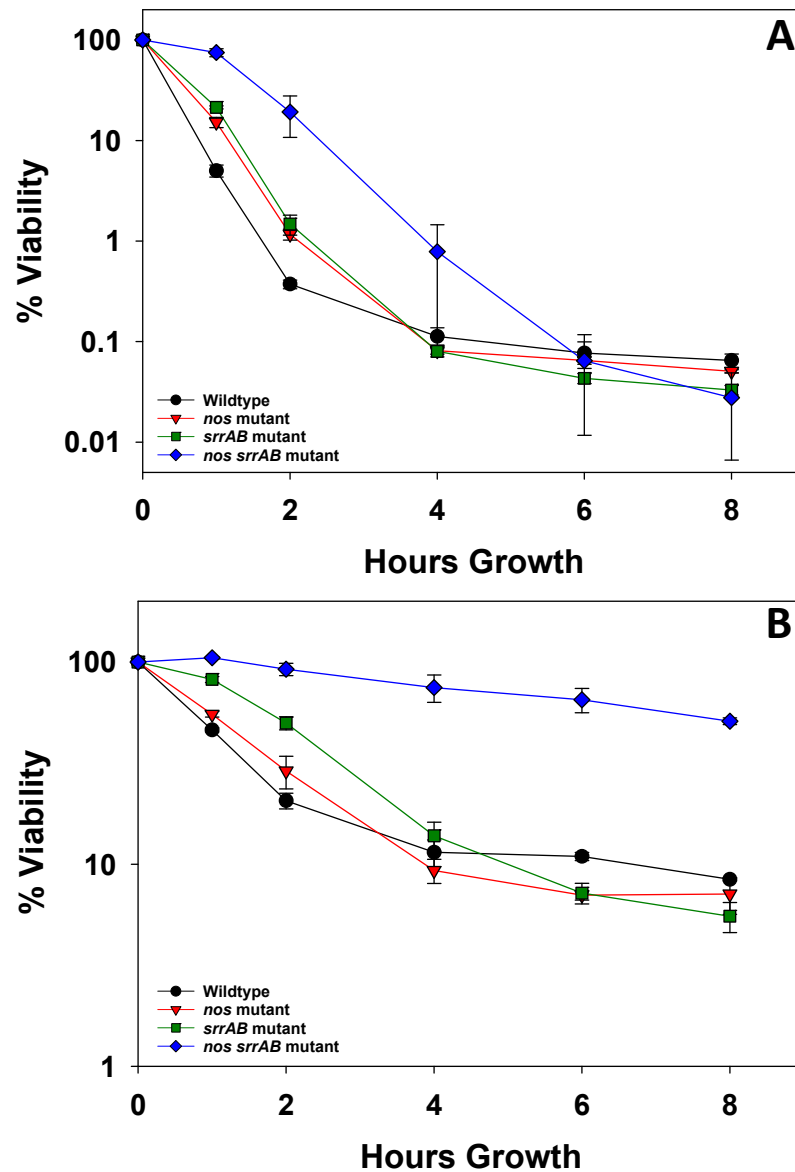


Figure S3: Contributions of saNOS and SrrAB to antibiotic killing. Early-exponential phase aerobic TSB-G cultures of UAMS-1 (wildtype) and isogenic *nos*, *srrAB*, and *nos srrAB* mutants were treated with final concentrations of either 30 $\mu\text{g/ml}$ ciprofloxacin (A) or 40 $\mu\text{g/ml}$ vancomycin (B), and CFU/ml were monitored at t=0 (just prior to antibiotic treatment), 1, 2, 4, 6, 8 hours post-treatment, as described in Materials and Methods. All data represent the average of n=3 independent experiments, error bars = SEM.

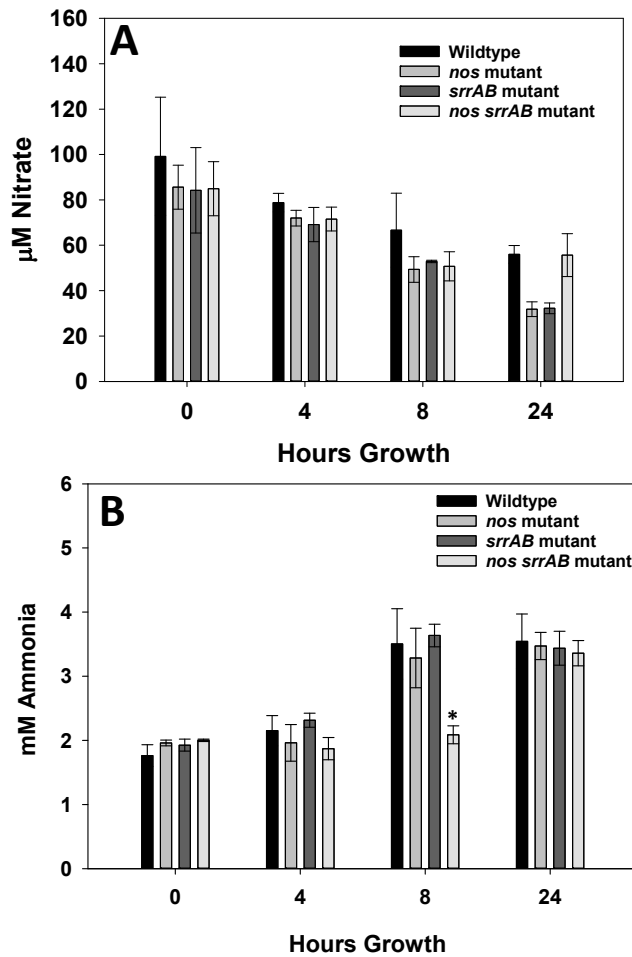


Figure S4: Nitrate and ammonia concentrations in supernatants. Extracellular nitrate and ammonia was measured from supernatants of wild-type, *nos* mutant, *srrAB* mutant, and *nos srrAB* mutant aerobic growth curves in TSB-G media. A. Nitrate measurements B. Ammonia measurements. For both A and B: Samples were collected at T = 0, 4, 8, 24 hours after inoculation. Measurements were performed using R-Biopharm kits in 96-well cell culture plates and each supernatant had an n=3 technical replicates and for each condition N=3 biological replicates, error bars = SEM). *P = 0.03 T-test (relative to wildtype).

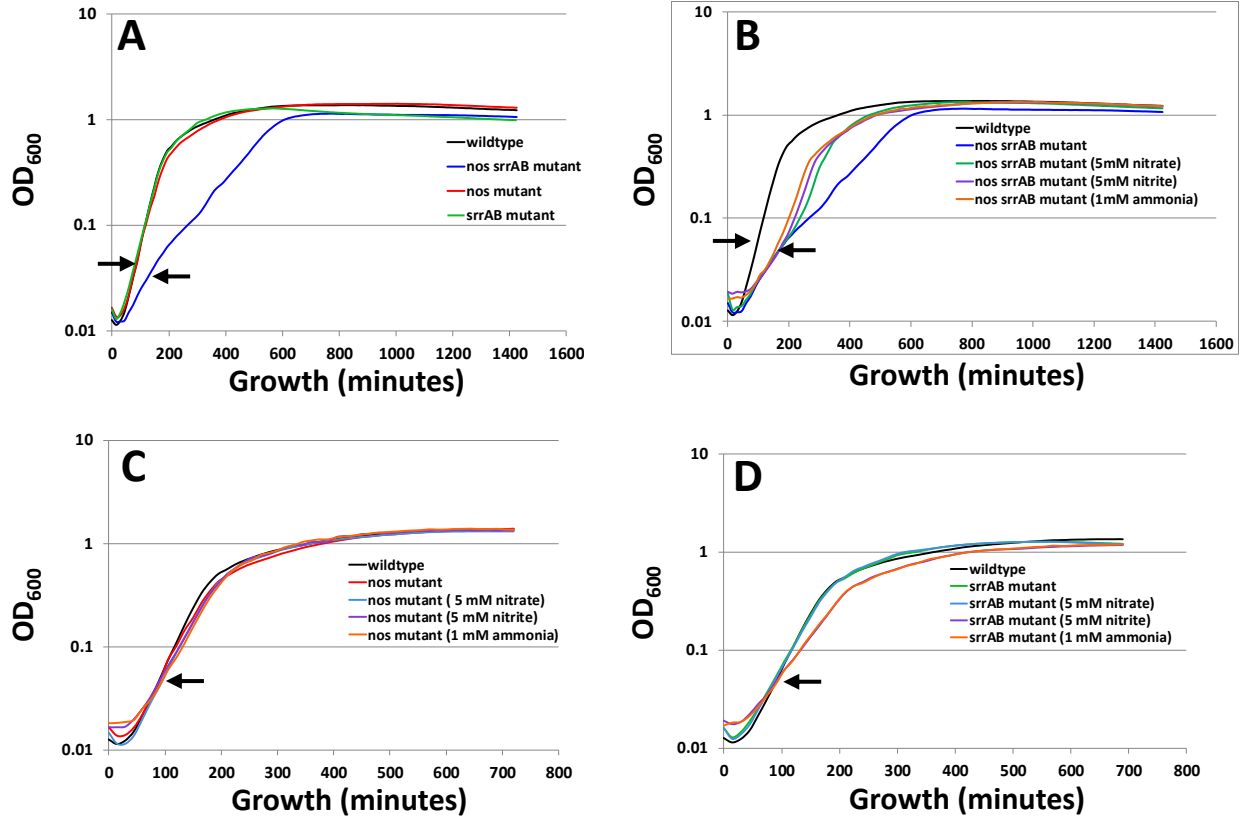


Figure S5: Bioscreen growth curves. Wildtype, *nos* mutant, *srrAB* mutant, and *nos srrAB* mutant were inoculated to a final $OD_{600} = 0.025$ in TSB-G and were grown untreated or supplemented with either 5 mM nitrate, 1 mM nitrite, or 1 mM ammonia. 200 μ l aliquots were dispensed into quadruplicate wells of a Bioscreen C plate. Cultures were incubated in a Bioscreen C plate reader with maximum shaking at 37°C and growth was monitored by measuring the OD_{600} every 15 minutes for 24 hours. Graphs are representative of $n=3$ biological replicates. Black arrows represent the linear region of the graph in which maximum specific growth rates were calculated for Figure 6.

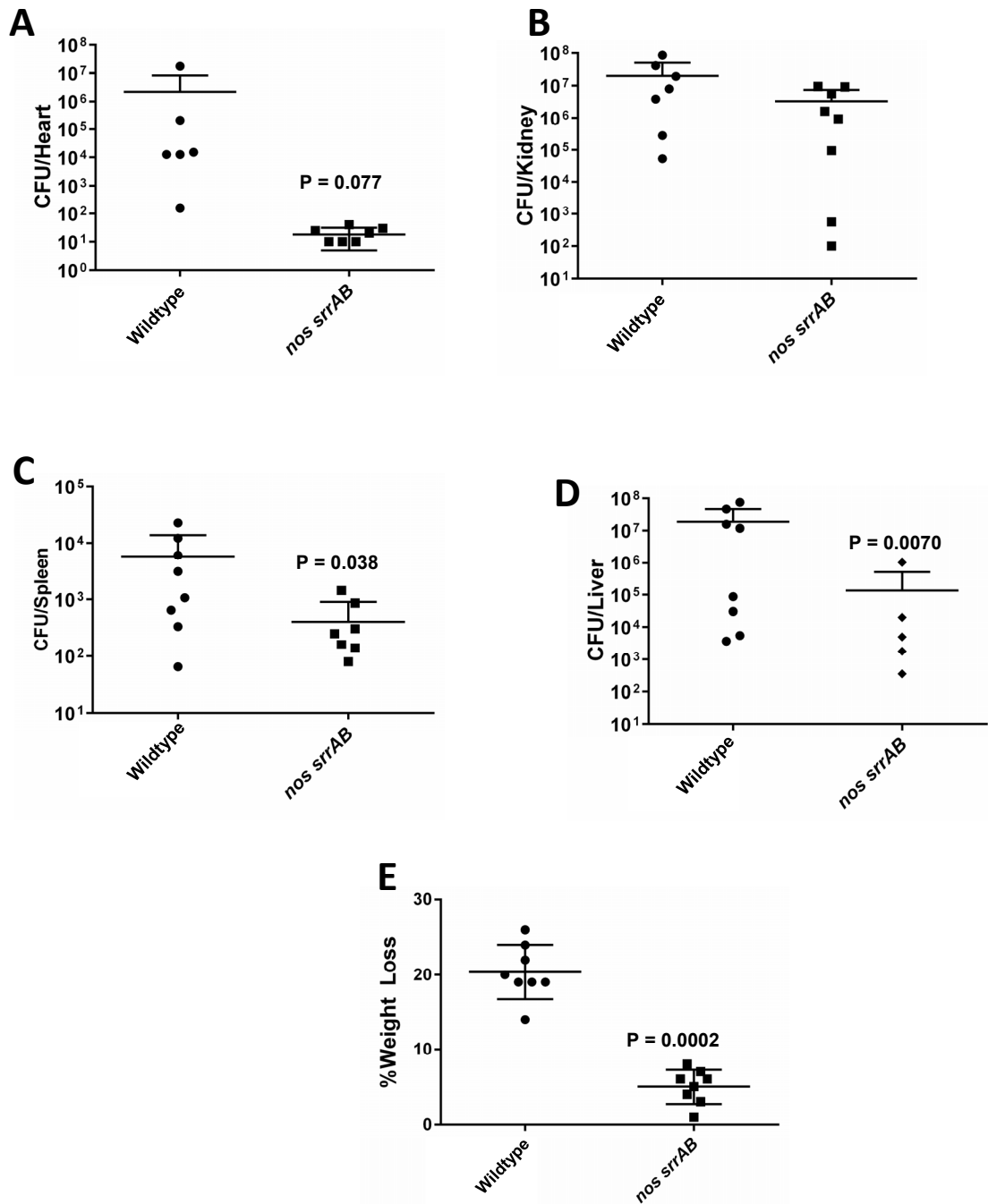


Figure S6: 4-day sepsis infection. UAMS-1 (wildtype; 3.95×10^7 CFU) and isogenic *nos srrAB* (3.9×10^7 CFU) mutant cultures were each retro-orbitally injected into 8-week-old C57BL/6 female mice (n=8 mice per group). Mice were euthanized 4-days post-infection, and organs were processed for CFU/organ determination as described in Materials and Methods. Graphs depict the calculated bacterial burdens for heart (A), kidney (B), spleen (C) and liver (D). The percent weight loss at 4-days post infection of each animal group is also reported (E). For A–E, data are graphed as scatter plots with mean (solid line) and standard deviation (error bars). Two-tailed P-values are reported for all significantly different comparisons to wild-type using a Mann-Whitney Test.

Table S1. List of bacterial strains and plasmids used in this study

Strain or plasmid name	Description	Reference or source
<i>E. coli</i> DH5 α	Host strain for construction of recombinant plasmids	(1)
<i>Staphylococcus aureus</i>		
RN4220	Easily transformable restriction deficient strain	(2)
UAMS-1	Osteomyelitis clinical isolate	(3)
KR1010	UAMS-1 <i>nos::erm</i> insertion mutant	(4)
KB6004	UAMS-1 Δ <i>srrAB</i> deletion mutant	(5)
KR1014	UAMS-1 <i>nos::erm</i> Δ <i>srrAB</i> mutant	This study
pTR27	<i>nos::erm</i> allele-replacement plasmid in pBT2; Erm ^R /Cm ^R	(4)
pBT2	Temperature-sensitive shuttle vector; Cm ^R /Amp ^R	(6)
pMK <i>nos</i>	<i>nos</i> complementation plasmid; Cm ^R	(4)
pMK4	Shuttle vector; Cm ^R /Amp ^R	(7)
pIHW58	<i>srrAB</i> complementation plasmid in pJB94; Tet ^R	(8)

Table S2. PCR primers used in this study

Primer	Purpose	Sequence (5'-3')	Reference or Source
sigA-F sigA-R	Real-time PCR	F - CAAGCAATCACTCGTGCAAT R - GGTGCTGGATCTCGACCTAA	(4)
sar0233 (<i>hmp</i>)	Real-time PCR	F - AGAGGCATGCAATCTTCAGC R - AGTGCGCAGTGTTTATATGC	(9)
sar0256 (<i>scdA</i>)	Real-time PCR	F - TGCGGCGGACAAGTAAGTAT R - GCGAACCTGGTGTATTCGTT	(9)
sar0218 (<i>pfIB</i>)	Real-time PCR	F - GCTGTAAAGCAGCCTACCG R - AGAAGCATATGCCCTTCAC	(9)
sar1032 (<i>qoxC</i>)	Real-time PCR	F - ACGCATGGTTGTCACGTATC R - TGTCTAATCCGCGTCGTTG	(9)
sar2680 (<i>ldh2</i>)	Real-time PCR	F - CTTGCAGTTTGGTCACAAGC R - TTCCGCTTTAGCTTCGCTAC	(9)
sar0234 (<i>ldh1</i>)	Real-time PCR	F - GGTGTTGCAATGGGATTAGC R - TGTGCGAACTTGCTTTGTTC	This Paper
sar2486 (<i>narG</i>)	Real-time PCR	F - CGGCAAGAGCAGTTATTTTCG R - GACCCAGGCGTTTGAATATG	(9)
sar2489 (<i>nirB</i>)	Real-time PCR	F - TGCAGAACATAACGGCAAAG R - TCCCTTGATCCGTTTCGTTT	This Paper
sar2493 (<i>narT</i>)	Real-time PCR	F - TATGGGGACGACTGGGTAAA R - GCGGTAAATCTGGTTCGTGT	This Paper
sar2714 (<i>arcA</i>)	Real-time PCR	F - AGCACGACGACGAGAATCAA R - AAACAAGTTCATCGCCGCCT	This Paper
sar2713 (<i>arcB</i>)	Real-time PCR	F - TGGTGTACCGGTGTGGAATG R - ACGTCCATCTCCAACGTAAG	This Paper
sar0184 (<i>argJ</i>)	Real-time PCR	F - GGTGCGTTTAAACGAGGCAAT R - TCCTTTAGCACTGCCACCAA	This Paper
sar0923 (<i>argG</i>)	Real-time PCR	F - GCATTGCGACCTGTACGTGA R - TCATTGCTCTGCCCATAG	This Paper
sar1142 (<i>otc</i>)	Real-time PCR	F - AGGTGCTGCCATTATGGGTA R - GTTGCCACCATTTTCAGCGG	This Paper
sar2255 (<i>rocF</i>)	Real-time PCR	F - CGCCAGGCACAGGTACTIONA R - CCGATTGTTTCAGCAGTATGGT	This Paper
sar2007 (<i>nos</i>)	Real-time PCR	F - TATGGTGCTAAAATGGCTTG R - ACGATGCTTCGTCAGTAACA	(4)

Supplemental References:

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5. Lewis AM, Matzdorf SS, Endres JL, Windham IH, Bayles KW, Rice KC. 2015. Examination of the *Staphylococcus aureus* nitric oxide reductase (saNOR) reveals its contribution to modulating intracellular NO levels and cellular respiration. Mol Microbiol 96:651-69. doi: 10.1111/mmi.12962. Epub 2015 Mar 16.
6. Bruckner R. 1997. Gene replacement in *Staphylococcus carnosus* and *Staphylococcus xylosus*. FEMS Microbiol Lett 151:1-8.
7. Sullivan MA, Yasbin RE, Young FE. 1984. New shuttle vectors for *Bacillus subtilis* and *Escherichia coli* which allow rapid detection of inserted fragments. Gene 29:21-6.
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