Table S1: DNA primers used in this study for recombineering.

Targeted mutation	Primer sequence	DNA template
Δ*U-Z* 1	gatggatcaactatattacgtccctgaggagggatgacaagtgtaggctggagctgcttc	pKD4
Δ*U-Z* 2	cgcccgatagcgcaacgtttatcgggcgtcttttacctcacatatgaatatcctccttagttcc	pKD4
Δ*H-Z* 1	acccagaccgagcgcgtcggctttacccggtacgtccatctgtgtaggctggagctgcttc	pKD4
Δ*H-Z* 2	cgcccgatagcgcaacgtttatcgggcgtcttttacctcacatatgaatatcctccttagttcc	pKD4
Δ*U-V* 1	ttgtagtctcacaattagcattggcttgcactctggcaatgtgtaggctggagctgcttc	pKD4
Δ*U-V* 2	taatattcggagggcaaacggttaatactgatcagtttgccatatgaatatcctccttagttcc	pKD4
Δ*U* 1	ttgtagtctcacaattagcattggcttgcactctggcaatgtgtaggctggagctgcttc	pKD4
Δ*U* 2	ggtgtaggcgctgaagttcttcgtgaagctgaactgagtacatatgaatatcctccttagttcc	pKD4
Δ*iprA* 1	aatgcatatgttatctttaagcaagccactacaggaattctgtgtaggctggagctgcttc	pKD4
Δ*iprA* 2	taatattcggagggcaaacggttaatactgatcagtttgccatatgaatatcctccttagttcc	pKD4
Δ*katN* 1	caacttcaatatactgtgcgagtgagcgaacctaatcctgcatatgaatatcctccttagttcc	pKD3
Δ*katN* 2	cgcagcctagttctgcgccagtgagaggatcaacggtgggtgtgtaggctggagctgcttc	pKD3
Δ*katG* 1	atgagcacgaccgacgatacccataacacgttatccactgtgtgtaggctggagctgcttc	pKD4
Δ*katG* 2	gcagatcgaaacggtccaggttcatcactttcacccatgccatatgaatatcctccttagttcc	pKD4
Δ*katE* 1	cgtgcatgatacccgtgaatcacagcccggcctggactcccatatgaatatcctccttagttcc	pKD3
Δ*katE* 2	gcacgcgaccagacacggtgtgccgccatcagcgtcagcatgtgtaggctggagctgcttc	pKD3
Δ*oxyR* 1	atgaatattcgtgatcttgaatatctggtggcgttagccgcatatgaatatcctccttagttcc	pKD3
Δ*oxyR* 2	taacgccttgtcgaaatggccatccattgcgccacggatggtgtaggctggagctgcttc	pKD3
Δ*dps* 1	ttaattacctgggacacaaacatcaagaggatatgagattcatatgaatatcctccttagttcc	pKD3
Δ*dps* 2	tcgaagtattcagggtagagatagatttattcgatgttggtgtgtaggctggagctgcttc	pKD3

Δ*ahpC* 1	aatttcgttaacttactcctcaacgaaaacacggaggaagtgtgtaggctggagctgcttc	pKD4
Δ*ahpC* 2	gtttgtaaggaacggtggtgcaatcgcctgcggcgaagaccatatgaatatcctccttagttcc	pKD4
Δ*tsaA* 1	gcccgcgttgcgttctaaaacccttaatattgcaggagaatgtgtaggctggagctgcttc	pKD3
Δ*tsaA* 2	tggaaatgttctcagccaggtatttagccacgccgtccggcatatgaatatcctccttagttcc	pKD3
ΔN10 1	ttgtagtctcacaattagcattggcttgcactctggcaatgtgtaggctggagctgcttc	pKD4
ΔN10 2	aacgcgtaccatgcttagaaaggcatttatcgagtctgtacatatgcattccttgcaataatgccatatgaatatcctccttagttcc	pKD4
ΔC10 1	gcgtaagggtaattacattgaaatgaataaaggcaaactgtaacaaaaatgttgtgtaggctggagctgcttc	pKD4
ΔC10 2	cgcccgatagcgcaacgtttatcgggcgtcttttacctcacatatgaatatcctccttagttcc	pKD4
Δ*iprA* 1 *E.coli*	cgcaaatgttatctgtagttaaacctcttcaggaatttggtgtgtaggctggagctgcttc	pKD3
Δ*iprA* 2 *E. coli*	tgaaggcaaacggttgatagcgaccagtttgcctttattccatatgaatatcctccttagttcc	pKD3
Δ*iprA* 1 *Enterobacter*	atgaacgttaatgcgaaaccactttctgaattaagccggctgtgtaggctggagctgcttc	pJW102
Δ*iprA* 2 *Enterobacter*	taatattccgtgggcaaacggttgatgctgaccagtttgccatatgaatatcctccttagttcc	pJW102

Table S2. Quality control information for RNA-Seq samples obtained via FastQC.

Sample	Sample yield (Mb)	Mean quality score	Total # reads	# reads with at least one alignment	% R1 reads with at least one reported alignment
χ3339 WT log	1,507	37.5	30,151,350	23,669,313	78.5
χ3339 WT stat	1,403	37.4	28,061,794	19,990,513	71.24
χ3339 Δ*iprA* log	1,812	36.6	36,257,174	28,330,268	78.14
χ3339 Δ*iprA* stat	1,416	37.4	28,323,658	19,884,125	70.2

Table S3: DNA primers used in this study for RT-qPCR and flagella analysis.

Target gene	Primer sequence
SL1344_1490 1	CAGGAAATGCAGGCGAACGGTGACGGCTGG
SL1344_1490 2	CATCACTTCAATAACGGTAACGCCGAGTTC
SL1344_1660 1	TCTTCCTAAACTTGCCAGAGCCACGTCCAA
SL1344_1660 2	GCTATAGCCGAGCTGCTCGGCCAGGGTGGC
spvR 1	TAACACTGATGGAAACAGGTTCCTTCAGTATC
spvR 2	TACAGGTGTTCCGGCCAGCCTGTTGATATC
spvB 1	TCCCGTCACCTGCTTCGCGTACGG
spvB 2	GGTCGCGTTGCCATACTGTACCTTGC
SL1344_2887 1	GAAGCTAACCCAGCTCAAAAACTCTACACT
SL1344_2887 2	CAACACAATCTTGATTACAGTCTCGAGTTC
SL1344_2185 1	GTGCAGCATGATACAAAGGTTGTGAGTATG
SL1344_2185 2	ACGTTTAATGTCACCATCATCGATATACCA
fimA 1	AACGGAGCCGACAGGATGCCGAAACCGGG
fimA 2	CTGCCAGGACCGGTAAACGCATTCGTGCGG
lpxC 1	CCGTTGAGCACCTGAATGCTGCTCTGGCGG
lpxC 2	TCTGGCGCATGAACGCATCCGCAGAGAAGT
FljB on 1	TCGGTATAAGACATTTTGACCAACTCAGCGCCATTA
FljB on 2	CGTATTAACATATATAGTGTAACGCGCTCACGATA
FliC on 1	TCGGTATAAGACATTTTGACCAACTCAGCGCCATTA
FliC on 2	TTTCAGACAATGAGGTAAACGTACCGACAGCA

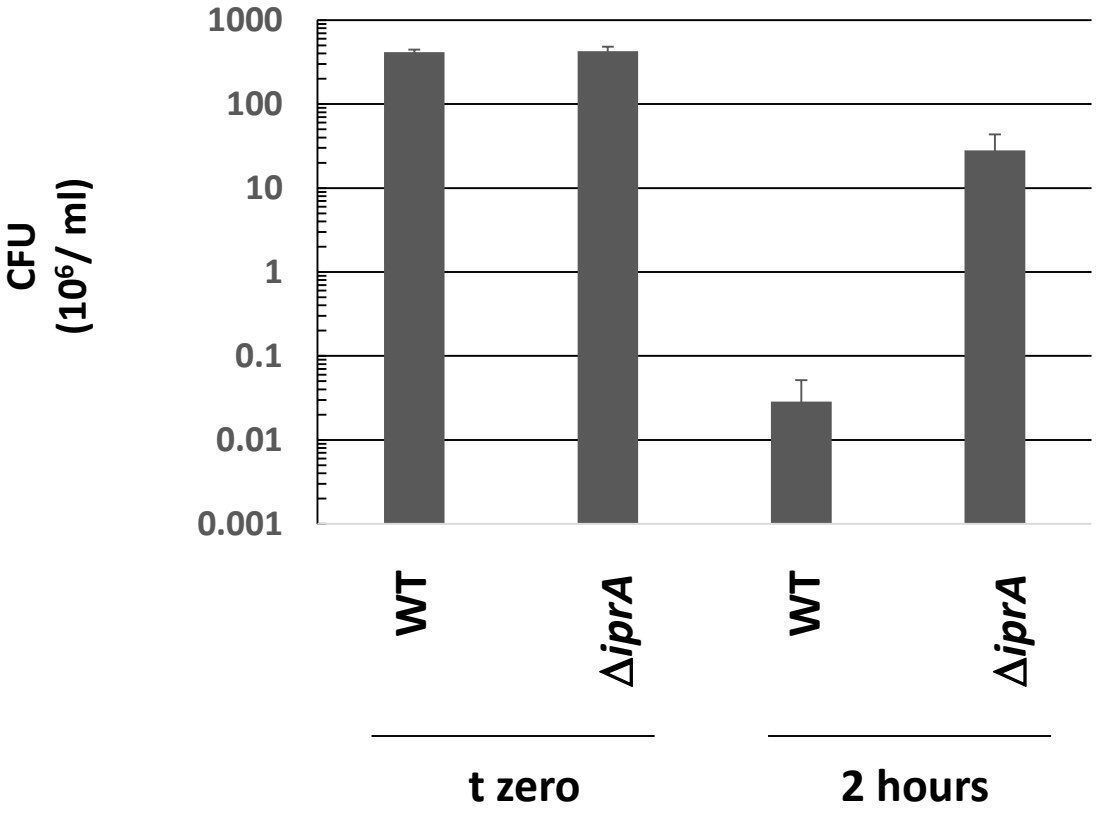


Figure S1: CFU levels of strains used in *S.* Typhimurium χ3339 WT vs. Δ*iprA* oxidative stress experiments. Cultures inoculated into fresh LB broth media were grown for 4 hours and then harvested for use in oxidative stress assays. The CFU level of the cultures was assayed before addition of the stress and then at 2 hours after stress addition (70 mM H_2O_2). Data is from two independent experiments and is representative of all experiments of this assay in terms of demonstrating equivalent CFU levels of WT and mutant at the start of the assay.

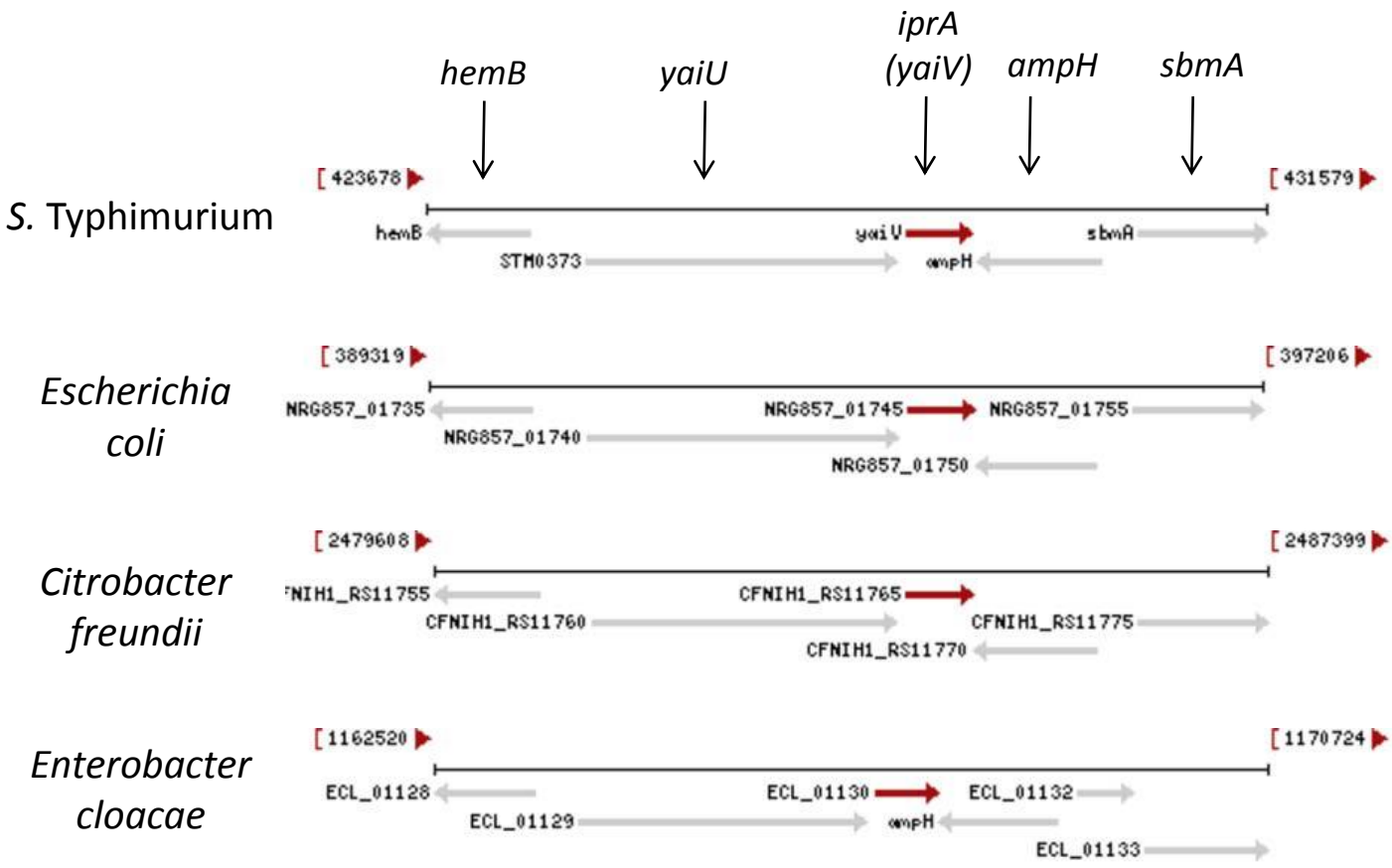


Figure S2: Synteny of the *iprA* gene locus across Enterobacteriaceae. The *iprA* gene is in red color for each genus. The specific strains used in this analysis were *S.* Typhimurium LT2, *E. coli* NRG 857C, *C. freundii* CFNIH1, and *E. cloacae* ATCC 13047.

Pssm-ID: 237999; Interval: 23-116; Cd Length: 115; Bit Score: 48.86; E-value: 3.52e-08

```
gi 16418876  23 TRFEFVNDKEIICSPDESNTHTFVILEGVVSLVR----GDKVLIGIVQAPFIFGLADGVAKKEAQYKLIAESGCIGYRLS 98
Cdd:cd00038  17 LEERRFPAGEVIIRQGDPADSLYIVLSGSVEVYKldedGREQIVGFLGPGDLFGELALLGNGPRSATVRALTDSELLVLP 96

gi 16418876  99 SSQTLAIIEQNQLWREAF 116
Cdd:cd00038  97 RSDFRRLLQEYPELARRL 114
```

gi 16418876 = query (IprA)

Cdd:cd00038 = consensus

Figure S3: Alignment of IprA predicted CAP effector binding domain with consensus. The *S.* Typhimurium IprA predicted CAP effector binding domain (amino acids 23 – 116) was aligned with the consensus domain sequence using the Conserved Domains tool via National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov). In the alignment, "gi 16418876" is the IprA sequence and "Cdd:cd00038" is the consensus.

```
#HMM        sYeliralLlelielpeelreninvlkyIqerTnLSRSsilkvLseLkkggyIeierGkLvkinkLPe
#MATCH      sY++ira+L+++ie++eelr++i v++yI++rT++SRS++++vL++L+kg+yIe+++GkL++in+LP+
#PP         8*********************************************************************5
#SEQ        SYDQIRATLMTMIEWDEELRSRIGVMNYIHQRTRVSRSVVAEVLAALRKGNYIEMNKGKLISINRLPS
(138-205)
```

#HMM = consensus sequence

#SEQ = query (IprA)

Envelope Start	End	Alignment Start	End	HMM From	To	HMM length	Bit score	E-value
138	205	138	205	1	68	68	101.4	1.90E-29

Figure S4: Alignment of the IprA predicted winged helix-turn-helix domain with the consensus. The predicted winged helix-turn-helix domain of the S. Typhimurium IprA protein (amino acids 138 – 205) was aligned with the consensus using the Pfam protein family search tool (http://pfam.xfam.org). In the alignment, #HMM is the consensus sequence and #SEQ is the IprA sequence.

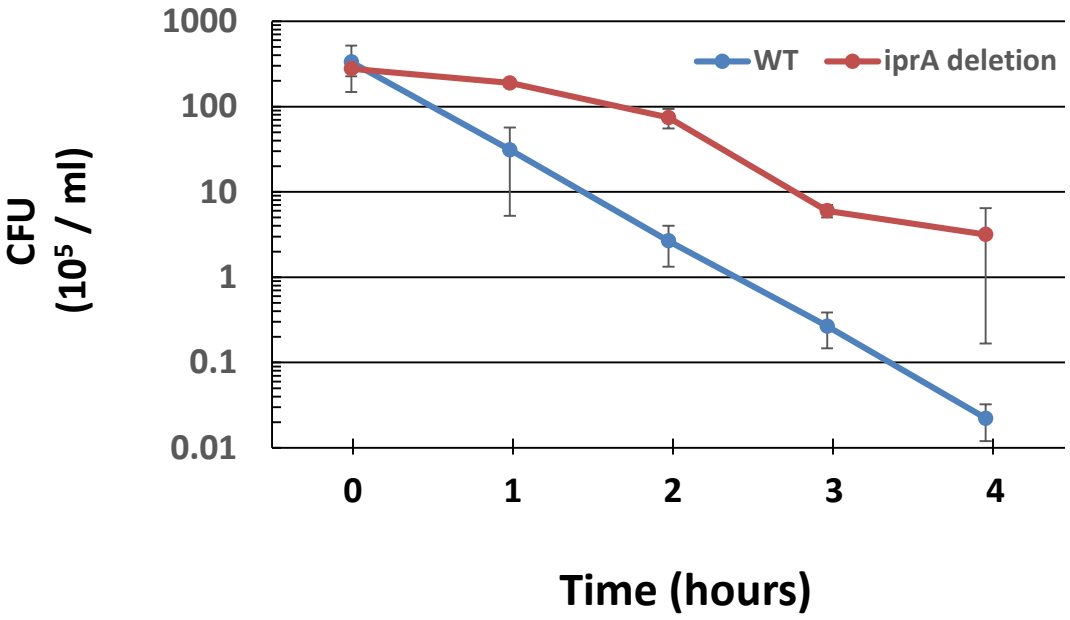
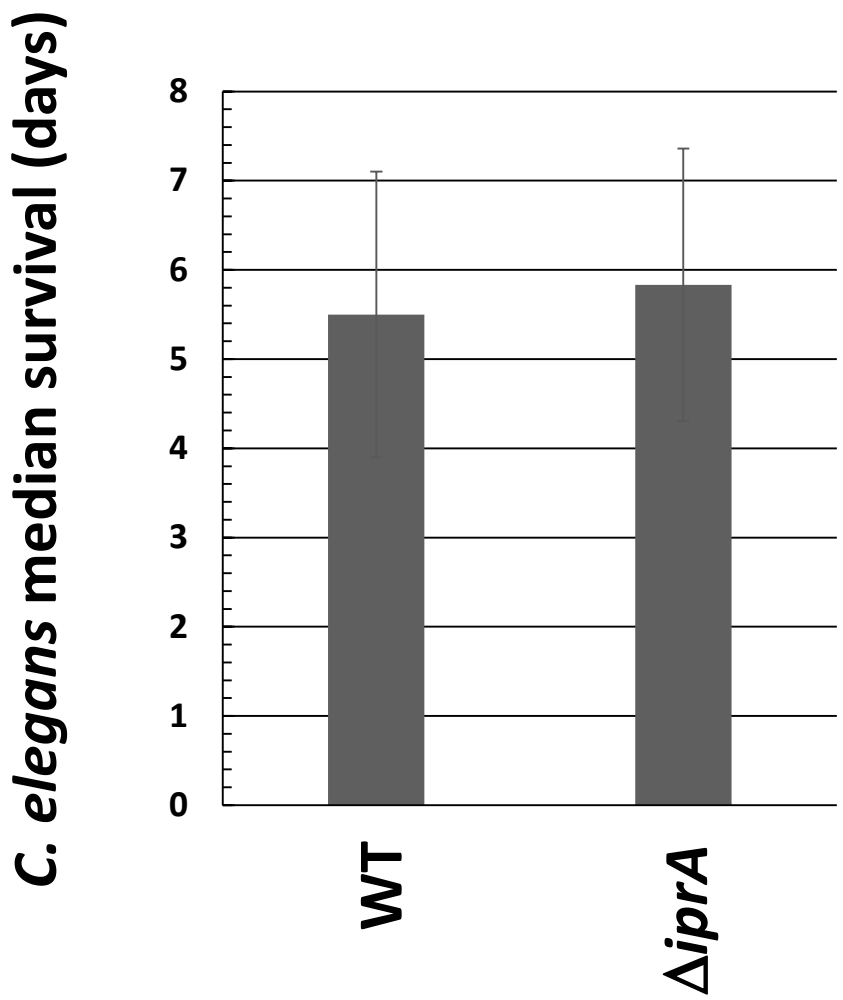


Figure S5: The Δ*iprA* mutation enhances survival in the presence of oxidative stress under growth curve conditions. Cultures of *S.* Typhimurium WT and Δ*iprA* strains were diluted into fresh LB broth media containing 5 mM hydrogen peroxide, grown shaking at 37 degrees C, and time point samples taken every hour for 4 hours. The samples were serial diluted and plated for CFU on LB agar plates. Data is the mean and standard deviation from three independent experiments.



***S.* Typhimurium χ3339**

Figure S6. Survival of *C. elegans* infected with *S.* Typhimurium WT and Δ*iprA* strains. Separate groups of approximately 100 worms were infected with either *S.* Typhimurium χ3339 WT or Δ*iprA* strains, and the survival of the worms was measured over 15 days. The data are the mean and standard deviation from 3 independent experiments.

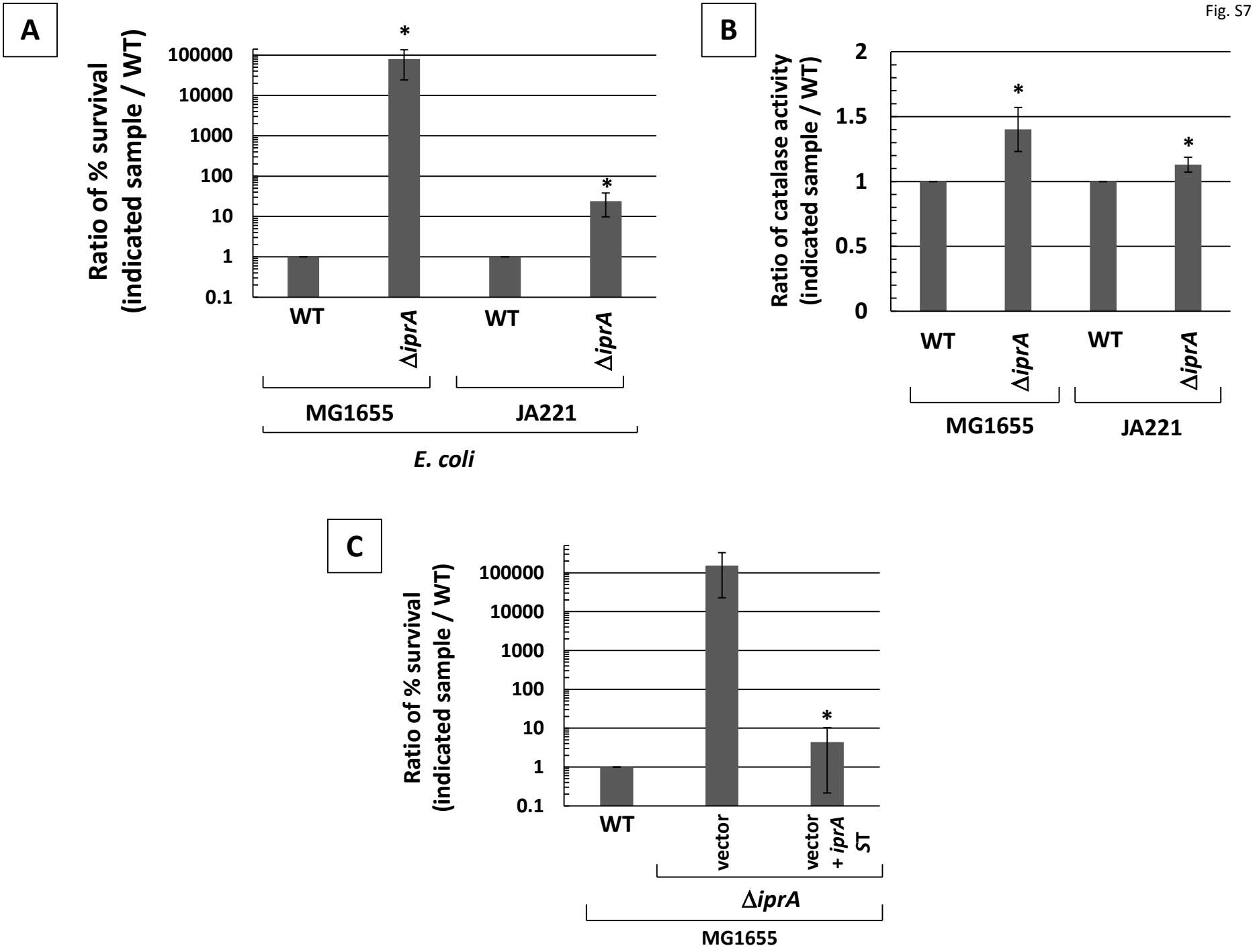

A
Ratio of % survival
(indicated sample / WT)
100000
10000
1000
100
10
1
0.1
*
*
WT
ΔiprA
WT
ΔiprA
MG1655
JA221
E. coli
B
Ratio of catalase activity
(indicated sample / WT)
2
1.5
1
0.5
0
*
*
WT
ΔiprA
WT
ΔiprA
MG1655
JA221
C
Ratio of % survival
(indicated sample / WT)
100000
10000
1000
100
10
1
0.1
*
WT
vector
vector + iprA ST
ΔiprA
MG1655

Figure S7: Characterization of *E. coli* MG1655 and JA221 Δ*iprA* strains. **Panel A**. A Δ*iprA* mutation was constructed in *E. coli* and transferred to *E. coli* strains MG1655 and JA221. The percent survival in oxidative stress of WT and Δ*iprA* was measured and calculated for a ratio to the corresponding WT strains. **Panel B**. Catalase activity was measured in the WT and Δ*iprA E. coli* MG1655 and JA221 strains and plotted as a ratio of each sample to the corresponding WT strain. **Panel C**. MG1655 Δ*iprA* strain containing plasmid vector and vector + *iprA S*T were assayed for oxidative stress survival and compared to the corresponding WT strain. The *iprA S*T gene is the WT *iprA* gene cloned from *S.* Typhimurium. Data in each panel are shown as the mean plus standard deviation, and observed differences from WT were found to be significant at p-value < 0.05 in all panels using t-test between WT and the indicated mutant sample (as marked via asterisk). In panel C, a t-test comparison was performed between vector and vector + *iprA* as indicated via asterisk.

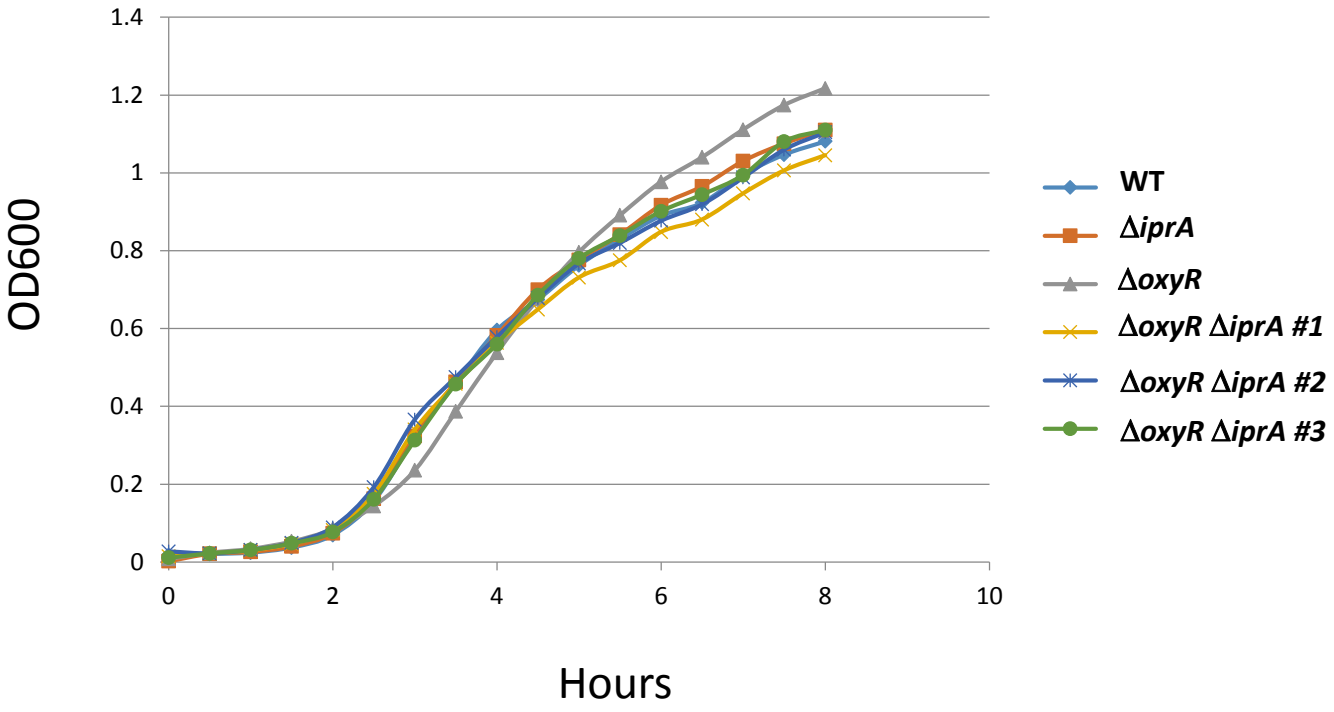


Figure S8: Growth curve measured via OD600 for *S.* Typhimurium χ3339 WT, Δ*iprA*, Δ*oxyR*, and Δ*iprA* Δ*oxyR* strains. Equal amounts of cells were used to inoculate fresh LB broth cultures that were incubated shaking at 37 degrees C. At the indicated time points, samples were assayed for OD600 measurements. Three independent Δ*iprA* Δ*oxyR* isolates were used in the assay.