Supplemental Results and Discussion

Francisella species are extremely resistant to polymyxin in comparison to other bacteria. We therefore set out to identify genes necessary for *F. novicida* polymyxin resistance. We initiated a screen of 470 transposon mutants from a library (1) representing 229 genes that have previously been identified as necessary for virulence *in vivo* and/or intracellular replication in mammalian cells. Each mutant was grown overnight in the presence of polymyxin B, and compared to wild-type. Mutants that failed to reach at least 75% of wild-type growth were deemed to have mutations in genes required for complete fitness in the presence of polymyxin (Supplemental Tables 1 and 2).

We identified 120 genes as playing roles in *F. novicida* resistance to polymyxin. The majority of these are categorized as having Unknown Function by COG analysis, while the remainder are primarily grouped into pathways necessary for the generation of envelope structures or within metabolic pathways that can act upstream of envelope biogenesis and modification (Supplemental Figure 2). Resistance to polymyxin is often mediated by alterations to the structure of lipid A and O-antigen, components of lipopolysaccharide (LPS) in the bacterial outer membrane. Notably, we identified *FTN_0544*, *FTN_0545*, and *lpxE* which have roles in lipid A modification and have previously been implicated in polymyxin resistance (2-4), providing validation for the results of the screen (Supplemental Table 1). Additionally, *wbtD*, *wbtF*, and *wbtH*, which are part of the O-antigen biosynthetic machinery were also identified (Supplemental Table 1)(5). To further confirm the results of the screen, we generated deletion mutants in two genes encoding proteins of unknown function, *FTN_0109* and *FTN_1254*. These deletion mutants demonstrated a significant decrease in polymyxin resistance compared to wild-type, providing additional support for screen's validity (Supplemental Figure 3).

In addition to a number of genes known to be involved in the biogenesis or modification of envelope structures, and numerous genes encoding hypothetical proteins, the screen also implicated numerous potential metabolic pathways in mediating polymyxin resistance (Supplemental Table 1 and

Supplemental Figure 2). These pathways may be involved in creating necessary precursors for envelope structures, and/or increasing metabolic output, allowing sufficient energy to resist and repair damage induced by polymyxin. In either case, the results suggest an important interplay between the metabolic status of the bacterial cell and its ability to resist the action of polymyxin. It is important to note that this screen does not differentiate between mutant strains which failed to grow in the presence of polymyxin, mutant strains which can replicate in polymyxin but subsequently are killed, and those mutant strains which are actively killed more effectively by polymyxin. However, this broad screen of 229 genes already implicated in *Francisella* virulence allows the foundation for future studies to determine their precise contribution to polymyxin resistance and virulence.

Supplemental Methods

Screen for polymyxin resistance determinants

Four hundred and seventy transposon mutants, representing 229 genes were obtained from the *Francisella* two-allele transposon mutant library (1, 6). Each transposon mutant was grown overnight in a well of a 96 well plate containing cation-adjusted Mueller Hinton broth (MH/C-A) with 0.2% L-cysteine (BD Biosciences). Subsequently, each mutant was diluted to an OD_{600} of 0.03 in MH/C-A containing 100µg/mL of polymyxin B (USB Corporation, Cleveland, OH). Following overnight growth at 37°C with aeration, the OD_{600} was measured and used to calculate the percent growth compared to wild-type bacteria. Strains that grew to an OD_{600} of less than 75% than that of wild-type were deemed to have increased sensitivity.

Bacterial growth kinetics.

The indicated strains were grown overnight and subsequently diluted to an OD_{600} of 0.03 in TSB with 0.2% L-cysteine or Chamberlain's Defined Media (CDM). Subcultures were placed at 37°C with aeration in a Biotek Synergy Mx plate reader and OD_{600} was measured each hour for 15 hours.

Lipid A isolation and analysis.

Total lipid A was isolated from the indicated strains as described previously (2). Lipid A was analyzed by LC/MS as described previously (2). Briefly, LC/MS of lipids was performed using a Shimadzu LC system coupled to a QSTAR XL quadrupole time-of-flight tandem mass spectrometer.

Surface charge analysis by zeta potential

Zeta electrokinetic potentials of the indicated strains were calculated as described previously (2). Briefly, bacteria were subcultured and grown to OD_{600} = 1.0, and subsequently washed and resuspended at a 5× concentration in 20 mM potassium chloride. Twenty microlitres of the concentrated bacteria were added to 3.2 ml of 20 mM potassium chloride in the zeta potential electrokinetic cuvette from Brookhaven

Instruments Corporation (BIC, Holtsville, NY). The bacterial cell sizes and zeta electrokinetic potentials were measured using the 90Plus size and zeta potential analyser (BIC). Data were analysed using BIC Zeta Potential Analyser Software Version 5.20, which corrects for bacterial cell size.

Antimicrobial resistance.

The indicated strains were grown overnight and subsequently diluted to an OD_{600} of 0.03 in MH/C-A with 0.2% L-cysteine containing the specified doses of Triton X (Fisher Scientific, Pittsburgh, PA), hydrogen peroxide (Fisher Scientific, Pittsburgh, PA), kanamycin (Teknova, Hollister, CA), and streptomycin (Teknova). Following overnight growth at 37°C with aeration, OD_{600} was measured and used to calculate the percent growth compared to the growth of the strain in media alone.

Intracellular survival.

Murine bone marrow-derived macrophages were infected as described in the Experimental Procedures with the indicated bacterial strains. At 4 hours post infection, macrophages were lysed with 1% saponin. Lysates were serially diluted in PBS and plated onto TSA containing 0.1% cysteine to enumerate colony forming units.

Campylobacter manipulations and experiments

The GB11 (wild-type) and its cognate Δ*cas9* deletion mutant have been described previously (7). Strains were routinely grown on Columbia blood agar plates containing 7% sheep blood (Becton Dickinson, Breda, The Netherlands), supplemented with vancomycin (Sigma-Aldrich, Zwijndrecht, The Netherlands) and chloramphenicol (Sigma-Aldrich) under micro-aerophilic conditions at 37°C using anaerobic jars and an Anoxomat (Mart Microbiology B.V., Drachten, The Netherlands). To measure bacterial permeability, plate-grown bacteria were recovered, washed in PBS, and diluted to a concentration of $7.5x10^7$ cfu/mL in PBS containing 30µg/mL ethidium bromide (Sigma-Aldrich). Fluorescence was measured immediately in a Fluostar Optima plate reader (BMG Labtech) using an excitation of 250nm

and an emission of 605nm. Erythromycin susceptibility was determined using an Epsilometer-test (bioMérieux, Zaltbommel, The Netherlands). Bacteria were diluted to a 1 MacFarland suspension, swabbed onto Columbia blood agar plates, and an E-test deposited. Plates were incubated overnight, as described above, and at 24 hours the MIC was determined.

Supplemental Figure Legends

Supplemental Figure 1. Model of the Cas9/dual RNA complex mediating *FTN_1103* repression. Cas9 associates with two small RNAs, tracrRNA and scaRNA. This complex is then targeted to the *FTN_1103* transcript, encoding a bacterial lipoprotein (BLP), and ultimately mediates the repression of BLP production by altering the stability of its mRNA. Since BLP can be recognized by TLR2, leading to a proinflammatory innate immune response, the ability of Cas9 to act as a regulatory element against this transcript is critical for *Francisella* evasion of the innate immune response.

Supplemental Figure 2. COG categories of genes identified as being involved in polymyxin B resistance. COG categories were assigned to each locus identified within the screen as defined by the *Francisella novicida* U112 genome database through NCBI (Accession #: NC_008601.1). Quantities of each COG category were plotted as percent of all categories identified within the screen.

Supplemental Figure 3. *FTN_1254* and *FTN_0109* contribute to *F. novicida* polymyxin resistance. Wild-type (WT), *FTN_0544*, *FTN_1254*, or *FTN_0109* deletion mutants were grown overnight in TSB with or without polymyxin B (200 ug/mL). Percent growth compared to untreated cultures is plotted (n=3). **; $p \leq 0.005$, ***; $p \leq 0.001$.

Supplemental Figure 4. Growth kinetics of the *cas9* deletion mutant in the presence of polymyxin B. Overnight cultures of wild-type (WT; circles) or the *cas9* deletion mutant (squares) were diluted to an OD_{600} of ~0.03 into the media containing indicated doses of polymyxin B in a 96-well plate. Cultures were incubated at 37°C with aeration in a Biotek Synergy Mx plate reader and OD_{600} was measured each hour for 18 hours (n=3).

Supplemental Figure 5. Complementation of the *cas9* deletion mutant restores polymyxin resistance. Wild-type (WT), *cas9* deletion mutant, or a *cas9*:complement strain were grown overnight

with or without polymyxin B (200 ug/mL). Percent growth compared to untreated cultures is plotted (n=3). **; $p \leq 0.005$.

Supplemental Figure 6. Other *cas* genes are not involved in polymyxin resistance. Wild-type (WT) or deletion mutants in the indicated *cas* genes were grown overnight with or without polymyxin B (400 ug/mL). Percent growth compared to untreated cultures is plotted (n=3). **; $p \leq 0.005$

Supplemental Figure 7. Cas9 is not involved in modification of lipid A. Total lipid A was analyzed by LC/MS from wild-type (WT), the *cas9* deletion mutant, or the *cas9*/1103 double deletion strain.

Supplemental Figure 8. Cas9 is not involved in alteration of cell surface charge. Cultures of wild-type (WT), the *cas9* deletion mutant, or the *cas9*/*1103* double deletion strain were subjected to zeta electrokinetic potential analysis. Data presented for each strain is pooled from 3 independent cultures, with multiple technical replicates.

Supplemental Figure 9. *FTN_1103* regulation by tracrRNA and scaRNA is necessary for polymyxin resistance. (A) Wild-type (WT), tracrRNA or tracrRNA/*1103* deletion mutants, or (B) WT, scaRNA or scaRNA/*1103* deletion mutants, were grown overnight in TSB containing the indicated concentrations of polymyxin B. Percent growth compared to untreated cultures is plotted (n=3). Data presented was generated during the same experiment as Figures 1a, b, utilizing the same controls, and plotted separately for clarity. **; $p \leq 0.005$.

Supplemental Figure 10. Cas9 regulatory axis provides resistance to Triton X. (A) Wild-type (WT), *cas9* and *cas9/1103* deletion mutants, (B) tracrRNA and tracrRNA/*1103* deletion mutants, or (C) scaRNA and scaRNA/*1103* deletion mutants were grown overnight in TSB, in the presence or absence of the non-ionic detergent Triton X (0.0125%). Percent growth compared to untreated cultures is plotted (n=3). Data

presented was generated during the same experiment, utilizing the same controls, and plotted separately for clarity. *; $p \leq 0.05$.

Supplemental Figure 11. Cas9 regulatory axis is not required for resistance to hydrogen peroxide. (A) Wild-type (WT), *cas9* and *cas9/1103* deletion mutants, (B) WT, tracrRNA and tracrRNA/*1103* deletion mutants, or (C) WT, scaRNA and scaRNA/*1103* deletion mutants were grown overnight in TSB containing the indicated concentrations of hydrogen peroxide. Percent growth compared to untreated cultures is plotted (n=3). Data presented was generated during the same experiment, utilizing the same controls, and plotted separately for clarity. *$p > 0.05$.

Supplemental Figure 12. Cas9 regulatory axis is required for resistance to kanamycin. Wild-type (WT), *cas9*, *cas9/1103*, tracrRNA, tracrRNA/*1103*, scaRNA, and scaRNA/*1103* deletion mutants were grown overnight in TSB containing the indicated concentrations of kanamycin. Percent growth compared to untreated cultures is plotted (n=3). *$p > 0.05$, ***; $p \leq 0.001$.

Supplemental Figure 13. Cas9 regulatory axis is required for resistance to streptomycin. Wild-type (WT), *cas9*, *cas9/1103*, tracrRNA, tracrRNA/*1103*, scaRNA, and scaRNA/*1103* deletion mutants were grown overnight in TSB containing the indicated concentrations of streptomycin. Percent growth compared to untreated cultures is plotted (n=3). *$p > 0.05$.

Supplemental Figure 14. *cas9* mutant does not have altered viability during growth in broth. Prior to propidium iodide staining (Figure 1c), wild-type (WT), *cas9*, or *cas9*/*1103* deletion mutants were grown to mid-log phase in TSB, washed and plated to enumerate colony forming units (n=3).

Supplemental Figure 15. Cas9 regulatory axis mutants exhibit wild-type growth kinetics in rich or synthetic media. Wild-type (WT), *cas9*, tracrRNA, scaRNA, *cas9/1103*, tracrRNA/*1103* and

scaRNA/*1103* deletion mutants were grown in (A) TSB or (B) Chamberlain's defined media (CHB) for 15 hours, and OD_{600} was measured every hour (n=3).

Supplemental Figure 16. *FTN_1103* regulation by tracrRNA and scaRNA is necessary for enhanced envelope integrity. Wild-type (WT), tracrRNA, tracrRNA/*1103*, scaRNA, or scaRNA/*1103* deletion mutants were grown to mid-log phase, washed, and stained with ethidium bromide. Fluorescence was measured at excitation 250nm and emission 605nm (n=3). **; $p \leq 0.005$, ***; $p \leq 0.001$.

Supplemental Figure 17. *FTN_1103* regulation by tracrRNA and scaRNA is necessary for enhanced envelope integrity during intracellular infection. (A) Bone marrow-derived macrophages were infected with wild-type (WT), tracrRNA, tracrRNA/*1103*, scaRNA, or scaRNA/*1103* deletion mutants at a multiplicity of infection (MOI) of 20:1 (bacteria per macrophage). At 4 hours post infection, macrophages were permeabilized with saponin and lysates were plated to enumerate intracellular bacterial levels (n=3). (B) Macrophages were infected as above, and at 4 hours post infection, macrophages were permeabilized with saponin and stained with anti-*Francisella* antibody (green), and propidium iodide (nucleic acids; red). Co-localization was quantified as no less than 50% PI overlap with *Francisella*, and 1,000 bacteria were counted for each strain. (C) Representative fluorescence micrographs of WT, tracrRNA, tracrRNA/*1103*, scaRNA, or scaRNA/*1103* deletion mutants. DAPI (DNA; blue), anti-*Francisella* antibody (green), and propidium iodide (nucleic acids; red). Arrows indicate representative PI and anti-*Francisella* co-localization. **; $p \leq 0.005$, ***; $p \leq 0.001$.

Supplemental Figure 18. *FTN_1103* regulation by tracrRNA and scaRNA promotes evasion of the inflammasome. Wild-type (WT), $ASC^{-/-}$, and $TLR2^{-/-}$, knockout macrophages were infected with WT, tracrRNA, tracrRNA/*1103*, scaRNA, or scaRNA/*1103* deletion mutants at a multiplicity of infection (MOI) of 20:1. At 5.5 hours post infection, cells were assayed for cytotoxicity through LDH release (n=3). *; $p \leq 0.05$, **; $p \leq 0.005$, ***; $p \leq 0.001$.

Supplemental Figure 19. Other CRISPR/Cas components are not required for evasion of the inflammasome. Wild-type bone marrow-derived macrophages were infected with wild-type (WT), *cas9*, *cas1*, *cas2*, *cas4*, tracrRNA, crRNA, or scaRNA deletion mutants at a multiplicity of infection (MOI) of 20:1. At 5.5 hours post infection, cells were assayed for cytotoxicity through LDH release (n=3). ***; $p \leq 0.001$.

Supplemental Figure 20. Sublethal treatment with polymyxin induces increased permeability without loss of bacterial viability. Wild-type bacteria were treated with 40µg/mL polymyxin B for 30min, at 37°C with aeration. (A) Treated and untreated cultures were plated and colony forming units enumerated. (B) Treated and untreated cultures were grown to mid-log phase, washed, and stained with ethidium bromide and fluorescence measured (n=3). ***; $p \leq 0.001$.

Supplemental Figure 21. Virulence of the *cas9* mutant is not restored in ASC$^{-/-}$ or TLR2$^{-/-}$ mice. (A) Wild-type (WT), ASC$^{-/-}$, TLR2$^{-/-}$, or ASC/TLR2-deficient mice were inoculated subcutaneously with 10^5 cfu of the *cas9* deletion strain. Forty-eight hours post infection, spleens were harvested and plated to quantify bacterial levels (n=5). (B, C) Groups of 5 (B) WT or TLR2$^{-/-}$ and (C) WT or ASC$^{-/-}$ mice were inoculated subcutaneously with 10^8 cfu of WT or *cas9* deletion strains. Mice were monitored for survival over 20 days. **; $p \leq 0.005$.

Supplemental Figure 22. ASC and TLR2 control inflammasome activation and cytokine response against *cas9* deletion mutants. (A) Wild-type (WT), TLR2$^{-/-}$, ASC$^{-/-}$ and ASC/TLR2-deficient bone marrow-derived macrophages were infected with wild-type (WT), *cas9*, or *cas9/1103* deletion mutants at a multiplicity of infection (MOI) of 20:1 (bacteria per macrophage). At 5.5 hours post infection, cells were assayed for cytotoxicity using the LDH release assay (n=3). (B) Identical infections as above were

performed and at 4 hours post infection, infection supernatants collected, and ELISA performed for the pro-inflammatory cytokine IL-6 (n=3). *; $p \leq 0.05$, **; $p \leq 0.005$.

Supplemental Figure 23. *Campylobacter jejuni* Cas9 controls envelope permeability and erythromycin resistance. (A) Cultures of wild-type GB11 (WT) and the *cas9* deletion mutant were washed, stained with ethidium bromide, and fluorescence measured (n=4). (B) MIC breakpoints as determined by erythromycin E-test for WT or the *cas9* deletion mutant. ***; $p \leq 0.001$.

Supplemental References

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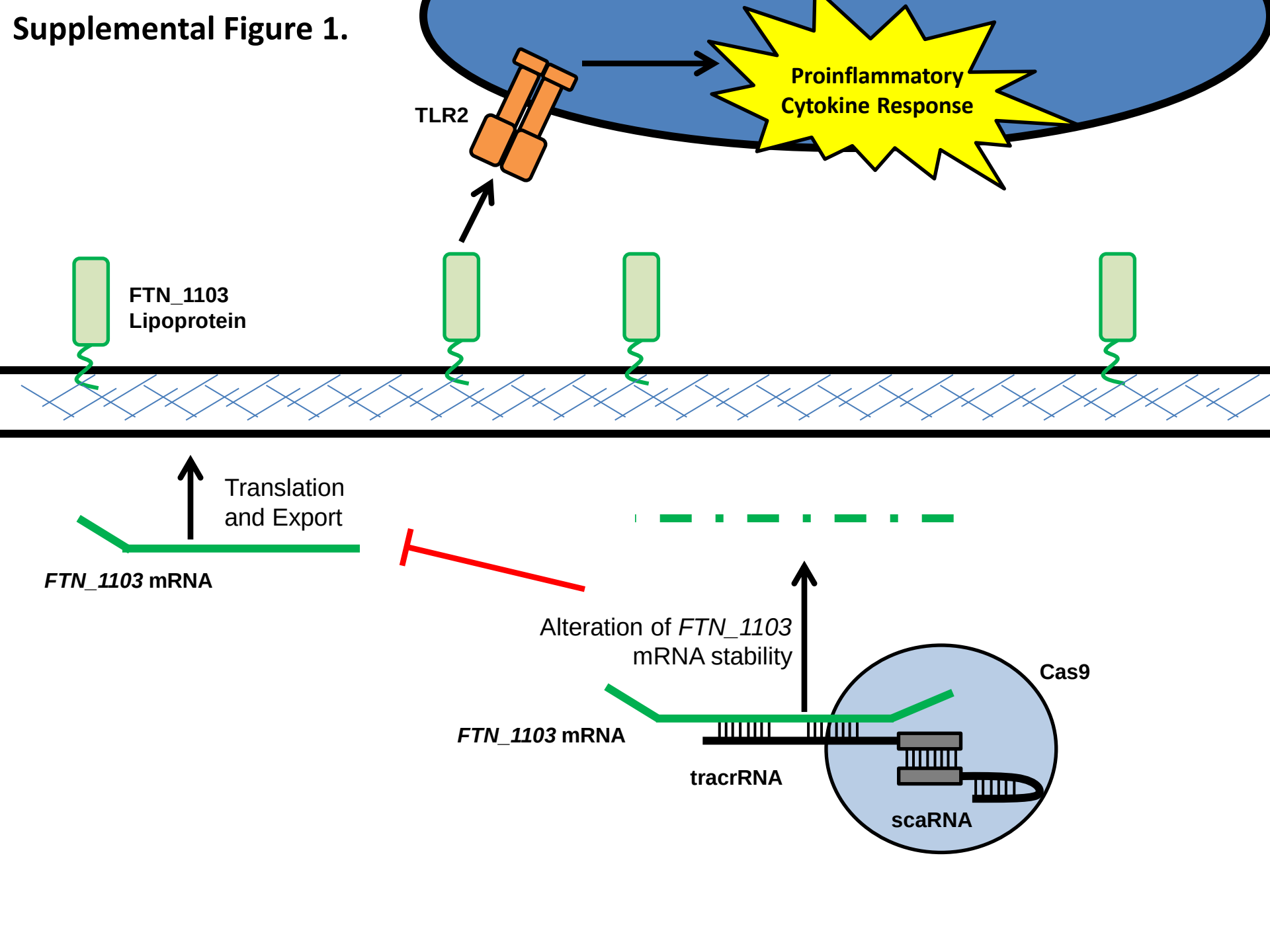
Supplemental Figure 1.



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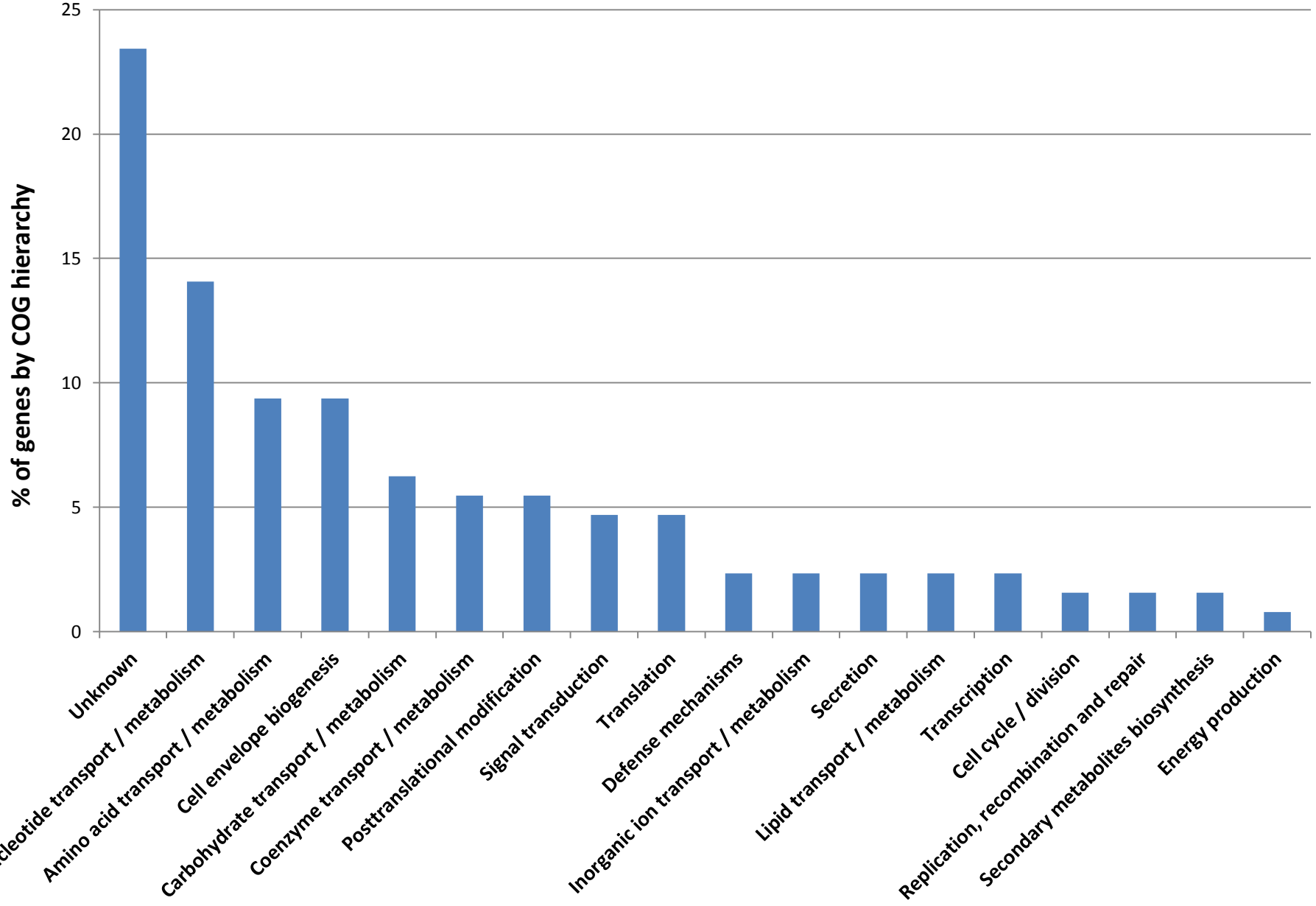

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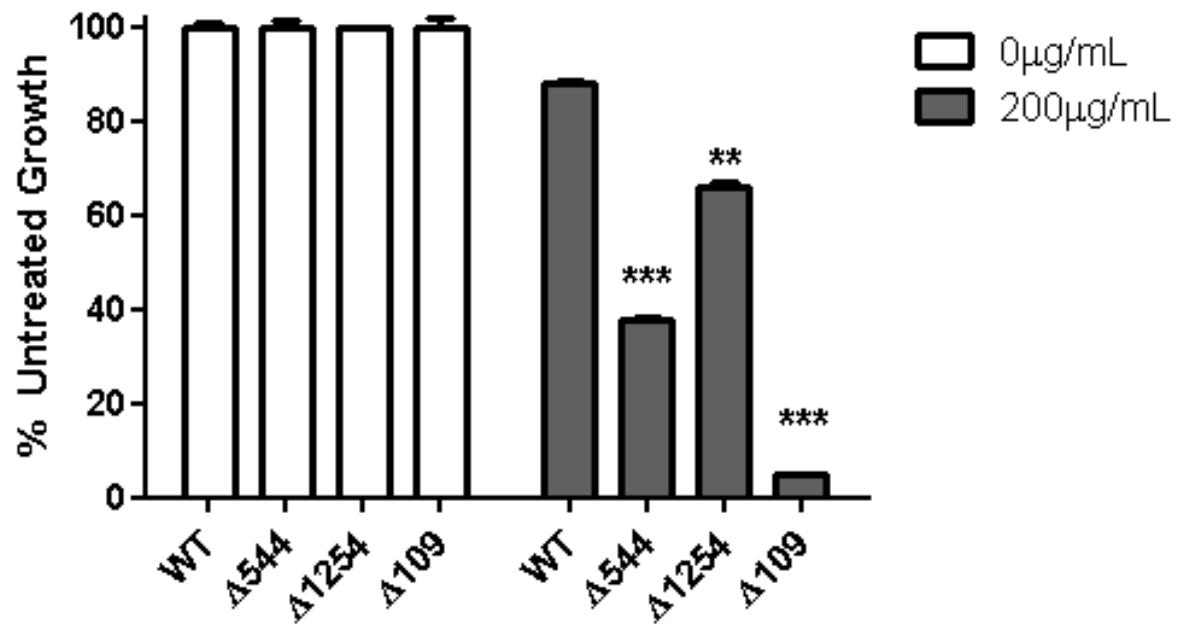

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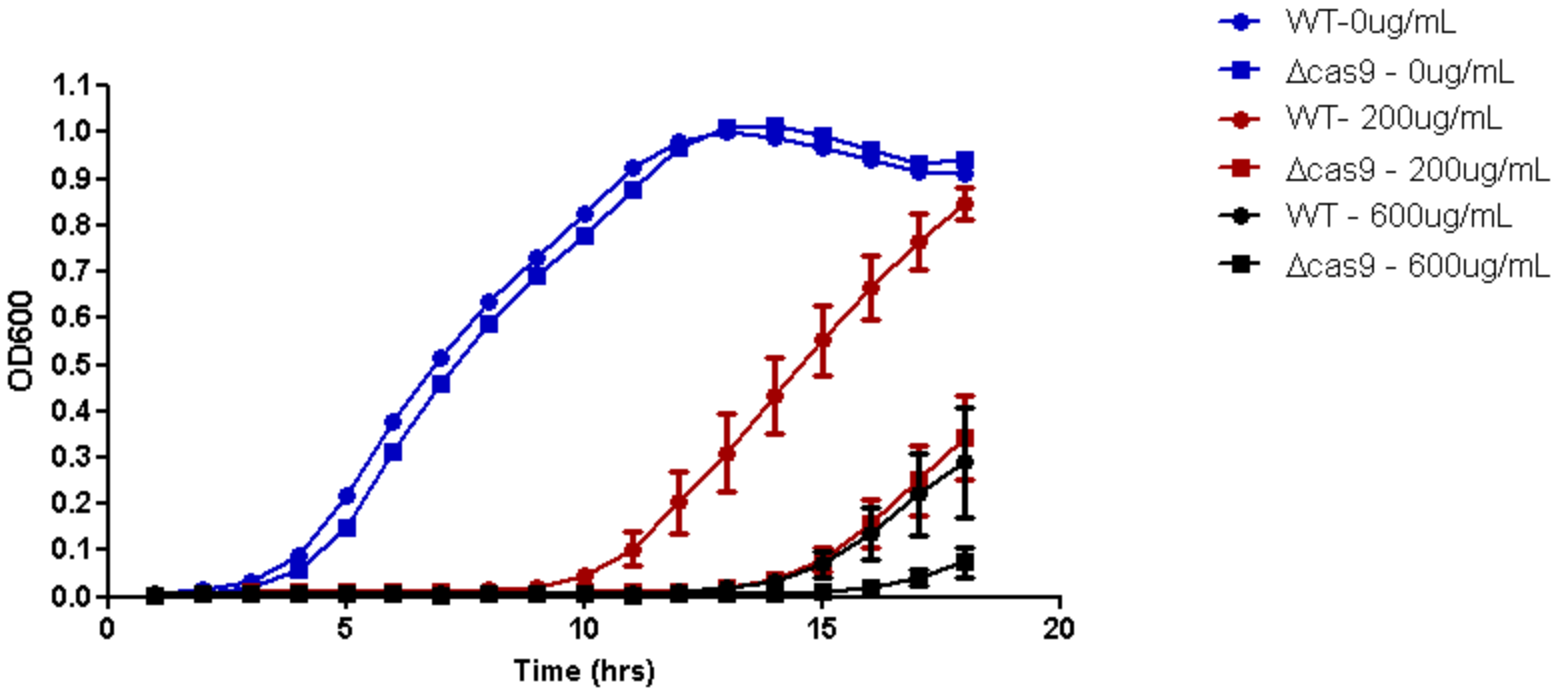

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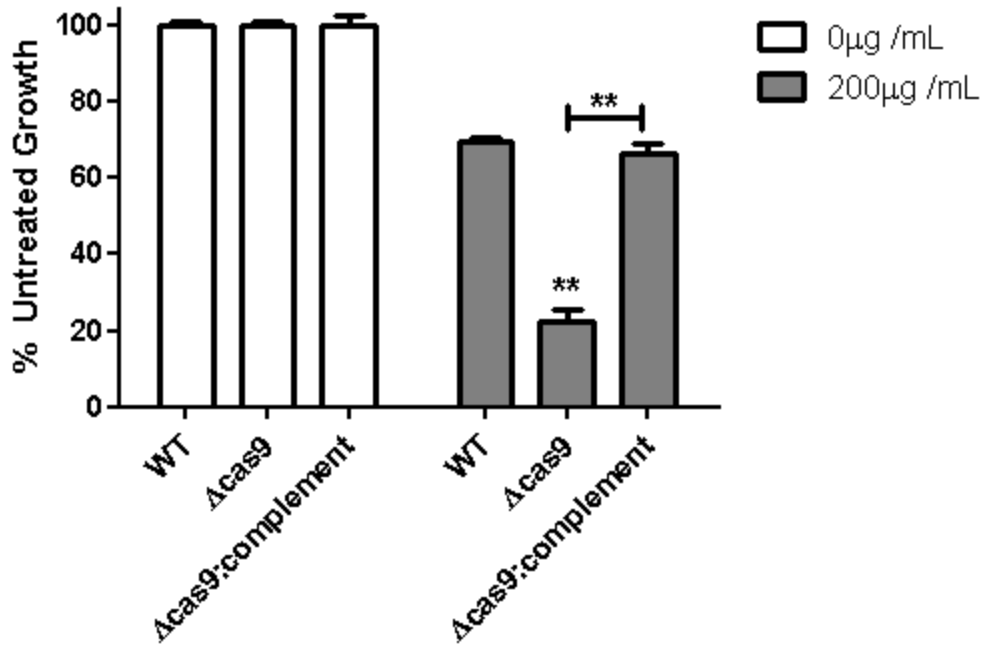

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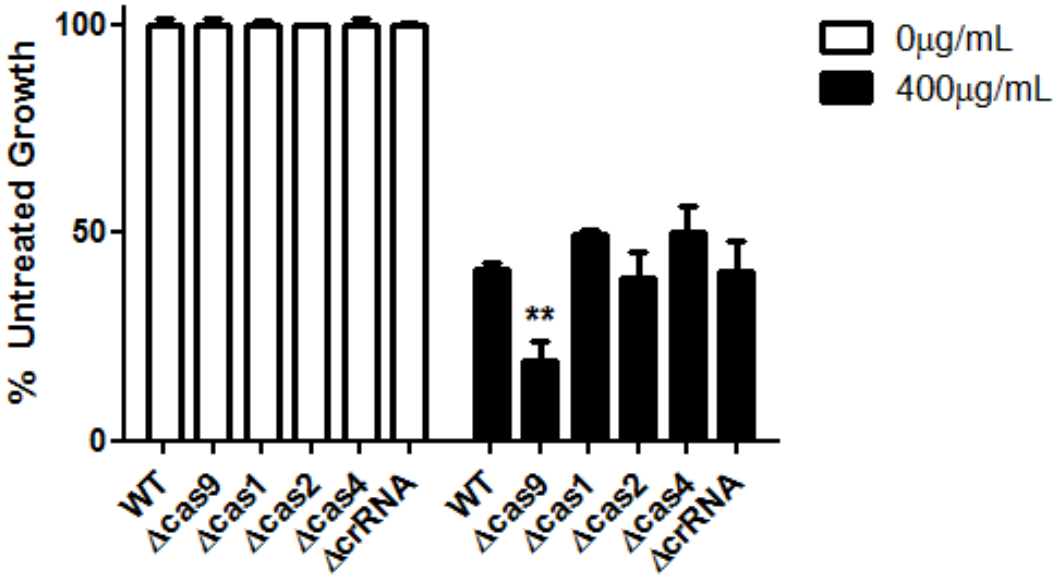

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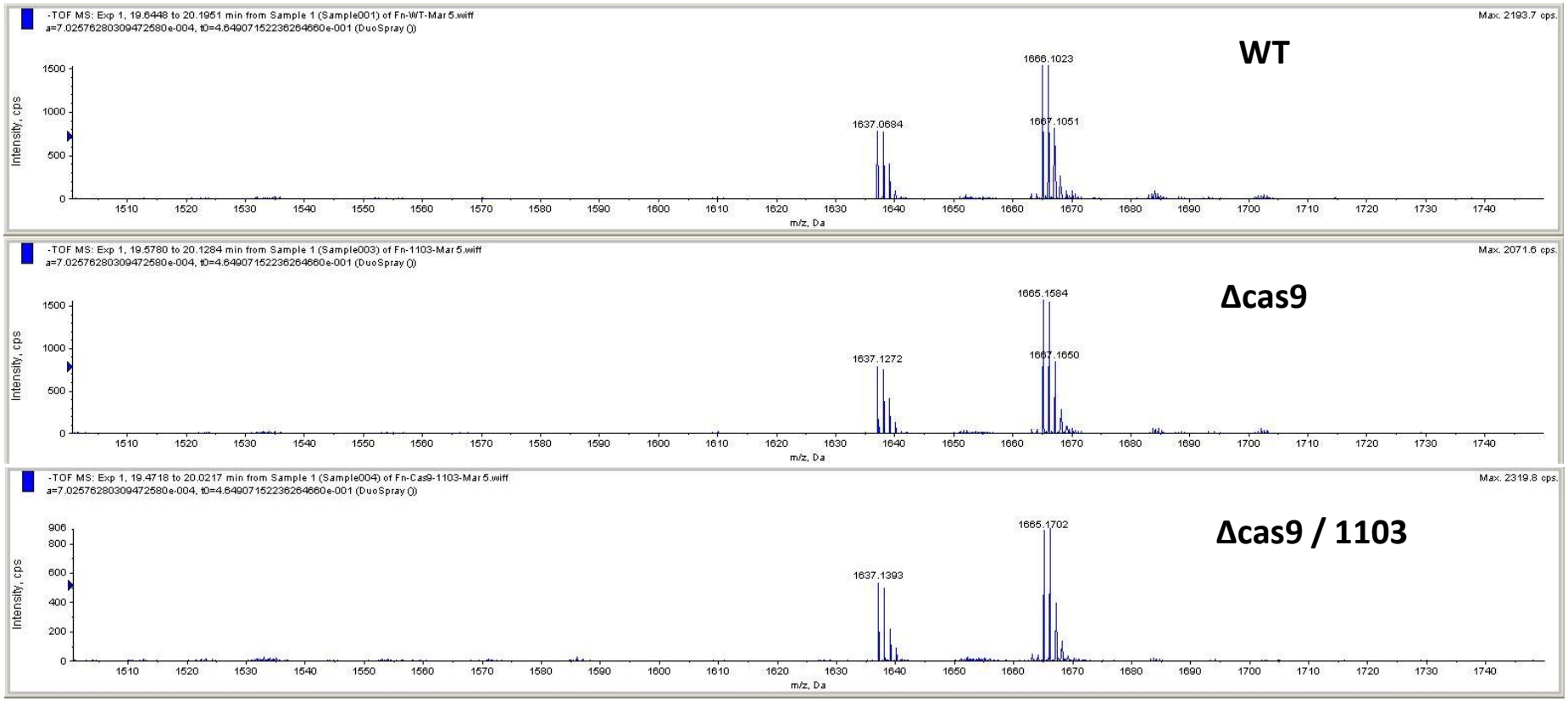

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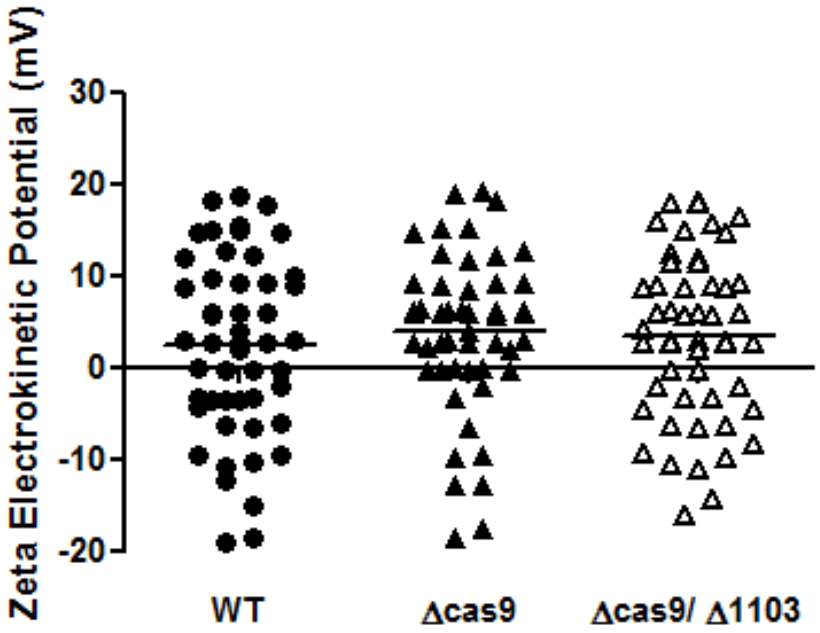

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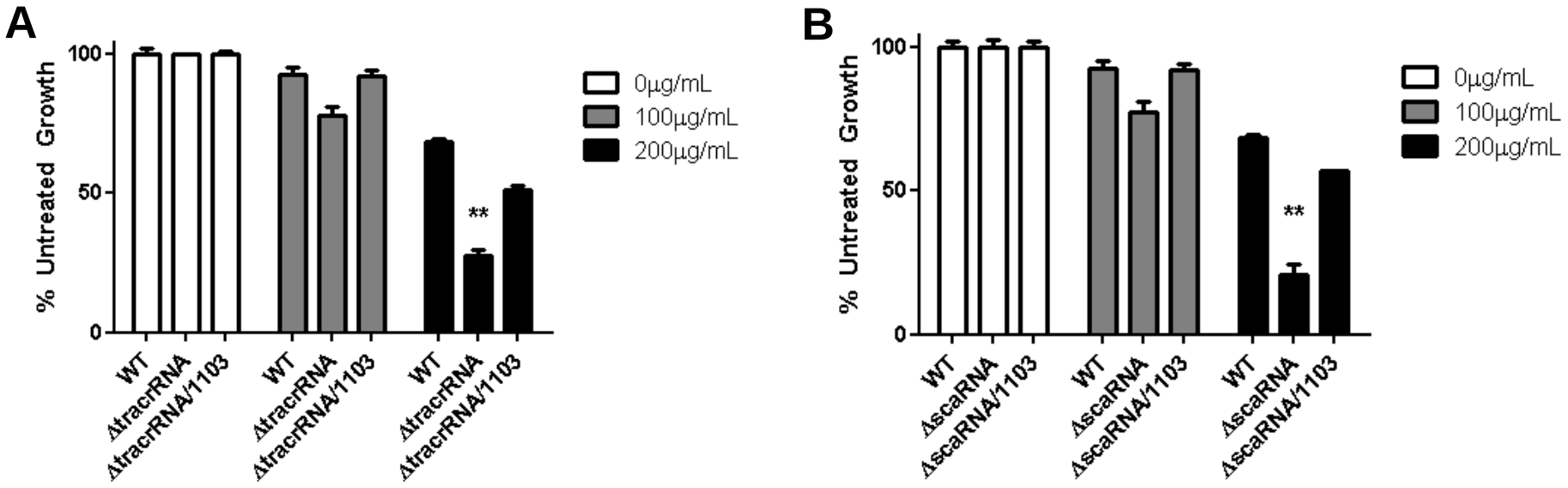

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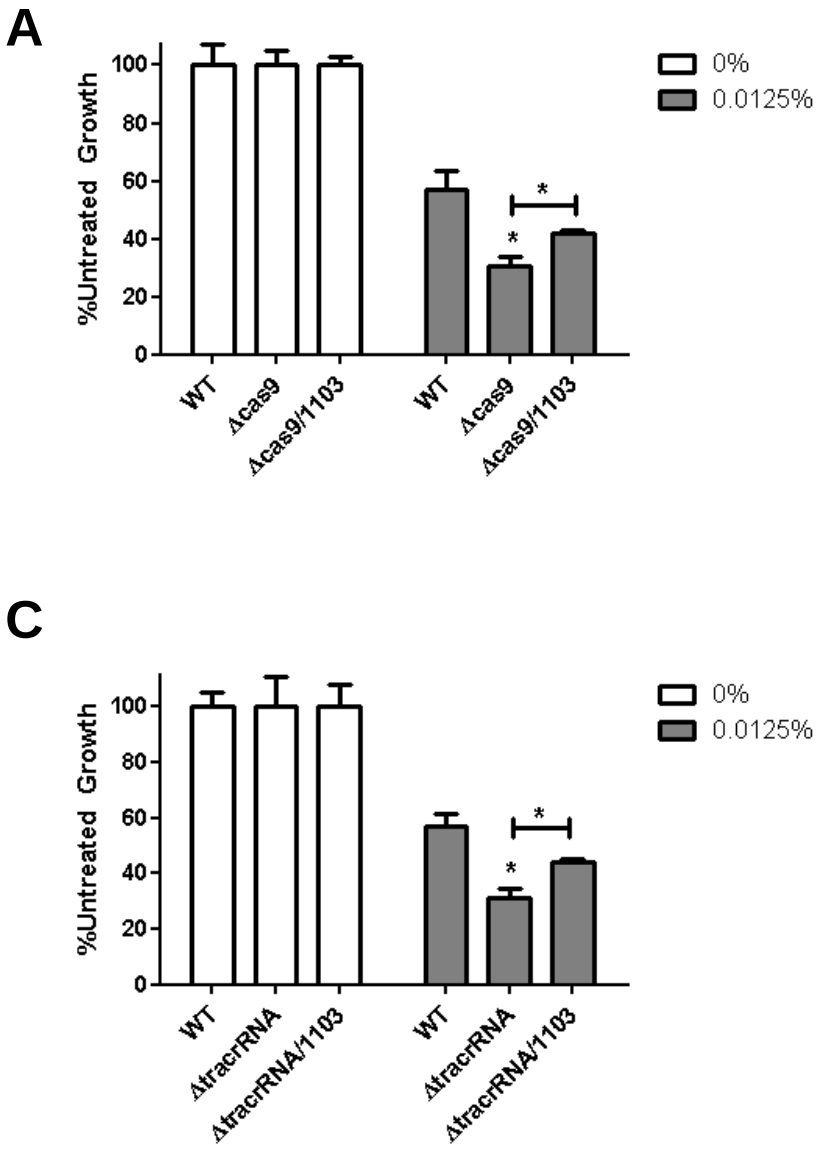

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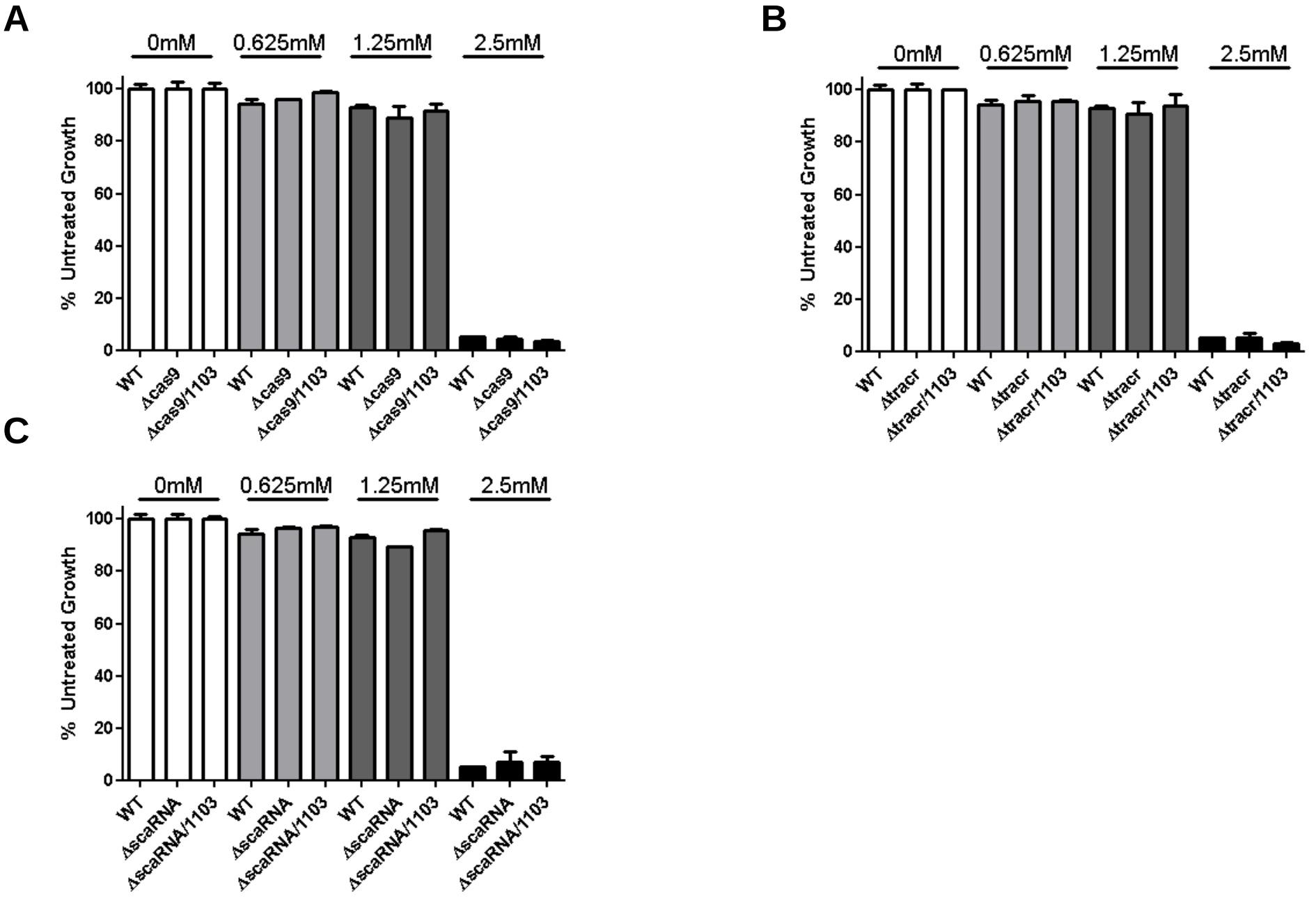

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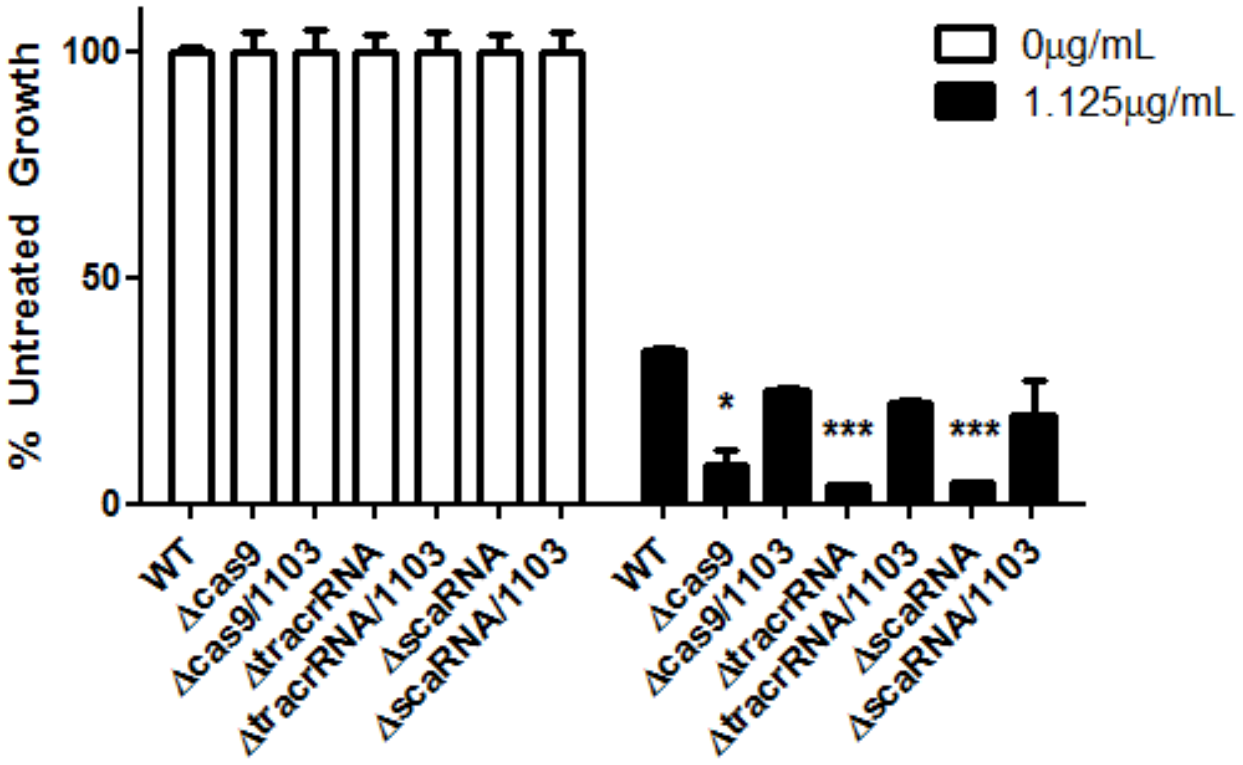

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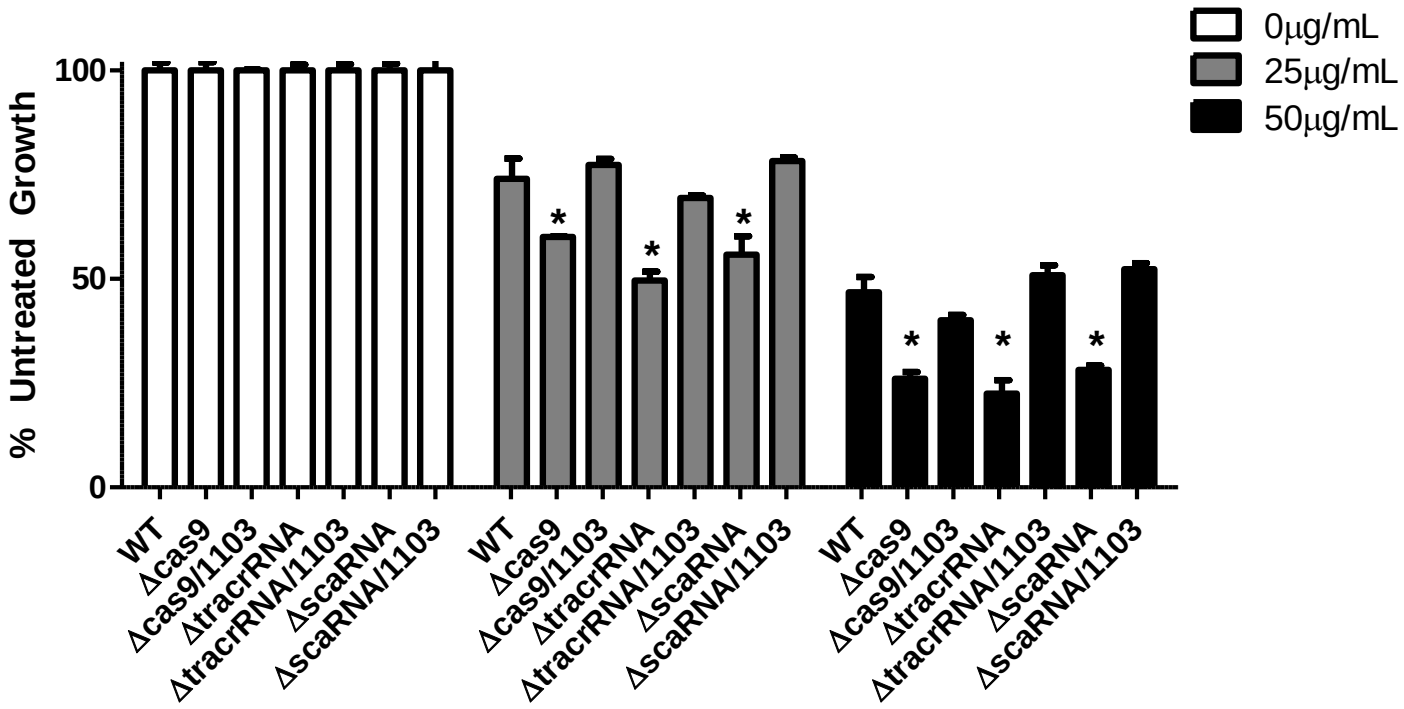

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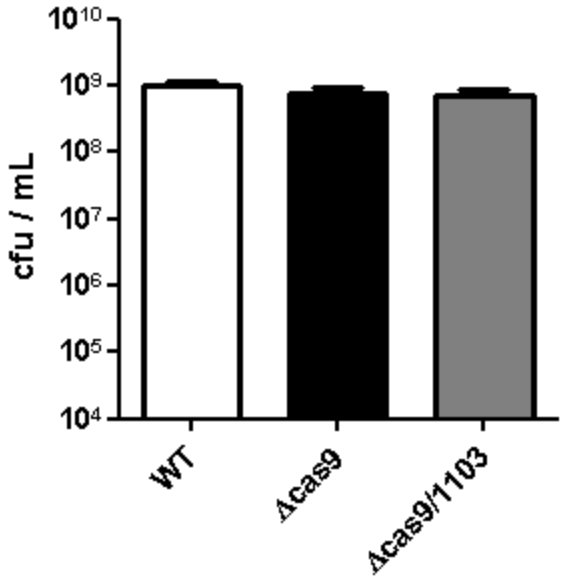

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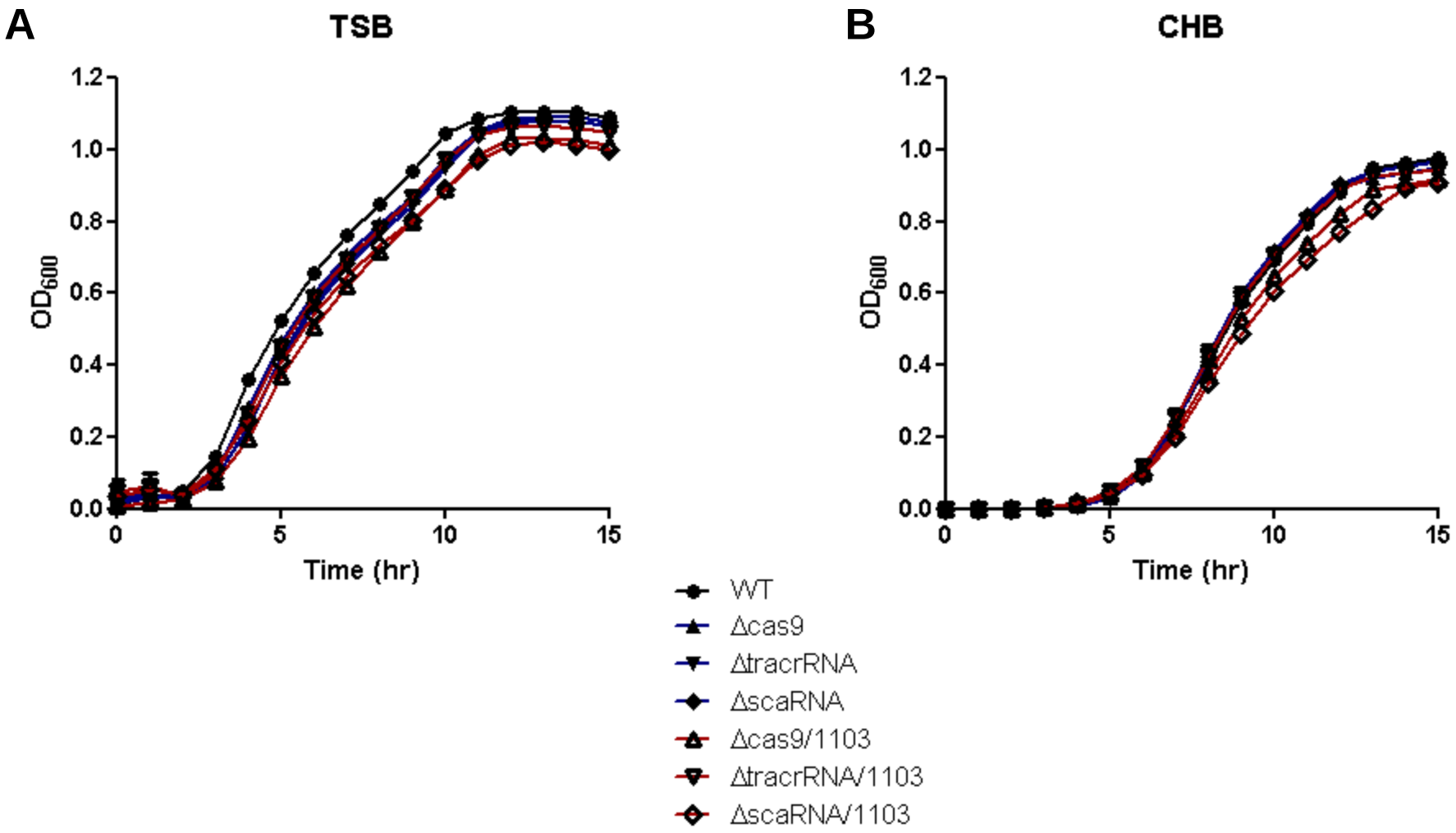

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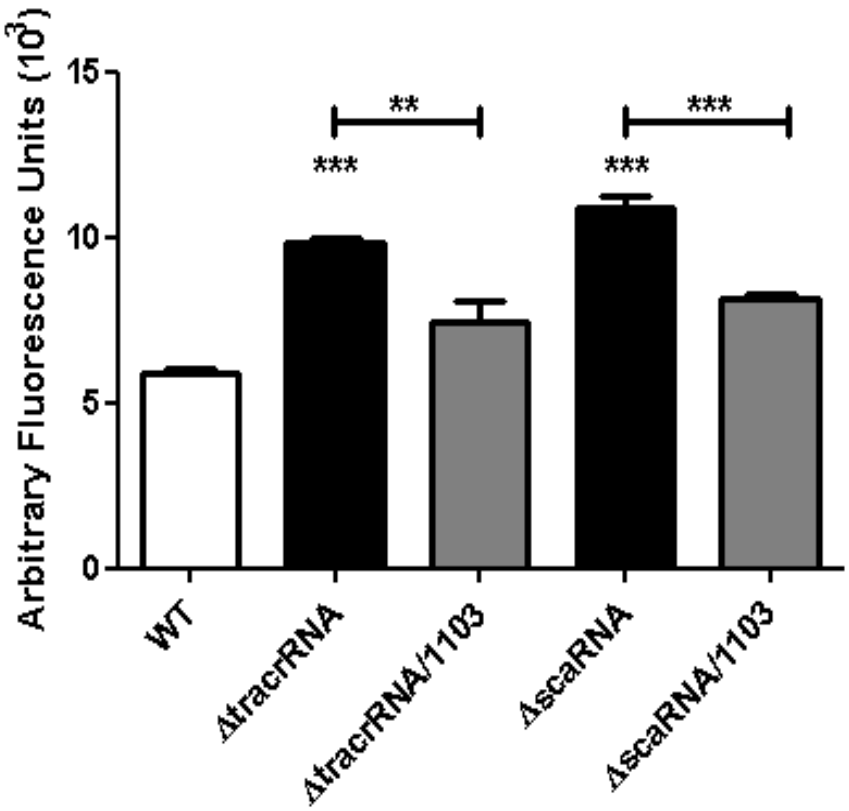

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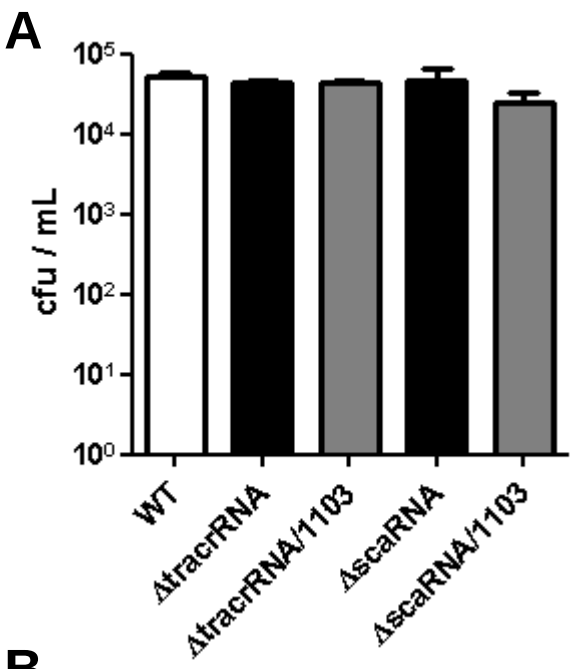

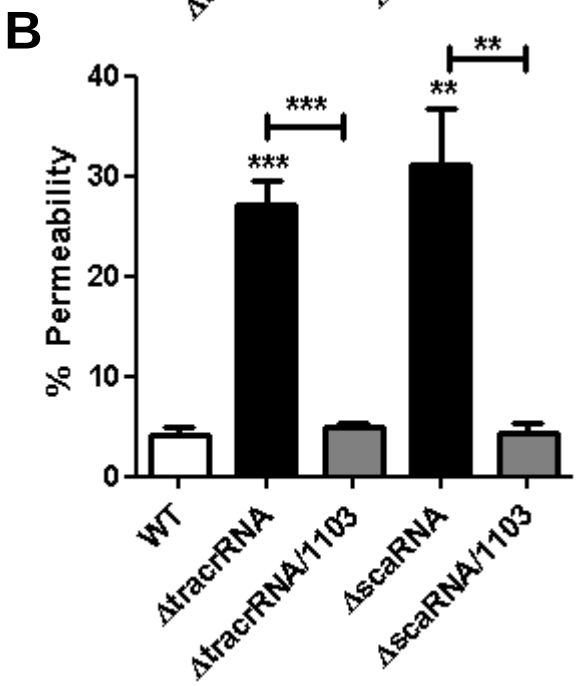

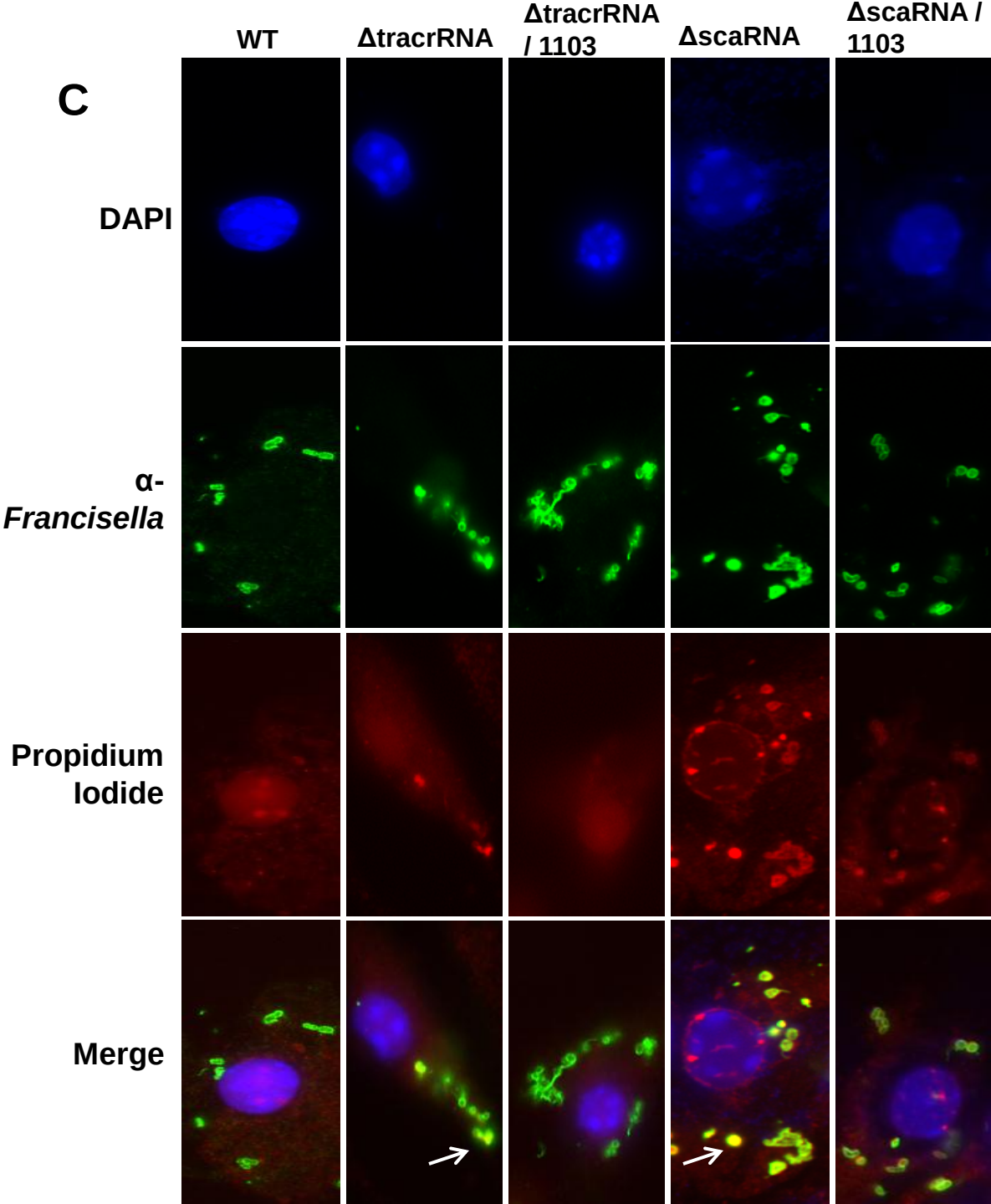

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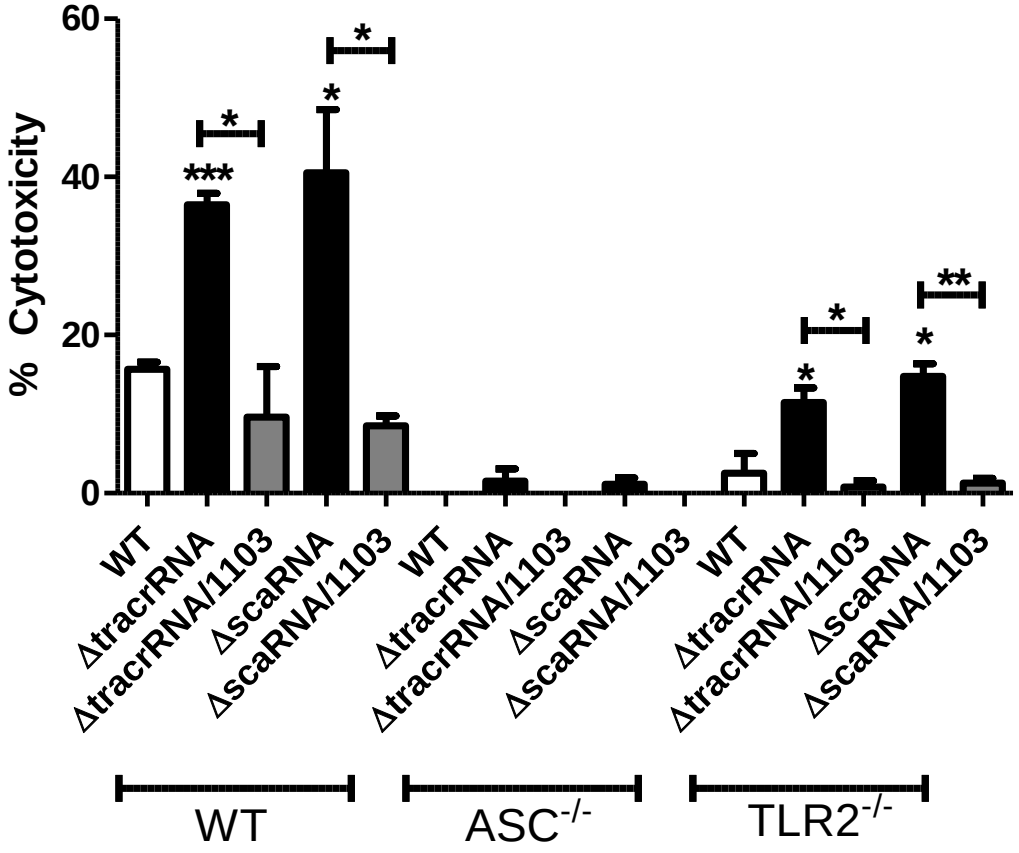

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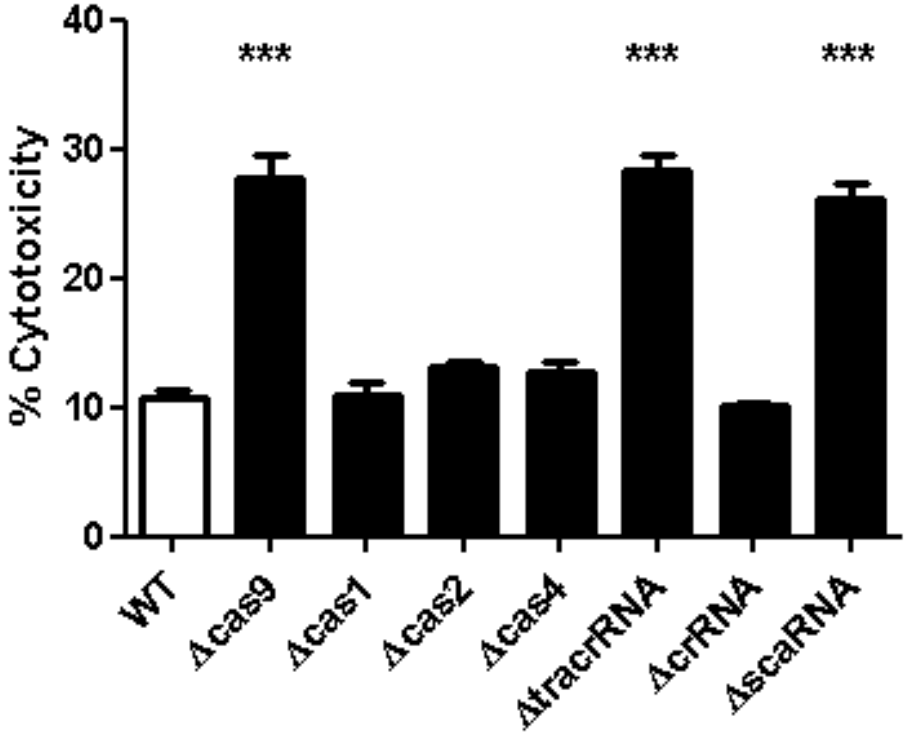

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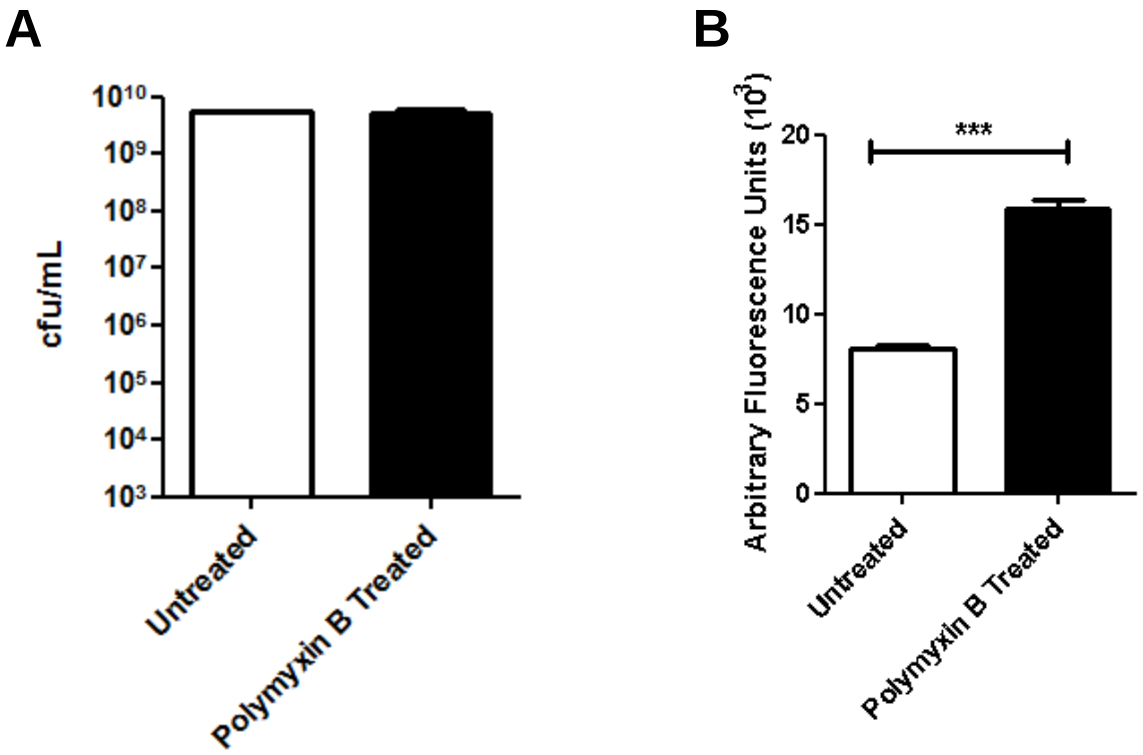
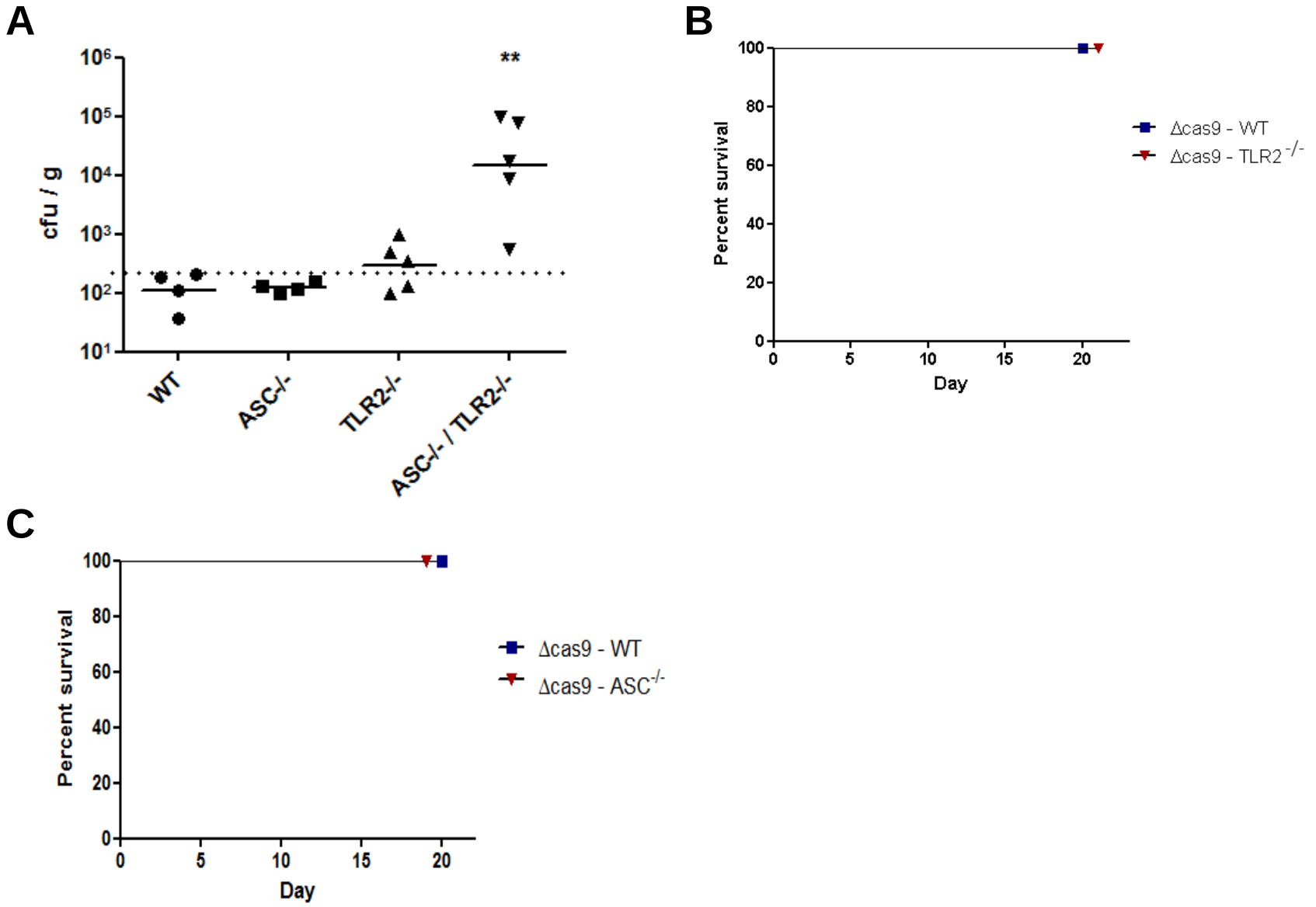
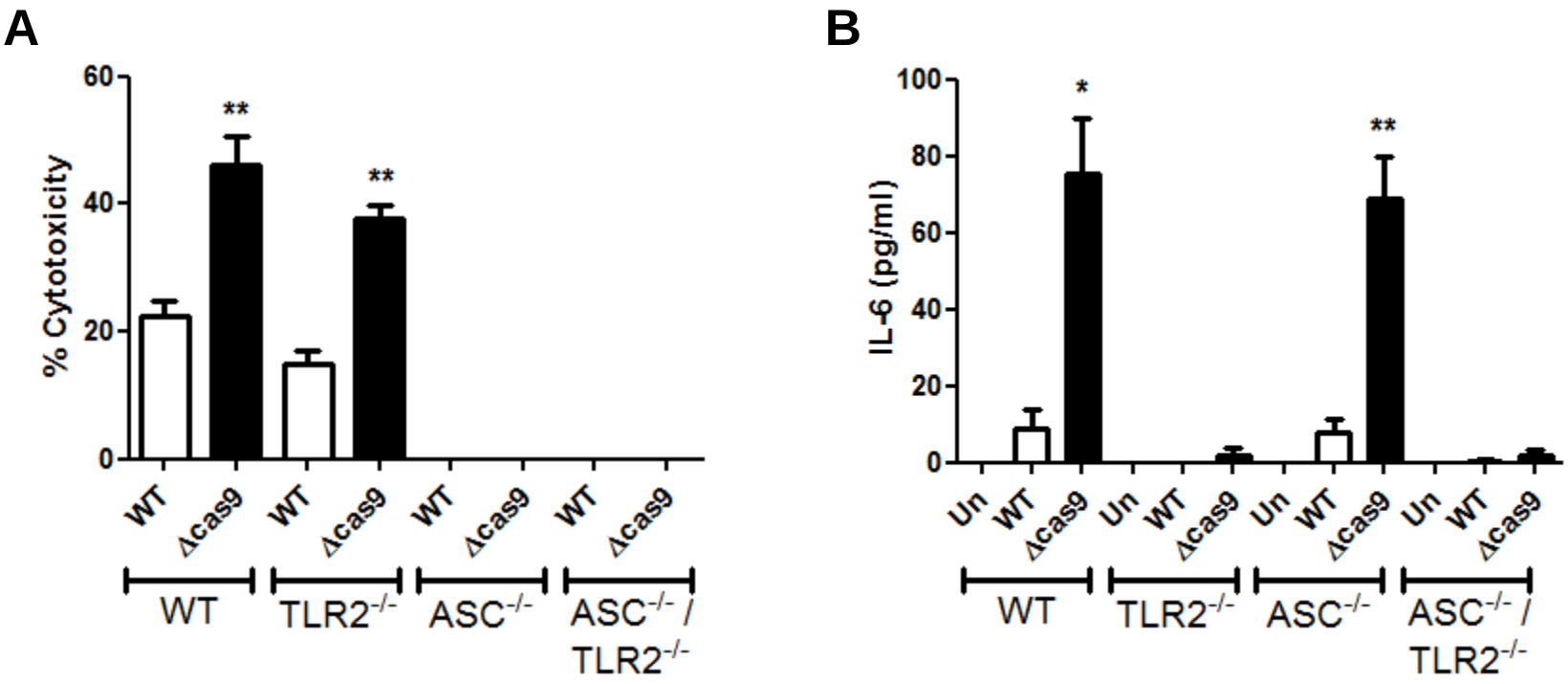


Supplemental Figure 21.

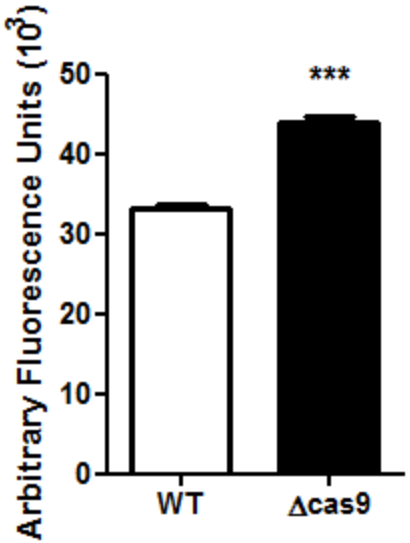


Supplemental Figure 22.

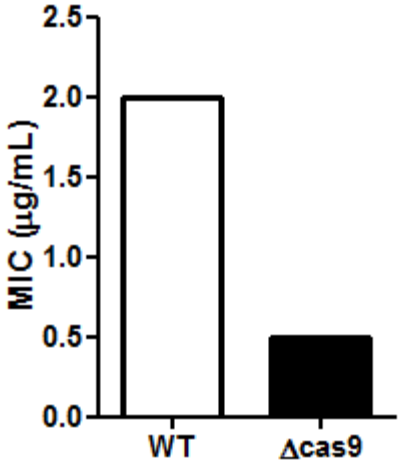


Supplemental Figure 23.

A



B



Supplemental Table 1. Transposon mutants with increased sensitivity to polymyxin B

Locus	Name	COG	Description	% WT Growth in Polymyxin
FTN_0019	*pyrB*	COG0540F	aspartate carbamoyltransferase	68.9
FTN_0021	*carA*	COG0505EF	carbamoyl phosphate synthase small subunit	62.4
FTN_0036	*pyrD*	COG0167F	dihydroorotate oxidase	68.7
FTN_0097	-	COG0814E	hydroxy/aromatic amino acid permease (HAAAP) family protein	73.0
FTN_0098	*gidB*	COG0357M	16S rRNA methyltransferase GidB	69.0
FTN_0109	-	-	hypothetical protein FTN_0109	0.2
FTN_0113	*ribC*	COG0307H	riboflavin synthase subunit alpha	0.0
FTN_0132	-	-	hypothetical protein FTN_0132	63.9
FTN_0177	*purH*	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	70.1
FTN_0178	*purA*	COG0104F	adenylosuccinate synthetase	57.0
FTN_0196	*cyoB*	COG0843C	cytochrome bo terminal oxidase subunit I	73.4
FTN_0197	*cyoC*	COG1845C	cytochrome bo terminal oxidase subunit III	65.7
FTN_0202	*pdxY*	COG2240H	pyridoxal kinase	68.1
FTN_0296	*lysP*	COG0833E	lysine:H+ symporter	28.5
FTN_0298	*glpX*	COG1494G	fructose 1,6-bisphosphatase II	68.5
FTN_0300	-	COG1215M	glycosyl transferase	63.5
FTN_0325	-	COG2854Q	membrane protein	71.9
FTN_0330	*minD*	COG2894D	septum site-determining protein MinD	71.0
FTN_0331	*minC*	COG0850D	septum site-determining protein MinC	64.9

FTN_0358	*rimO*	COG0621J	ribosomal protein S12 methylthiotransferase	73.7
FTN_0416	*lpxE*	COG0671I	lipid A 1-phosphatase	52.6
FTN_0417	*folD*	COG0190H	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohyd...	29.6
FTN_0419	*purM*	COG0150F	phosphoribosylaminoimidazole synthetase	72.6
FTN_0421	*purN*	COG0299F	phosphoribosylglycinamide formyltransferase	70.8
FTN_0422	*purE*	COG0041F	N5-carboxyaminoimidazole ribonucleotide mutase	69.0
FTN_0427	-	-	hypothetical protein FTN_0427	60.6
FTN_0434	*parB*	COG1475K	chromosome partition protein B	68.8
FTN_0436	-	COG3240IR	hypothetical protein FTN_0436	68.4
FTN_0444	-	-	membrane protein	48.1
FTN_0494	-	-	hypothetical protein FTN_0494	62.6
FTN_0495	-	COG4692G	BNR/Asp-box repeat-containing protein	67.0
FTN_0507	*gcvP1*	COG0403E	glycine dehydrogenase subunit 1	72.2
FTN_0514	*pgm*	COG0033G	phosphoglucomutase	61.9
FTN_0515	*glgC*	COG0448G	glucose-1-phosphate adenylyltransferase	55.6
FTN_0534	-	COG1289S	hypothetical protein FTN_0534	74.4
FTN_0544	*naxD*	COG3394S	N-acetylhexosamine deacetylase	36.5
FTN_0545	-	COG0463M	glycosyl transferase	4.3
FTN_0546	-	COG1807M	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	1.0
FTN_0554	-	COG0219J	RNA methyltransferase	57.3
FTN_0561	*apaH*	COG0639T	diadenosine tetraphosphatase	53.7

FTN_0593	*sucD*	COG0074C	succinyl-CoA synthetase, alpha subunit	72.0
FTN_0594	*sucC*	COG0045C	succinyl-CoA synthetase subunit beta	63.5
FTN_0599	-	-	hypothetical protein FTN_0599	55.6
FTN_0624	-	COG0814E	serine permease	74.0
FTN_0651	*cdd*	COG0295F	cytidine deaminase	69.0
FTN_0669	*deoD*	COG0813F	purine nucleoside phosphorylase	65.0
FTN_0672	*secA*	COG0653U	preprotein translocase subunit SecA	66.8
FTN_0690	*deaD*	COG0513LKJ	DEAD/DEAH box helicase	73.3
FTN_0719	-	-	hypothetical protein FTN_0719	60.9
FTN_0728	-	COG0053P	Co/Zn/Cd cation transporter	73.4
FTN_0757	*cas9*	-	CRISPR/Cas associated protein	69.9
FTN_0772	-	COG0545O	hypothetical protein FTN_0772	72.5
FTN_0806	-	COG1472G	glycosyl hydrolase family protein	60.0
FTN_0814	*bioF*	COG0156H	8-amino-7-oxononanoate synthase	73.1
FTN_0815	*bioB*	COG0502H	biotin synthase	74.4
FTN_0816	*bioA*	COG0161H	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	66.8
FTN_0842	*aroG*	COG0722E	phospho-2-dehydro-3-deoxyheptonate aldolase	68.3
FTN_0848	-	COG0531E	amino acid antiporter	65.0
FTN_0855	-	-	hypothetical protein FTN_0855	74.0
FTN_0945	*rsuA*	COG1187J	16S rRNA pseudouridine synthase	50.1
FTN_0998	-	COG2898S	potassium channel protein	69.0
FTN_0999	*udhA*	COG1249C	soluble pyridine nucleotide transhydrogenase	71.0

FTN_1016	-	COG1335Q	hypothetical protein FTN_1016	72.6
FTN_1055	*lon*	COG0466O	DNA-binding, ATP-dependent protease La	70.8
FTN_1056	*clpX*	COG1219O	ATP-dependent protease ATP-binding subunit ClpX	5.1
FTN_1057	*clpP*	COG0740OU	ATP-dependent Clp protease proteolytic subunit	64.1
FTN_1058	*tig*	COG0544O	trigger factor	74.0
FTN_1064	-	COG1702T	PhoH family protein ATPase	72.5
FTN_1066	-	COG4535P	HlyC/CorC family transporter-associated protein	68.2
FTN_1091	*aroA*	COG0128E	3-phosphoshikimate 1-carboxyvinyltransferase	59.4
FTN_1107	*metIQ*	COG1464P	methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	69.7
FTN_1111	-	COG0769M	Mur ligase family protein	64.3
FTN_1133	-	-	Ohr-like protein	72.3
FTN_1146	-	COG0436E	aspartate aminotransferase	68.2
FTN_1199	-	-	hypothetical protein FTN_1199	70.9
FTN_1201	*capB*	COG0769M	capsule biosynthesis protein CapB	70.7
FTN_1211	-	COG1011R	haloacid dehalogenase-like hydrolase	74.2
FTN_1212	-	COG0438M	glycosyl transferases group 1 family protein	73.3
FTN_1213	-	COG1215M	glycosyl transferase family protein	65.5
FTN_1217	-	COG1132V	ABC transporter ATP-binding protein	74.0
FTN_1219	*galE*	COG1087M	UDP-glucose 4-epimerase	63.7
FTN_1240	-	COG0271T	hypothetical protein FTN_1240	50.7
FTN_1240	-	COG0271T	hypothetical protein FTN_1240	64.4

FTN_1254	-	-	hypothetical protein FTN_1254	64.7
FTN_1263	*comL*	COG4105R	competence lipoprotein ComL	73.0
FTN_1272	-	COG3104E	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	68.0
FTN_1277	-	COG1538MU	outer membrane efflux protein	59.5
FTN_1311	-	-	hypothetical protein FTN_1311	67.0
FTN_1312	-	-	hypothetical protein FTN_1312	74.7
FTN_1313	-	-	hypothetical protein FTN_1313	52.5
FTN_1314	-	-	hypothetical protein FTN_1314	70.9
FTN_1315	-	-	hypothetical protein FTN_1315	71.8
FTN_1316	-	COG3455S	hypothetical protein FTN_1316	74.2
FTN_1317	-	-	hypothetical protein FTN_1317	70.2
FTN_1323	*iglB*	COG3517S	intracellular growth locus protein B	74.7
FTN_1421	*wbtH*	COG0367E	glutamine amidotransferase/asparagine synthase	72.5
FTN_1425	*wbtF*	COG0451MG	NAD dependent epimerase	67.8
FTN_1427	*wbtD*	COG0438M	group 1 glycosyl transferase	59.5
FTN_1470	*ispA*	COG0142H	geranyl diphosphate synthase/farnesyl diphosphate synthase	2.0
FTN_1471	*pcs*	COG1183I	phosphatidylcholine synthase	73.8
FTN_1500	-	-	hypothetical protein FTN_1500	66.5
FTN_1513	*xerC*	COG4973L	site-specific recombinase	73.6
FTN_1518	*relA*	COG0317TK	GDP pyrophosphokinase/GTP pyrophosphokinase	68.7
FTN_1538	*groEL*	COG0459O	chaperonin GroEL	71.5
FTN_1551	*ampD*	COG3023V	N-acetyl-anhydromuramyl-L-alanine amidase	57.8
FTN_1597	*prfC*	COG4108J	peptide chain release factor 3	57.0
FTN_1602	*deoB*	COG1015G	phosphopentomutase	74.5
FTN_1610	-	COG0841V	RND efflux transporter	74.4

FTN_1633	*apt*	COG0503F	adenine phosphoribosyltransferase	60.2
FTN_1653	-	-	hypothetical protein FTN_1653	74.7
FTN_1699	*purL*	COG0046F	phosphoribosylformylglycinamidine synthase	66.0
FTN_1700	*purF*	COG0034F	amidophosphoribosyltransferase	73.8
FTN_1715	*kdpD*	COG2205T	two component regulator, sensor histidine kinase kdpD	61.7
FTN_1743	*clpB*	COG0542O	chaperone clpB	70.5
FTN_1745	*purT*	COG0027F	phosphoribosylglycinamide formyltransferase 2	72.2
FTN_1762	-	COG0488R	putative ABC transporter ATP-binding protein	68.5

Supplemental Table 2. Percent wild-type growth of each transposon mutant in polymyxin B

Locus Tag	Gene name	COG	Gene product	% WT growth in polymyxin	Library Plate	Well
FTN_0113	*ribC*	COG0307H	riboflavin synthase subunit alpha	0	NR-8043	E03
FTN_0109	-	-	hypothetical protein FTN_0109	0.2	NR-8048	G06
FTN_0546	-	COG1807M	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	1.0	NR-8060	A06
FTN_1470	*ispA*	COG0142H	geranyl diphosphate synthase/farnesyl diphosphate synthase	2.0	NR-8058	F05
FTN_0113	*ribC*	COG0307H	riboflavin synthase subunit alph	4.0	NR-8060	C12
FTN_0545	-	COG0463M	glycosyl transferase	4.3	NR-8040	D09
FTN_1056	*clpX*	COG1219O	ATP-dependent protease ATP-binding subunit ClpX	5.1	NR-8061	H09
FTN_0545	-	COG0463M	glycosyl transferase	5.9	NR-8055	G11
FTN_0546	-	COG1807M	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	11.9	NR-8050	D09
FTN_0296	*lysP*	COG0833E	lysine:H+ symporter	28.5	NR-8058	A05
FTN_0417	*folD*	COG0190H	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohyd...	29.6	NR-8047	G04
FTN_0544	*naxD*	COG3394S	N-acetylhexosamine deacteylase	36.5	NR-8055	F02
FTN_0544	*naxD*	COG3394S	N-acetylhexosamine deacteylase	40.6	NR-8052	G01
FTN_0444	-	-	membrane protein	48.1	NR-8061	C10
FTN_0945	*rsuA*	COG1187J	16S rRNA pseudouridine synthase	50.1	NR-8064	E06
FTN_1240	-	COG0271T	hypothetical protein FTN_1240	50.7	NR-8058	C11
FTN_0444	-	-	membrane protein	51.4	NR-8047	C03
FTN_1313	-	-	hypothetical protein FTN_1313	52.5	NR-8046	F07
FTN_0416	*lpxE*	COG0671I	lipid A 1-phosphatase	52.6	NR-8043	E11
FTN_0561	*apaH*	COG0639T	diadenosine tetraphosphatase	53.7	NR-8056	H07
FTN_0599	-	-	hypothetical protein FTN_0599	55.6	NR-8052	G11
FTN_0515	*glgC*	COG0448G	glucose-1-phosphate adenylyltransferase	55.6	NR-8046	F05
FTN_1597	*prfC*	COG4108J	peptide chain release factor 3	57.0	NR-8063	F06
FTN_0178	*purA*	COG0104F	adenylosuccinate synthetase	57.0	NR-8037	A05

FTN_0554	-	COG0219J	RNA methyltransferase	57.3	NR-8049	F08
FTN_1551	*ampD*	COG3023V	N-acetyl-anhydromuranmyl-L-alanine amidase	57.8	NR-8048	E10
FTN_0178	*purA*	COG0104F	adenylosuccinate synthetase	59.2	NR-8065	G11
FTN_1091	*aroA*	COG0128E	3-phosphoshikimate 1-carboxyvinyltransferase	59.4	NR-8064	E08
FTN_1277	-	COG1538MU	outer membrane efflux protein	59.5	NR-8049	G08
FTN_1427	*wbtD*	COG0438M	group 1 glycosyl transferase	59.5	NR-8065	G01
FTN_0806	-	COG1472G	glycosyl hydrolase family protein	60.0	NR-8065	C03
FTN_1633	*apt*	COG0503F	adenine phosphoribosyltransferase	60.2	NR-8064	G01
FTN_0427	-	-	hypothetical protein FTN_0427	60.6	NR-8036	D12
FTN_0513	*glgB*	COG0296G	glycogen branching protein	60.9	NR-8066	D01
FTN_0719	-	-	hypothetical protein FTN_0719	60.9	NR-8047	A05
FTN_1715	*kdpD*	COG2205T	two component regulator, sensor histidine kinase kdpD	61.7	NR-8065	D11
FTN_0416	*lpxE*	COG0671I	lipid A 1-phosphatase	61.8	NR-8054	B11
FTN_0514	*pgm*	COG0033G	phosphoglucomutase	61.9	NR-8064	H04
FTN_0021	*carA*	COG0505EF	carbamoyl phosphate synthase small subunit	62.4	NR-8064	D08
FTN_0494	-	-	hypothetical protein FTN_0494	62.6	NR-8036	D02
FTN_0594	*sucC*	COG0045C	succinyl-CoA synthetase subunit beta	63.5	NR-8040	G06
FTN_0300	-	COG1215M	glycosyl transferase	63.5	NR-8060	F06
FTN_1219	*galE*	COG1087M	UDP-glucose 4-epimerase	63.7	NR-8064	C10
FTN_0132	-	-	hypothetical protein FTN_0132	63.9	NR-8036	A02
FTN_1057	*clpP*	COG0740OU	ATP-dependent Clp protease proteolytic subunit	64.1	NR-8044	E02
FTN_1111	-	COG0769M	Mur ligase family protein	64.3	NR-8054	B01
FTN_1240	-	COG0271T	hypothetical protein FTN_1240	64.4	NR-8049	E10
FTN_1254	-	-	hypothetical protein FTN_1254	64.7	NR-8065	C05
FTN_0331	*minC*	COG0850D	septum site-determining protein MinC	64.9	NR-8060	F09
FTN_0945	*rsuA*	COG1187J	16S rRNA pseudouridine synthase	65.0	NR-8047	E08
FTN_0848	-	COG0531E	amino acid antiporter	65.0	NR-8054	C07
FTN_0669	*deoD*	COG0813F	purine nucleoside phosphorylase	65.0	NR-8065	E02
FTN_1213	-	COG1215M	glycosyl transferase family protein	65.5	NR-8066	D03
FTN_0296	*lysP*	COG0833E	lysine:H+ symporter	65.7	NR-8058	B04
FTN_0506	*gcvH*	COG0509E	glycine cleavage system H protein	65.7	NR-8061	C05

FTN_0197	*cyoC*	COG1845C	cytochrome bo terminal oxidase subunit III	65.7	NR-8056	C11
FTN_1699	*purL*	COG0046F	phosphoribosylformylglycinamidine synthase	66.0	NR-8065	E03
FTN_0494	-	-	hypothetical protein FTN_0494	66.5	NR-8057	B06
FTN_1500	-	-	hypothetical protein FTN_1500	66.5	NR-8064	C05
FTN_0672	*secA*	COG0653U	preprotein translocase subunit SecA	66.8	NR-8046	G03
FTN_0816	*bioA*	COG0161H	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	66.8	NR-8047	H01
FTN_0495	-	COG4692G	BNR/Asp-box repeat-containing protein	67.0	NR-8048	H03
FTN_1311	-	-	hypothetical protein FTN_1311	67.0	NR-8051	G10
FTN_1357	*recB*	COG1074L	ATP-dependent exonuclease V subunit beta	67.2	NR-8053	B08
FTN_1056	*clpX*	COG1219O	ATP-dependent protease ATP-binding subunit ClpX	67.3	NR-8036	A06
FTN_0561	*apaH*	COG0639T	diadenosine tetraphosphatase	67.4	NR-8056	H07
FTN_1551	*ampD*	COG3023V	N-acetyl-anhydromuranmyl-L-alanine amidase	67.7	NR-8066	E04
FTN_0296	*lysP*	COG0833E	lysine:H+ symporter	67.7	NR-8046	E12
FTN_1425	*wbtF*	COG0451MG	NAD dependent epimerase	67.8	NR-8066	E05
FTN_1272	-	COG3104E	proton-dependent oligopeptide transporter (POT) family protein, di- or tripeptide:H+ symporter	68.0	NR-8050	B10
FTN_0202	*pdxY*	COG2240H	pyridoxal kinase	68.1	NR-8054	D06
FTN_1066	-	COG4535P	HlyC/CorC family transporter-associated protein	68.2	NR-8062	G03
FTN_1146	-	COG0436E	aspartate aminotransferase	68.2	NR-8036	B07
FTN_0842	*aroG*	COG0722E	phospho-2-dehydro-3-deoxyheptonate aldolase	68.3	NR-8066	G04
FTN_0436	-	COG3240IR	hypothetical protein FTN_0436	68.4	NR-8062	C03
FTN_0848	-	COG0531E	amino acid antiporter	68.4	NR-8036	D05
FTN_0298	*glpX*	COG1494G	fructose 1,6-bisphosphatase II	68.5	NR-8056	D09
FTN_1762	-	COG0488R	putative ABC transporter ATP-binding protein	68.5	NR-8058	F09
FTN_0036	*pyrD*	COG0167F	dihydroorotate oxidase	68.7	NR-8066	G12
FTN_1518	*relA*	COG0317TK	GDP pyrophosphokinase/GTP pyrophosphokinase	68.7	NR-8055	F10
FTN_1091	*aroA*	COG0128E	3-phosphoshikimate 1-carboxyvinyltransferase	68.7	NR-8058	D09
FTN_0434	*parB*	COG1475K	chromosome partition protein B	68.8	NR-8065	H12
FTN_0019	*pyrB*	COG0540F	aspartate carbamoyltransferase	68.9	NR-8037	C03
FTN_0098	*gidB*	COG0357M	16S rRNA methyltransferase GidB	69.0	NR-8055	D05
FTN_0651	*cdd*	COG0295F	cytidine deaminase	69.0	NR-8055	D09

FTN_0422	*purE*	COG0041F	N5-carboxyaminoimidazole ribonucleotide mutase	69.0	NR-8066	H09
FTN_0998	-	COG2898S	potassium channel protein	69.0	NR-8059	C12
FTN_1470	*ispA*	COG0142H	geranyl diphosphate synthase/farnesyl diphosphate synthase	69.2	NR-8046	B03
FTN_1107	*metlQ*	COG1464P	methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	69.7	NR-8054	G08
FTN_0098	*gidB*	COG0357M	16S rRNA methyltransferase GidB	69.8	NR-8046	C06
FTN_0757	*cas9*	-	CRISPR/Cas associated protein	69.9	NR-8058	H09
FTN_1715	*kdpD*	COG2205T	two component regulator, sensor histidine kinase kdpD	69.9	NR-8043	H03
FTN_1038	-	COG0670R	hypothetical protein FTN_1038	70.0	NR-8056	H01
FTN_0177	*purH*	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	70.1	NR-8046	D12
FTN_0554	-	COG0219J	RNA methyltransferase	70.1	NR-8066	A05
FTN_1317	-	-	hypothetical protein FTN_1317	70.2	NR-8062	E10
FTN_0757	*cas9*	-	CRISPR/Cas associated protein	70.3	NR-8056	D11
FTN_1743	*clpB*	COG0542O	chaperone clpB	70.5	NR-8064	F04
FTN_1201	*capB*	COG0769M	capsule biosynthesis protein CapB	70.7	NR-8053	E03
FTN_0421	*purN*	COG0299F	phosphoribosylglycinamide formyltransferase	70.8	NR-8064	D04
FTN_1055	*lon*	COG0466O	DNA-binding, ATP-dependent protease La	70.8	NR-8045	E04
FTN_1199	-	-	hypothetical protein FTN_1199	70.9	NR-8054	G10
FTN_1314	-	-	hypothetical protein FTN_1314	70.9	NR-8054	A06
FTN_0330	*minD*	COG2894D	septum site-determining protein MinD	71.0	NR-8043	D01
FTN_0999	*udhA*	COG1249C	soluble pyridine nucleotide transhydrogenase	71.0	NR-8053	G08
FTN_1057	*clpP*	COG0740OU	ATP-dependent Clp protease proteolytic subunit	71.3	NR-8057	D05
FTN_1538	*groEL*	COG0459O	chaperonin GroEL	71.5	NR-8047	E04
FTN_0515	*glgC*	COG0448G	glucose-1-phosphate adenylyltransferase	71.6	NR-8065	C02
FTN_1315	-	-	hypothetical protein FTN_1315	71.8	NR-8062	A05
FTN_0325	-	COG2854Q	membrane protein	71.9	NR-8053	E09
FTN_0593	*sucD*	COG0074C	succinyl-CoA synthetase, alpha subunit	72.0	NR-8044	A06
FTN_0507	*gcvP1*	COG0403E	glycine dehydrogenase subunit 1	72.2	NR-8063	H03

FTN_1745	*purT*	COG0027F	phosphoribosylglycinamide formyltransferase 2	72.2	NR-8063	H08
FTN_1133	-	-	Ohr-like protein	72.3	NR-8046	E04
FTN_1357	*recB*	COG1074L	ATP-dependent exonuclease V subunit beta	72.3	NR-8042	E09
FTN_1064	-	COG1702T	PhoH family protein ATPase	72.5	NR-8035	A04
FTN_0772	-	COG0545O	hypothetical protein FTN_0772	72.5	NR-8056	C02
FTN_1421	*wbtH*	COG0367E	glutamine amidotransferase/asparagine synthase	72.5	NR-8062	H02
FTN_1016	-	COG1335Q	hypothetical protein FTN_1016	72.6	NR-8056	F09
FTN_0419	*purM*	COG0150F	phosphoribosylaminoimidazole synthetase	72.6	NR-8064	D05
FTN_0132	-	-	hypothetical protein FTN_0132	72.8	NR-8036	C02
FTN_0177	*purH*	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	72.8	NR-8065	F08
FTN_0097	-	COG0814E	hydroxy/aromatic amino acid permease (HAAAP) family protein	73.0	NR-8048	F08
FTN_1263	*comL*	COG4105R	competence lipoprotein ComL	73.0	NR-8048	G09
FTN_0331	*minC*	COG0850D	septum site-determining protein MinC	73.0	NR-8042	F06
FTN_0814	*bioF*	COG0156H	8-amino-7-oxononanoate synthase	73.1	NR-8056	F05
FTN_1317	-	-	hypothetical protein FTN_1317	73.1	NR-8036	B06
FTN_0690	*deaD*	COG0513LKJ	DEAD/DEAH box helicase	73.3	NR-8060	D08
FTN_1212	-	COG0438M	glycosyl transferases group 1 family protein	73.3	NR-8062	A01
FTN_0021	*carA*	COG0505EF	carbamoyl phosphate synthase small subunit	73.3	NR-8046	A09
FTN_0196	*cyoB*	COG0843C	cytochrome bo terminal oxidase subunit I	73.4	NR-8052	E03
FTN_0728	-	COG0053P	Co/Zn/Cd cation transporter	73.4	NR-8047	G03
FTN_0594	*sucC*	COG0045C	succinyl-CoA synthetase subunit beta	73.5	NR-8057	E02
FTN_1513	*xerC*	COG4973L	site-specific recombinase	73.6	NR-8048	E09
FTN_1254	-	-	hypothetical protein FTN_1254	73.6	NR-8066	C05
FTN_0358	*rimO*	COG0621J	ribosomal protein S12 methylthiotransferase	73.7	NR-8055	E09
FTN_1471	*pcs*	COG1183I	phosphatidylcholine synthase	73.8	NR-8040	D11
FTN_1700	*purF*	COG0034F	amidophosphoribosyltransferase	73.8	NR-8055	B12
FTN_1058	*tig*	COG0544O	trigger factor	74.0	NR-8053	B10
FTN_1217	-	COG1132V	ABC transporter ATP-binding protein	74.0	NR-8053	G01
FTN_0624	-	COG0814E	serine permease	74.0	NR-8064	H07

FTN_0855	-	-	hypothetical protein FTN_0855	74.0	NR-8062	D10
FTN_1211	-	COG1011R	haloacid dehalogenase-like hydrolase	74.2	NR-8053	G04
FTN_1316	-	COG3455S	hypothetical protein FTN_1316	74.2	NR-8055	A04
FTN_0534	-	COG1289S	hypothetical protein FTN_0534	74.4	NR-8054	H05
FTN_0815	*bioB*	COG0502H	biotin synthase	74.4	NR-8056	B10
FTN_1610	-	COG0841V	RND efflux transporter	74.4	NR-8054	B03
FTN_1602	*deoB*	COG1015G	phosphopentomutase	74.5	NR-8051	B10
FTN_0436	-	COG3240IR	hypothetical protein FTN_0436	74.6	NR-8040	H04
FTN_1055	*lon*	COG0466O	DNA-binding, ATP-dependent protease La	74.7	NR-8051	E07
FTN_1312	-	-	hypothetical protein FTN_1312	74.7	NR-8048	D06
FTN_1653	-	-	hypothetical protein FTN_1653	74.7	NR-8047	A11
FTN_1323	*iglB*	COG3517S	intracellular growth locus protein B	74.7	NR-8055	A06
FTN_1655	*rluC*	COG0564J	ribosomal large subunit pseudouridine synthase C	75.0	NR-8064	A09
FTN_1684	-	COG0019E	diaminopimelate decarboxylase	75.0	NR-8064	C12
FTN_0183	-	COG0803P	periplasmic solute binding family protein	75.0	NR-8055	A09
FTN_0822	-	COG0147EH	para-aminobenzoate synthase component I	75.1	NR-8040	C06
FTN_0298	*glpX*	COG1494G	fructose 1,6-bisphosphatase II	75.2	NR-8047	D09
FTN_0624	-	COG0814E	serine permease	75.3	NR-8054	A08
FTN_0666	*uvrA*	COG0178L	excinuclease ABC subunit A	75.5	NR-8066	D09
FTN_1558	*xerD*	COG4974L	site-specific recombinase	75.5	NR-8043	C10
FTN_0096	-	COG3619S	hypothetical protein FTN_0096	75.6	NR-8048	E08
FTN_0429	-	COG4372S	hypothetical protein FTN_0429	75.6	NR-8048	G12
FTN_0506	*gcvH*	COG0509E	glycine cleavage system H protein	75.6	NR-8049	G01
FTN_1066	-	COG4535P	HlyC/CorC family transporter-associated protein	75.7	NR-8045	B05
FTN_1091	*aroA*	COG0128E	3-phosphoshikimate 1-carboxyvinyltransferase	75.8	NR-8046	A01
FTN_0109	-	-	hypothetical protein FTN_0109	76.0	NR-8054	E12
FTN_0122	*recA*	COG0468L	recombinase A	76.0	NR-8035	D07
FTN_1500	-	-	hypothetical protein FTN_1500	76.3	NR-8048	C07
FTN_1313	-	-	hypothetical protein FTN_1313	76.4	NR-8057	F02
FTN_0122	*recA*	COG0468L	recombinase A	76.5	NR-8066	E09
FTN_1050	*hflX*	COG2262R	protease, GTP-binding subunit	76.6	NR-8058	A04
FTN_1097	-	COG1335Q	isochorismatase hydrolase family protein	76.6	NR-8054	F03

FTN_1200	*capC*	-	capsule biosynthesis protein CapC	76.6	NR-8052	G05
FTN_1318	-	-	hypothetical protein FTN_1318	76.6	NR-8054	F08
FTN_1558	*xerD*	COG4974L	site-specific recombinase	76.6	NR-8053	A03
FTN_0504	-	COG1982E	lysine decarboxylase	76.6	NR-8066	D07
FTN_0289	*proQ*	COG3109T	activator of osmoprotectant transporter ProP	76.7	NR-8036	D01
FTN_0821	-	COG0318IQ	AMP-binding protein	76.8	NR-8036	E05
FTN_0728	-	COG0053P	Co/Zn/Cd cation transporter	76.9	NR-8053	A07
FTN_1617	-	COG0642T	two-component regulator, sensor histidine kinase	76.9	NR-8054	A01
FTN_1133	-	-	Ohr-like protein	76.9	NR-8059	G08
FTN_1582	-	-	hypothetical protein FTN_1582	76.9	NR-8060	B01
FTN_0358	*rimO*	COG0621J	ribosomal protein S12 methylthiotransferase	77.0	NR-8048	E03
FTN_0330	*minD*	COG2894D	septum site-determining protein MinD	77.1	NR-8043	C09
FTN_1277	-	COG1538MU	outer membrane efflux protein	77.2	NR-8054	F05
FTN_1608	*dsbB*	COG1495O	disulfide bond formation protein	77.3	NR-8064	A08
FTN_0210	-	-	hypothetical protein FTN_0210	77.3	NR-8042	E07
FTN_0419	*purM*	COG0150F	phosphoribosylaminoimidazole synthetase	77.4	NR-8042	E12
FTN_0495	-	COG4692G	BNR/Asp-box repeat-containing protein	77.4	NR-8061	D05
FTN_1107	*metlQ*	COG1464P	methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	77.4	NR-8065	F04
FTN_0119	-	COG2825M	hypothetical protein FTN_0119	77.5	NR-8057	D03
FTN_1146	-	COG0436E	aspartate aminotransferase	77.5	NR-8057	B10
FTN_0337	*fumA*	COG1951C	fumerate hydratase	77.6	NR-8045	D06
FTN_1699	*purL*	COG0046F	phosphoribosylformylglycinamidine synthase	77.6	NR-8040	D02
FTN_1242	-	COG0586S	DedA family protein	77.6	NR-8052	B12
FTN_0234	*pgsA*	COG0558I	phosphatidylglycerophosphate synthetase	77.6	NR-8040	B01
FTN_0720	-	COG1414K	IclR family transcriptional regulator	77.6	NR-8054	G01
FTN_1750	-	COG0204I	acyltransferase	77.7	NR-8044	B05
FTN_0297	-	COG2945R	hypothetical protein FTN_0297	77.8	NR-8062	B05
FTN_1318	-	-	hypothetical protein FTN_1318	77.8	NR-8048	H06
FTN_1209	*cphB*	COG4242QP	cyanophycinase	77.8	NR-8055	F05
FTN_1362	-	-	hypothetical protein FTN_1362	77.9	NR-8055	E08
FTN_1362	-	-	hypothetical protein FTN_1362	78.0	NR-8038	G09

FTN_1322	*iglC*	-	intracellular growth locus protein C	78.1	NR-8052	H02
FTN_1426	*wbtE*	COG0677M	UDP-glucose/GDP-mannose dehydrogenase	78.1	NR-8054	H10
FTN_0728	-	COG0053P	Co/Zn/Cd cation transporter	78.1	NR-8048	H04
FTN_1326	*anmK*	COG2377O	anhydro-N-acetylmuramic acid kinase	78.1	NR-8048	C11
FTN_0020	*carB*	COG0458EF	carbamoyl phosphate synthase large subunit	78.2	NR-8042	D03
FTN_0756	*fopA*	COG2885M	OmpA family protein	78.3	NR-8063	G12
FTN_1219	*galE*	COG1087M	UDP-glucose 4-epimerase	78.3	NR-8064	E10
FTN_1425	*wbtF*	COG0451MG	NAD dependent epimerase	78.3	NR-8040	E08
FTN_1219	*galE*	COG1087M	UDP-glucose 4-epimerase	78.3	NR-8050	C05
FTN_0210	-	-	hypothetical protein FTN_0210	78.4	NR-8042	D07
FTN_1613	-	COG1619V	U61 family peptidase	78.4	NR-8046	D11
FTN_1656	-	COG1485R	ATPase	78.5	NR-8050	B11
FTN_0664	*fimT*	COG4970NU	Type IV pili, pilus assembly protein	78.5	NR-8057	A06
FTN_1058	*tig*	COG0544O	trigger factor	78.6	NR-8040	A06
FTN_0560	*ksgA*	COG0030J	dimethyladenosine transferase	78.7	NR-8053	D06
FTN_0210	-	-	hypothetical protein FTN_0210	78.7	NR-8063	G07
FTN_1273	-	COG0318IQ	long chain fatty acid CoA ligase	78.8	NR-8066	A07
FTN_0427	-	-	hypothetical protein FTN_0427	78.9	NR-8054	A05
FTN_0429	-	COG4372S	hypothetical protein FTN_0429	78.9	NR-8053	F10
FTN_1090	-	-	hypothetical protein FTN_1090	79.0	NR-8036	C05
FTN_1264	*rluD*	COG0564J	ribosomal large subunit pseudouridine synthase D	79.0	NR-8065	C11
FTN_1201	*capB*	COG0769M	capsule biosynthesis protein CapB	79.0	NR-8044	C01
FTN_1617	-	COG0642T	two-component regulator, sensor histidine kinase	79.0	NR-8042	E05
FTN_0096	-	COG3619S	hypothetical protein FTN_0096	79.1	NR-8057	C09
FTN_1309	*pdpA*	-	hypothetical protein FTN_1309	79.1	NR-8065	E06
FTN_1029	-	COG3155Q	isoprenoid biosynthesis protein with amidotransferase-like domain	79.2	NR-8057	F06
FTN_0505	*gcvT*	COG0404E	glycine cleavage system aminomethyltransferase T	79.3	NR-8041	C06
FTN_1209	*cphB*	COG4242QP	cyanophycinase	79.4	NR-8038	E10
FTN_1048	*hflK*	COG0330O	HflK-HflC membrane protein complex, HflK	79.5	NR-8041	E03
FTN_0560	*ksgA*	COG0030J	dimethyladenosine transferase	79.5	NR-8056	C05

FTN_0689	*ppiC*	COG0760O	parvulin-like peptidyl-prolyl isomerase domain-containing protein	79.6	NR-8059	D08
FTN_0534	-	COG1289S	hypothetical protein FTN_0534	79.6	NR-8047	F04
FTN_1513	*xerC*	COG4973L	site-specific recombinase	79.6	NR-8065	E12
FTN_1684	-	COG0019E	diaminopimelate decarboxylase	79.6	NR-8064	E12
FTN_1111	-	COG0769M	Mur ligase family protein	79.6	NR-8040	F04
FTN_0593	*sucD*	COG0074C	succinyl-CoA synthetase, alpha subunit	79.7	NR-8057	H02
FTN_0893	-	-	hypothetical protein FTN_0893	79.7	NR-8061	D08
FTN_1324	*iglA*	COG3516S	intracellular growth locus protein A	79.7	NR-8061	A04
FTN_0690	*deaD*	COG0513LKJ	DEAD/DEAH box helicase	79.8	NR-8041	G12
FTN_1586	-	COG2814G	major facilitator superfamily sugar transporter	79.8	NR-8051	B07
FTN_1705	-	COG0826O	U32 family peptidase	79.8	NR-8047	E01
FTN_0672	*secA*	COG0653U	preprotein translocase subunit SecA	79.8	NR-8052	F04
FTN_1715	*kdpD*	COG2205T	two component regulator, sensor histidine kinase kdpD	79.8	NR-8055	B07
FTN_1064	-	COG1702T	PhoH family protein ATPase	79.9	NR-8061	E03
FTN_0514	*pgm*	COG0033G	phosphoglucomutase	80.1	NR-8045	C12
FTN_1218	-	COG0438M	group 1 glycosyl transferase	80.1	NR-8062	E08
FTN_1433	-	-	hypothetical protein FTN_1433	80.1	NR-8060	B06
FTN_0599	-	-	hypothetical protein FTN_0599	80.1	NR-8066	G06
FTN_1613	-	COG1619V	U61 family peptidase	80.1	NR-8057	H10
FTN_1313	-	-	hypothetical protein FTN_1313	80.4	NR-8043	D06
FTN_0494	-	-	hypothetical protein FTN_0494	80.4	NR-8063	C09
FTN_1038	-	COG0670R	hypothetical protein FTN_1038	80.4	NR-8036	D07
FTN_1382	-	-	hypothetical protein FTN_1382	80.6	NR-8055	C03
FTN_1548	*groEL*	COG0459O	chaperonin GroEL	80.6	NR-8040	B07
FTN_0818	-	COG0657I	lipase/esterase	80.6	NR-8036	D08
FTN_1316	-	COG3455S	hypothetical protein FTN_1316	80.6	NR-8040	F08
FTN_1097	-	COG1335Q	isochorismatase hydrolase family protein	80.7	NR-8052	A01
FTN_0756	*fopA*	COG2885M	OmpA family protein	80.7	NR-8061	H10
FTN_1048	*hflK*	COG0330O	HflK-HflC membrane protein complex, HflK	80.7	NR-8059	D12
FTN_1218	-	COG0438M	group 1 glycosyl transferase	80.8	NR-8041	C04

FTN_1319	*pdpC*	-	hypothetical protein FTN_1319	80.9	NR-8054	F01
FTN_0177	*purH*	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	80.9	NR-8040	H02
FTN_1242	-	COG0586S	DedA family protein	80.9	NR-8043	G08
FTN_1252	-	COG3049M	choloylglycine hydrolase family protein	81.1	NR-8058	G09
FTN_1257	-	-	hypothetical protein FTN_1257	81.1	NR-8057	B07
FTN_0855	-	-	hypothetical protein FTN_0855	81.2	NR-8047	A04
FTN_0407	-	COG0833E	amino acid ABC transporter permease	81.3	NR-8053	G07
FTN_0925	-	-	hypothetical protein FTN_0925	81.4	NR-8058	H11
FTN_1321	*iglD*	-	intracellular growth locus protein D	81.5	NR-8063	B02
FTN_1410	*bfr*	COG2193P	bacterioferritin	81.5	NR-8061	C12
FTN_0818	-	COG0657I	lipase/esterase	81.6	NR-8036	C08
FTN_0266	*htpG*	COG0326O	heat shock protein 90	81.6	NR-8050	F02
FTN_0325	-	COG2854Q	membrane protein	81.7	NR-8046	C03
FTN_1750	-	COG0204I	acyltransferase	81.8	NR-8064	A10
FTN_0297	-	COG2945R	hypothetical protein FTN_0297	81.8	NR-8042	C01
FTN_0643	-	-	hypothetical protein FTN_0643	81.9	NR-8055	A08
FTN_0842	*aroG*	COG0722E	phospho-2-dehydro-3-deoxyheptonate aldolase	82.0	NR-8041	G10
FTN_1501	-	COG0025P	monovalent cation:proton antiporter-1	82.0	NR-8045	E10
FTN_1157	-	COG1217T	GTP binding translational elongation factor Tu and G family protein	82.0	NR-8061	D10
FTN_0817	-	COG2050Q	hypothetical protein FTN_0817	82.1	NR-8040	F09
FTN_1597	*prfC*	COG4108J	peptide chain release factor 3	82.1	NR-8043	F01
FTN_0544	*naxD*	COG3394S	galactosamine deacteylase	82.2	NR-8062	D08
FTN_0756	*fopA*	COG2885M	OmpA family protein	82.2	NR-8038	G11
FTN_1633	*apt*	COG0503F	adenine phosphoribosyltransferase	82.2	NR-8035	B09
FTN_0020	*carB*	COG0458EF	carbamoyl phosphate synthase large subunit	82.3	NR-8043	B03
FTN_0505	*gcvT*	COG0404E	glycine cleavage system aminomethyltransferase T	82.3	NR-8045	E03
FTN_1745	*purT*	COG0027F	phosphoribosylglycinamide formyltransferase 2	82.3	NR-8050	E09
FTN_1548	-	COG1520S	hypothetical protein FTN_1548	82.4	NR-8043	A01
FTN_1657	-	COG2271G	major facilitator transporter	82.5	NR-8052	G02

FTN_1319	*pdpC*	-	hypothetical protein FTN_1319	82.5	NR-8035	G09
FTN_0507	*gcvP1*	COG0403E	glycine dehydrogenase subunit 1	82.6	NR-8040	E04
FTN_0822	-	COG0147EH	para-aminobenzoate synthase component I	82.7	NR-8062	H01
FTN_1320	-	-	hypothetical protein FTN_1320	82.7	NR-8059	E10
FTN_1744	*chiB*	COG3469G	chitinase	82.7	NR-8058	G04
FTN_0817	-	COG2050Q	hypothetical protein FTN_0817	82.7	NR-8051	A06
FTN_1656	-	COG1485R	ATPase	82.9	NR-8060	C04
FTN_0643	-	-	hypothetical protein FTN_0643	83.0	NR-8042	A02
FTN_0818	-	COG0657I	lipase/esterase	83.0	NR-8046	C10
FTN_1312	-	-	hypothetical protein FTN_1312	83.1	NR-8057	H04
FTN_0664	*fimT*	COG4970NU	Type IV pili, pilus assembly protein	83.1	NR-8045	C11
FTN_1586	-	COG2814G	major facilitator superfamily sugar transporter	83.1	NR-8043	B02
FTN_0633	*katG*	COG0376P	peroxidase/catalase	83.2	NR-8040	A05
FTN_1743	*clpB*	COG0542O	chaperone clpB	83.2	NR-8059	H05
FTN_1607	*cca*	COG0617J	tRNA CCA-pyrophosphorylase	83.3	NR-8046	G12
FTN_0624	-	COG0814E	serine permease	83.3	NR-8040	H08
FTN_0535	-	COG2814G	drug:H+ antiporter-1 (DHA1) family protein	83.3	NR-8053	A09
FTN_0198	*cyoD*	COG3125C	cytochrome bo terminal oxidase subunit IV	83.4	NR-8061	F07
FTN_0593	*sucD*	COG0074C	succinyl-CoA synthetase, alpha subunit	83.4	NR-8061	B09
FTN_0422	*purE*	COG0041F	N5-carboxyaminoimidazole ribonucleotide mutase	83.4	NR-8042	F12
FTN_1438	-	COG1250I	fusion product of 3-hydroxacyl-CoA dehydrogenase and acyl-CoA-binding protein	83.4	NR-8041	E09
FTN_1050	*hflX*	COG2262R	protease, GTP-binding subunit	83.6	NR-8042	E08
FTN_1256	-	-	hypothetical protein FTN_1256	83.7	NR-8062	H12
FTN_1325	*pdpD*	-	hypothetical protein FTN_1325	83.7	NR-8058	H01
FTN_1654	-	COG2271G	major facilitator transporter	83.7	NR-8058	G07
FTN_1311	-	-	hypothetical protein FTN_1311	83.7	NR-8043	F12
FTN_0132	-	-	hypothetical protein FTN_0132	83.9	NR-8063	G03
FTN_1112	*cphA*	COG0769M	cyanophycin synthetase	83.9	NR-8061	B03
FTN_1263	*comL*	COG4105R	competence lipoprotein ComL	83.9	NR-8060	G10
FTN_1276	-	COG1566V	membrane fusion protein	83.9	NR-8061	A02
FTN_1682	*frgA*	COG4264Q	siderophore biosynthesis protein	83.9	NR-8058	H10

FTN_0812	*bioD*	COG0132H	dethiobiotin synthetase	84.0	NR-8051	C10
FTN_0719	-	-	hypothetical protein FTN_0719	84.0	NR-8039	G09
FTN_0925	-	-	hypothetical protein FTN_0925	84.0	NR-8045	G06
FTN_0097	-	COG0814E	hydroxy/aromatic amino acid permease (HAAAP) family protein	84.0	NR-8059	H10
FTN_0771	-	COG1651O	protein-disulfide isomerase	84.2	NR-8058	F12
FTN_1326	*anmK*	COG2377O	anhydro-N-acetylmuramic acid kinase	84.2	NR-8061	F03
FTN_1744	*chiB*	COG3469G	chitinase	84.3	NR-8045	D11
FTN_1058	*tig*	COG0544O	trigger factor	84.3	NR-8038	G01
FTN_1427	*wbtD*	COG0438M	group 1 glycosyl transferase	84.3	NR-8035	B05
FTN_0035	*pyrF*	COG0284F	orotidine-5'-phosphate decarboxylase	84.3	NR-8063	E04
FTN_1321	*iglD*	-	intracellular growth locus protein D	84.3	NR-8061	E05
FTN_0430	-	-	hypothetical protein FTN_0430	84.5	NR-8040	E09
FTN_1016	-	COG1335Q	hypothetical protein FTN_1016	84.6	NR-8043	A09
FTN_0211	*pcp*	COG2039O	pyrrolidone carboxylylate peptidase	84.7	NR-8053	E10
FTN_0407	-	COG0833E	amino acid ABC transporter permease	84.8	NR-8041	F04
FTN_1657	-	COG2271G	major facilitator transporter	84.8	NR-8044	G09
FTN_0197	*cyoC*	COG1845C	cytochrome bo terminal oxidase subunit III	84.9	NR-8050	D07
FTN_0816	*bioA*	COG0161H	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	85.0	NR-8060	E06
FTN_0666	*uvrA*	COG0178L	excinuclease ABC subunit A	85.0	NR-8045	E09
FTN_1211	-	COG1011R	haloacid dehalogenase-like hydrolase	85.1	NR-8035	E11
FTN_1427	*wbtD*	COG0438M	group 1 glycosyl transferase	85.2	NR-8058	D12
FTN_1310	*pdpB*	COG3523S	hypothetical protein FTN_1310	85.3	NR-8039	G10
FTN_1220	-	COG2148M	lipopolysaccharide synthesis sugar transferase	85.3	NR-8040	C12
FTN_1683	-	COG2814G	drug:H+ antiporter-1 (DHA1) family protein	85.3	NR-8044	D12
FTN_0812	*bioD*	COG0132H	dethiobiotin synthetase	85.5	NR-8035	A12
FTN_1421	*wbtH*	COG0367E	glutamine amidotransferase/asparagine synthase	85.5	NR-8040	C03
FTN_1705	-	COG0826O	U32 family peptidase	85.5	NR-8062	G04
FTN_1007	*rplY*	COG1825J	50S ribosomal protein L25	85.6	NR-8036	H08
FTN_0019	*pyrB*	COG0540F	aspartate carbamoyltransferase	85.7	NR-8063	A02
FTN_0431	-	COG3307M	hypothetical protein FTN_0431	85.8	NR-8060	H05

FTN_1107	*metlQ*	COG1464P	methionine uptake transporter (MUT) family protein, membrane and periplasmic protein	86.1	NR-8044	A02
FTN_0266	*htpG*	COG0326O	heat shock protein 90	86.2	NR-8044	A08
FTN_1518	*relA*	COG0317TK	GDP pyrophosphokinase/GTP pyrophosphokinase	86.2	NR-8041	C09
FTN_0620	-	COG2271G	major facilitator transporter	86.3	NR-8058	C09
FTN_1277	-	COG1538MU	outer membrane efflux protein	86.3	NR-8063	D05
FTN_1548	-	COG1520S	hypothetical protein FTN_1548	86.5	NR-8061	F12
FTN_1426	*wbtE*	COG0677M	UDP-glucose/GDP-mannose dehydrogenase	86.5	NR-8045	H08
FTN_1750	-	COG0204I	acyltransferase	86.6	NR-8057	D04
FTN_1214	-	COG1215M	glycosyl transferase family protein	86.7	NR-8053	B07
FTN_1254	-	-	hypothetical protein FTN_1254	86.8	NR-8036	G07
FTN_0812	*bioD*	COG0132H	dethiobiotin synthetase	86.9	NR-8050	H08
FTN_0620	-	COG2271G	major facilitator transporter	86.9	NR-8035	E06
FTN_1157	-	COG1217T	GTP binding translational elongation factor Tu and G family protein	87.0	NR-8041	F11
FTN_0358	*rimO*	COG0621J	ribosomal protein S12 methylthiotransferase	87.1	NR-8045	G10
FTN_0731	-	COG5006R	hypothetical protein FTN_0731	87.1	NR-8044	D01
FTN_0410	-	COG0436E	aspartate aminotransferase	87.2	NR-8035	B06
FTN_0689	*ppiC*	COG0760O	parvulin-like peptidyl-prolyl isomerase domain-containing protein	87.2	NR-8035	B03
FTN_1090	-	-	hypothetical protein FTN_1090	87.3	NR-8052	C12
FTN_0823	*pabA*	COG0512EH	anthranilate synthase component II	87.4	NR-8035	H06
FTN_0120	-	COG0607P	rhodanese-related sulfurtransferase	87.5	NR-8053	A11
FTN_1431	*wbtA*	COG1086MG	dTDP-glucose 4,6-dehydratase	87.5	NR-8057	B09
FTN_1501	-	COG0025P	monovalent cation:proton antiporter-1	87.5	NR-8057	H12
FTN_1683	-	COG2814G	drug:H+ antiporter-1 (DHA1) family protein	87.5	NR-8058	E01
FTN_1256	-	-	hypothetical protein FTN_1256	87.5	NR-8041	B06
FTN_0806	-	COG1472G	glycosyl hydrolase family protein	87.6	NR-8036	H01
FTN_1745	*purT*	COG0027F	phosphoribosylglycinamide formyltransferase 2	87.6	NR-8063	A05
FTN_0431	-	COG3307M	hypothetical protein FTN_0431	87.7	NR-8044	A10
FTN_0651	*cdd*	COG0295F	cytidine deaminase	87.8	NR-8051	D03
FTN_1315	-	-	hypothetical protein FTN_1315	87.8	NR-8048	G08

FTN_0410	-	COG0436E	aspartate aminotransferase	88.0	NR-8059	B07
FTN_1214	-	COG1215M	glycosyl transferase family protein	88.0	NR-8063	B10
FTN_1131	*putA*	COG4230C	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	88.1	NR-8044	C10
FTN_0289	*proQ*	COG3109T	activator of osmoprotectant transporter ProP	88.1	NR-8058	E05
FTN_1750	-	COG0204I	acyltransferase	88.3	NR-8053	H02
FTN_1682	*frgA*	COG4264Q	siderophore biosynthesis protein	88.4	NR-8047	B07
FTN_0183	-	COG0803P	periplasmic solute binding family protein	88.5	NR-8058	C01
FTN_0669	*deoD*	COG0813F	purine nucleoside phosphorylase	88.5	NR-8038	H09
FTN_0599	-	-	hypothetical protein FTN_0599	88.6	NR-8048	A10
FTN_1654	-	COG2271G	major facilitator transporter	88.6	NR-8050	A12
FTN_1438	-	COG1250I	fusion product of 3-hydroxacyl-CoA dehydrogenase and acyl-CoA-binding protein	88.6	NR-8052	F03
FTN_0999	*udhA*	COG1249C	soluble pyridine nucleotide transhydrogenase	88.7	NR-8035	G04
FTN_1214	-	COG1215M	glycosyl transferase family protein	88.7	NR-8048	A07
FTN_1159	*ggt*	COG0405E	gamma-glutamyltranspeptidase	88.9	NR-8050	H10
FTN_0202	*pdxY*	COG2240H	pyridoxal kinase	89.0	NR-8039	D03
FTN_0430	-	-	hypothetical protein FTN_0430	89.1	NR-8057	F04
FTN_0643	-	-	hypothetical protein FTN_0643	89.1	NR-8051	F07
FTN_1323	*iglB*	COG3517S	intracellular growth locus protein B	89.3	NR-8044	G02
FTN_1582	-	-	hypothetical protein FTN_1582	89.3	NR-8042	E11
FTN_1610	-	COG0841V	RND efflux transporter	89.5	NR-8036	G04
FTN_0814	*bioF*	COG0156H	8-amino-7-oxononanoate synthase	89.9	NR-8041	E11
FTN_0513	*glgB*	COG0296G	glycogen branching protein	90.0	NR-8039	F12
FTN_0633	*katG*	COG0376P	peroxidase/catalase	90.0	NR-8052	D04
FTN_1273	-	COG0318IQ	long chain fatty acid CoA ligase	90.0	NR-8048	B09
FTN_1252	-	COG3049M	choloylglycine hydrolase family protein	90.3	NR-8038	E09
FTN_1423	*wbtG*	COG0438M	group 1 glycosyl transferase	90.4	NR-8051	F12
FTN_0036	*pyrD*	COG0167F	dihydroorotate oxidase	90.5	NR-8037	D06
FTN_0561	*apaH*	COG0639T	diadenosine tetraphosphatase	90.7	NR-8039	C12
FTN_0120	-	COG0607P	rhodanese-related sulfurtransferase	90.9	NR-8050	A04
FTN_1310	*pdpB*	COG3523S	hypothetical protein FTN_1310	90.9	NR-8052	A09

FTN_1325	*pdpD*	-	hypothetical protein FTN_1325	91.1	NR-8036	F02
FTN_1276	-	COG1566V	membrane fusion protein	91.5	NR-8064	C03
FTN_1213	-	COG1215M	glycosyl transferase family protein	92.0	NR-8037	D07
FTN_1518	*relA*	COG0317TK	GDP pyrophosphokinase/GTP pyrophosphokinase	92.1	NR-8040	B02
FTN_1322	*iglC*	-	intracellular growth locus protein C	92.4	NR-8048	G02
FTN_1357	*recB*	COG1074L	ATP-dependent exonuclease V subunit beta	92.4	NR-8038	H07
FTN_1324	*iglA*	COG3516S	intracellular growth locus protein A	92.8	NR-8039	C08
FTN_1431	*wbtA*	COG1086MG	dTDP-glucose 4,6-dehydratase	92.8	NR-8040	G03
FTN_0731	-	COG5006R	hypothetical protein FTN_0731	93.1	NR-8037	F11
FTN_1257	-	-	hypothetical protein FTN_1257	93.3	NR-8037	B01
FTN_1220	-	COG2148M	lipopolysaccharide synthesis sugar transferase	93.6	NR-8061	G05
FTN_0505	*gcvT*	COG0404E	glycine cleavage system aminomethyltransferase T	93.6	NR-8037	D04
FTN_1743	*clpB*	COG0542O	chaperone clpB	93.7	NR-8045	F03
FTN_0211	*pcp*	COG2039O	pyrrolidone carboxylylate peptidase	93.9	NR-8038	B01
FTN_0561	*apaH*	COG0639T	diadenosine tetraphosphatase	93.9	NR-8039	C12
FTN_1159	*ggt*	COG0405E	gamma-glutamyltranspeptidase	94.1	NR-8051	F06
FTN_1762	-	COG0488R	putative ABC transporter ATP-binding protein	94.1	NR-8046	E09
FTN_1112	*cphA*	COG0769M	cyanophycin synthetase	94.1	NR-8045	H04
FTN_1199	-	-	hypothetical protein FTN_1199	94.2	NR-8038	C05
FTN_0823	*pabA*	COG0512EH	anthranilate synthase component II	94.2	NR-8052	B05
FTN_1655	*rluC*	COG0564J	ribosomal large subunit pseudouridine synthase C	94.4	NR-8038	D08
FTN_1682	*frgA*	COG4264Q	siderophore biosynthesis protein	94.4	NR-8038	G04
FTN_1410	*bfr*	COG2193P	bacterioferritin	94.6	NR-8047	B12
FTN_1417	*manB*	COG1109G	phosphomannomutase	94.7	NR-8065	F11
FTN_1684	-	COG0019E	diaminopimelate decarboxylase	94.9	NR-8045	B09
FTN_0720	-	COG1414K	IclR family transcriptional regulator	94.9	NR-8038	A11
FTN_0265	*rplQ*	COG0203J	50S ribosomal protein L17	95.2	NR-8037	E11
FTN_1602	*deoB*	COG1015G	phosphopentomutase	95.5	NR-8038	E05
FTN_1255	-	COG1442M	glycosyl transferase family protein	95.7	NR-8039	C11
FTN_0535	-	COG2814G	drug:H+ antiporter-1 (DHA1) family protein	96.2	NR-8038	B04
FTN_0815	*bioB*	COG0502H	biotin synthase	96.3	NR-8037	G05

FTN_1029	-	COG3155Q	isoprenoid biosynthesis protein with amidotransferase-like domain	96.3	NR-8038	F11
FTN_1264	*rluD*	COG0564J	ribosomal large subunit pseudouridine synthase D	96.6	NR-8038	G05
FTN_1683	-	COG2814G	drug:H+ antiporter-1 (DHA1) family protein	96.7	NR-8037	G08
FTN_1254	-	-	hypothetical protein FTN_1254	97.2	NR-8036	H07
FTN_1608	*dsbB*	COG1495O	disulfide bond formation protein	97.2	NR-8039	A10
FTN_0035	*pyrF*	COG0284F	orotidine-5\'-phosphate decarboxylase	97.3	NR-8038	D10
FTN_0196	*cyoB*	COG0843C	cytochrome bo terminal oxidase subunit I	98.0	NR-8039	B03
FTN_0504	-	COG1982E	lysine decarboxylase	98.8	NR-8039	B11
FTN_1683	-	COG2814G	drug:H+ antiporter-1 (DHA1) family protein	98.9	NR-8052	E12
FTN_1212	-	COG0438M	glycosyl transferases group 1 family protein	99.1	NR-8039	F08
FTN_0893	-	-	hypothetical protein FTN_0893	99.4	NR-8037	E12
FTN_1423	*wbtG*	COG0438M	group 1 glycosyl transferase	99.4	NR-8037	A12
FTN_0198	*cyoD*	COG3125C	cytochrome bo terminal oxidase subunit IV	99.9	NR-8046	F12
FTN_0421	*purN*	COG0299F	phosphoribosylglycinamide formyltransferase	100.6	NR-8038	C03
FTN_0813	*bioC*	-	biotin synthesis protein BioC	101.2	NR-8038	H12
FTN_0998	-	COG2898S	potassium channel protein	101.2	NR-8039	D11
FTN_1320	-	-	hypothetical protein FTN_1320	101.2	NR-8037	H05
FTN_0487	*rpsU*	COG0828J	30S ribosomal protein S21	101.4	NR-8038	A01
FTN_1217	-	COG1132V	ABC transporter ATP-binding protein	101.4	NR-8038	G03
FTN_1309	*pdpA*	-	hypothetical protein FTN_1309	101.4	NR-8039	D04
FTN_1433	-	-	hypothetical protein FTN_1433	104.8	NR-8039	F07
FTN_1131	*putA*	COG4230C	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	105.4	NR-8038	G10
FTN_1412	-	COG0202K	DNA-directed RNA polymerase subunit alpha	105.4	NR-8038	D11
FTN_1417	*manB*	COG1109G	phosphomannomutase	105.9	NR-8050	G02
FTN_1314	-	-	hypothetical protein FTN_1314	111.5	NR-8037	G10
FTN_1309	*pdpA*	-	hypothetical protein FTN_1309	123.5	NR-8039	F04

Supplemental Table 3. Primers used in this study

Primer name	***Sequence***
0109 Arm1 FWD	cacccagttttaaaagaggt
0109 Arm 1 REV	ttatcgataccgtcgacctcactaaatttccatgatttaataac
0109 frt_sKAN_frt FWD	gttattaaatcatggaaatttagtgaggtcgacggtatcgataa
0109 frt_sKAN_frt REV	ttatttaggattacttatttaatttgcatagctgcaggatcgata
0109 Arm 2 FWD	tatcgatcctgcagctatgcaaattaaataagtaatcctaaataa
0109 Arm 2 REV	tttcctataggcaacattga
0430 Arm1 FWD	tttacttagatactctagctg
0430 Arm 1 REV	ttatcgataccgtcgacctctagtattacctgttatttcatta
0430 frt_sKAN_frt FWD	taatgaaataacaggtaatactagaggtcgacggtatcgataa
0430 frt_sKAN_frt REV	tcttataaaaagacggcaaaaagcatagctgcaggatcgata
0430 Arm 2 FWD	tatcgatcctgcagctatgctttttgccgtctttttataaga
0430 Arm 2 REV	aaaaatcgtactgctttagaat