| 1 | Supplemental material for: |
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| 3 4 | PASTA kinase signaling regulates peptidoglycan synthesis in <i>Enterococcus faecalis</i> by direct inhibition of UDP-N-acetylglucosamine 1-carboxyvinyl transferase activity |
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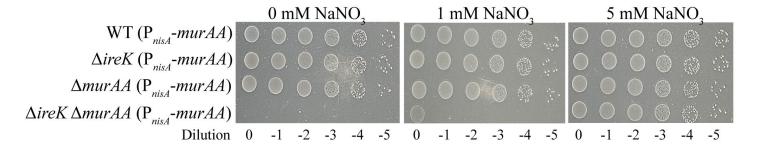


Figure S1 | *murAA* and *ireK* are synthetically lethal. Cultures grown in the presence of 5 mM NaNO₃ were washed, subjected to 10-fold serial dilutions, and spotted on MHB supplemented as indicated and incubated at 37 °C for 24 h. Results are representative of a minimum of 2 independent biological replicates. Strains were Wildtype/ P_{nisA} -murAA, OG1/pJLL288; $\Delta ireK/P_{nisA}$ -murAA, JL206/pJLL288; $\Delta murAA/P_{nisA}$ -murAA, JL626/pJLL288; and $\Delta ireK$ $\Delta murAA/P_{nisA}$ -murAA, DDJ470/pJLL288.

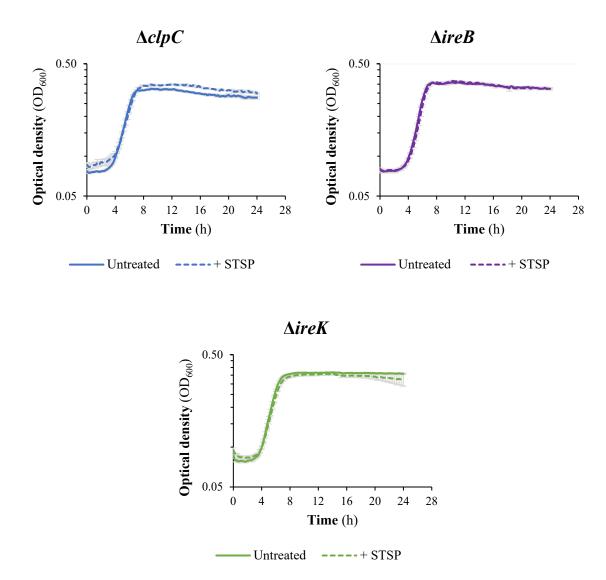


Figure S2 | Staurosporine (STSP) does not alter growth of the $\triangle ireK$, $\triangle clpC$, or $\triangle ireB$ mutants. Growth curves for the indicated *E. faecalis* strains grown at 37 °C with 10 μ M STSP or equivalent volume DMSO (untreated) as a vehicle control. Growth curves represent an average of 3 independent replicates within each experiment and error bars show standard deviation (too small to see in many cases). Strains were $\triangle ireK$, JL206; $\triangle ireB$, JL367, $\triangle clpC$, CM35.

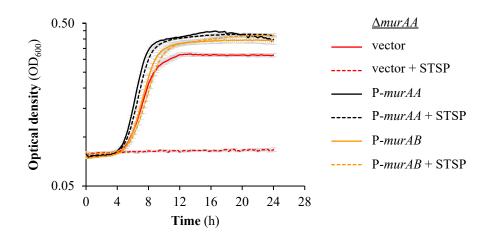


Figure S3 | Overexpression of *murAA* or *murAB* restores growth of the *murAA* deletion strain in the presence of staurosporine. Growth curves for the indicated *E. faecalis* strains grown at 37 °C with 10 μ M STSP or equivalent volume DMSO as a vehicle control. Growth curves depict the average of 3 independent replicates with error bars indicating standard deviation. Strains were $\Delta murAA$ /vector, JL626/pJRG9; $\Delta murAA$ /P-murAA, JL626/pDDJ99 and $\Delta murAA$ /P-murAB, JL626/pJLL217.

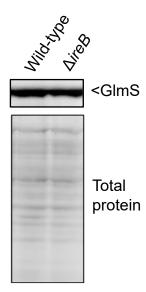


Figure S4 | Loss of IreB does not alter the steady-state abundance of GlmS. Immunoblot analysis on total cell lysates of wild-type and $\triangle ireB$ strains of *E. faecalis* collected during exponential phase. Blots were probed with custom anti-serum to GlmS followed by an HRP-conjugated secondary antibody. NoStain reagent was used for detection of total protein. Immunoblot is representative of three independent biological replicates. Strains are wild-type, OG1; $\triangle ireB$, JL367.

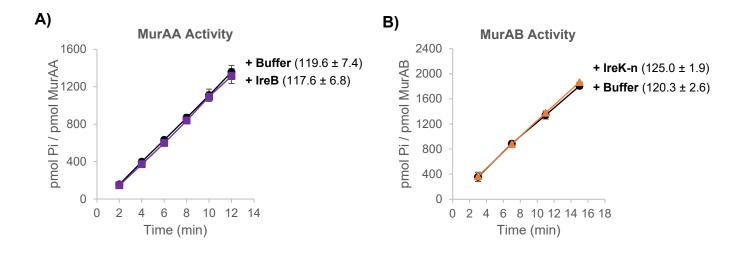


Figure S5 | (A) IreB does not inhibit enzymatic activity of MurAA. UNAG-CTase activity of purified, recombinant MurAA was measured in the presence of 10-fold molar excess purified wild-type IreB (purple squares) or equivalent volume buffer (black circles). Data represent the average of 6 replicate reactions ± standard deviation. The reaction rate was calculated as the average slope for data points between 2 and 12 min and is reported in parentheses. (B) IreK kinase domain used for IreB phosphorylation does not impact MurAB activity. UNAG-CTase activity of purified, recombinant MurAB was measured in the presence of IreK kinase domain at the concentration used for *in vitro* phosphorylation of IreB (IreK-n; orange triangles) or buffer (black circles). Data represent the average of 3 replicates ± standard deviation. The reaction rate was calculated as the average slope for data points between 3 and 15 min and is reported in parentheses.

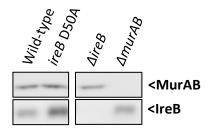


Figure S6 | **The IreB D50A variant is expressed in** *E. faecalis.* Immunoblot analysis was performed on lysates collected during exponential phase for the indicated strains using anti-sera to MurAB and IreB followed by an Alexa Fluor 647-conjugated secondary antibody. Blot is representative of two biological replicates. The left and right sections for each represent a single image from which intervening lanes that were not relevant to this analysis were removed for clarity. Strains were wild-type, OG1; *ireB* D50A, CM70; Δ*ireB*, JL367; Δ*murAB*, CM1.

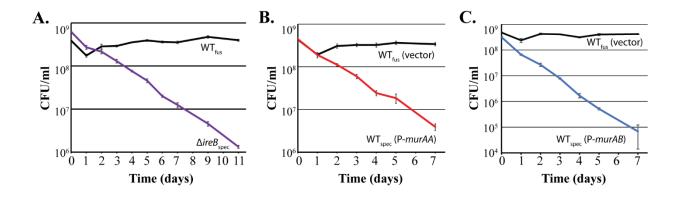


Figure S7 The fitness defect resulting from unregulated MurAA and MurAB is not due to the antibiotic marker. *E. faecalis* strains grown in MH broth (chloramphenicol was supplemented when plasmid containing strains were used) were normalized, mixed 1:1 for co-culture and subsequently diluted into fresh MH broth. Samples were plated for CFU (at Day 0 through Day 11 for panel A, and Day 0 through Day 7 for panels B and C) on MH agar plates supplemented with spectinomycin or fusidic acid to enumerate differentially marked strains. (A) Co-culture of wild-type (WT) with the $\Delta ireB$ deletion mutant. (B) Co-culture of wild-type and the MurAA overexpression strain. (C) Co-culture of wild-type and the MurAB overexpression strain. Data represents four biological replicates. Strains were: WT_{fus}, CK138, fusidic acid resistant wild-type; $\Delta ireB_{\rm spec}$, JL598, spectinomycin resistant $\Delta ireB$ mutant; WTspec,OG1Sp, spectinomycin resistant wild-type; vector, pJRG9; P-murAA, pDDJ99; P-murAB, pJLL217.

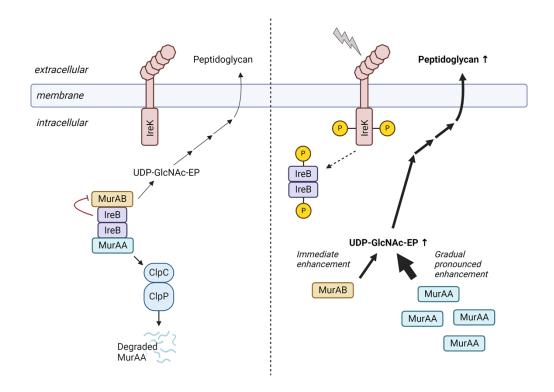


Figure S8 | **Model in which IreB provides coordinated, but differential regulation of MurAA and MurAB.** When IreK is not activated, IreB remains unphosphorylated and physically interacts with both MurAA and MurAB simultaneously. Under these conditions MurAA is targeted for degradation by the ClpCP complex and accordingly its cellular abundance is low. Meanwhile, the enzymatic activity of MurAB is inhibited by IreB. Thus, synthesis of UDP-N-acetylglucosamine enolpyruvate (UDP-GlcNAc-EP), and subsequently entry of substrates into the peptidoglycan synthesis pathway, is restricted. Following activation of IreK, such as during exposure to cell envelope stress, IreB becomes phosphorylated by IreK and is no longer competent to interact with either MurAA or MurAB. This results in an immediate enhancement of the enzymatic activity of MurAB, providing a modest increase in synthesis of UDP-GlcNAc-EP. MurAA also gradually begins to accumulate in cells given that is no longer targeted for degradation by ClpCP. Accumulation of MurAA appears to result in a more dramatic increase in peptidoglycan synthesis and has consequences of growth and resistance to cephalosporin antibiotics.

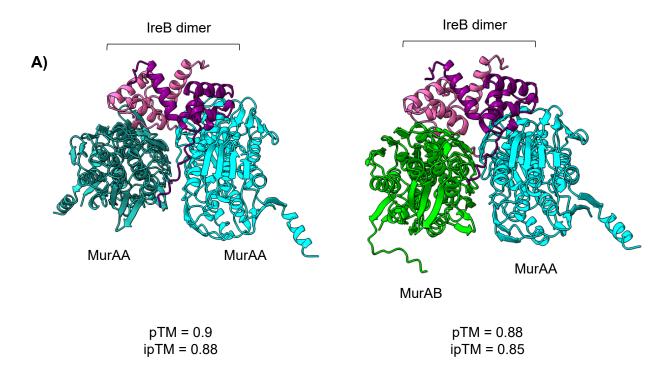


Figure S9 | **AlphaFold3 modeling**. Prediction complexes between (A) two monomers of MurAA (cyan and teal; WP_002356562.1) and an IreB homodimer (purple and pink; WP_002357937.1) and (B) the IreB homodimer and one monomer each of MurAA (cyan; WP_002356562.1) and MurAB (light green; WP_002357969.1).

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

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Agar-plate growth assays for depletion strain. Overnight cultures grown in MH broth supplemented with 10 µg/ml erythromycin and 5 mM NaNO₃ for induction of plasmid-borne murAA expression were centrifuged. The pellets were washed 2x with MH broth to remove residual NaNO₃ prior to normalization. Ten-fold serial dilutions were then prepared and 4 µl spotted on MH agar plates supplemented with 10 ug/ml erythromycin and NaNO3 as indicated. Immunoblot analysis. Stationary-phase cultures were diluted to $OD_{600} = 0.01$ in MHB and incubated at 37 °C with shaking. Cultures were grown until $OD_{600} \sim 0.2$ and harvested by mixing with an equal volume of cold EtOH/acetone (1:1). After harvesting, cells were pelleted by centrifugation and washed once with water. To prepare total cell lysates, bacteria were suspended in lysozyme buffer (10 mM Tris, 50 mM NaCl, 20% sucrose [pH 8]), normalized to equivalent OD₆₀₀, treated with lysozyme (5 mg ml⁻¹) for 30 min at 37°C, mixed with Laemmli SDS sample buffer containing 100 mM DTT and boiled for 5 min. After SDS-PAGE, proteins were transferred to polyvinylidene difluoride (PVDF; Bio-Rad) using a Transblot Turbo system (Bio-Rad) and incubated with No-Stain Protein Labeling reagent (Invitrogen) when indicated for visualization of total protein prior to blocking with 5% skim milk in Tris-buffered saline. Membranes were then probed with custom rabbit anti-GlmS, MurAB or IreB polyclonal antiserum followed by either goat anti-rabbit, Alexa Fluor 647-conjugated secondary antibody (Invitrogen) or goat anti-rabbit horseradish peroxidase-conjugated secondary antibody (Invitrogen) as indicated in the figure legend. Imaging of membranes was performed using an Amersham Typhoon 5 (Cytiva, Marlborough, MA) for Alexa Fluor 647-conjugated secondary antibody and No-Stain reagent or using Super-Signal (Thermo Fisher Scientific, Waltham, MA) on a ChemiDoc Touch System (Bio-Rad, Hercules, CA) for HRP-conjugated secondary antibody.

| Strain or plasmid | Relevant genotype or description ^a | Source or reference |
|-------------------|--|---------------------|
| Chuaina | | reference |
| Strains E. coli | | |
| DH5α | routine cloning host | Lab stock |
| TOP10 | routine cloning host | Lab stock |
| DHM1 | cya rec reporter strain for protein-protein interaction detection | Lab stock |
| BL21 (DE3) | Protein overexpression host | Lab stock |
| C43 (DE3) | Protein overexpression host optimized for toxic proteins | Lucigen |
| E. faecalis | | |
| OG1 | Wild-type reference strain (MLST 1) | (1) |
| JL626 | OG1 ΔmurAA | (2) |
| JL367 | OG1 ΔireB | (3) |
| CM32 | OG1 ΔireB ΔmurAA | This work |
| CM62 | OG1 ΔmurAA ΔclpC | This work |
| CM70 | OG1 ireB D50A | This work |
| CM71 | OG1 ireB D50A ΔmurAA | This work |
| CM1 | OG1 ΔmurAB | (2) |
| OG1RF | Wild-type reference strain (MLST 1) | (4) |
| JG4 | Ceftriaxone-resistant suppressor mutant of OG1RF $\Delta ireK$; | (5) |
| | carries D50A mutation in <i>ireB</i> | |
| DDJ470 (pJLL288) | OG1 $\triangle ireK \triangle murAA (P_{nisA}-murAA)$ | This work |
| OG1Sp | Spontaneous Sp ^R derivative of OG1 | (6) |
| CK138 | Spontaneous Fa ^R derivative of OG1 | (7) |
| JL597 | CK138 ∆ireB | This work |
| JL598 | OG1Sp Δ <i>ireB</i> | This work |
| Plasmids | D. | |
| рЈН086 | E. faecalis allelic exchange vector (Cm ^R); pheS* counterselection | (8) |
| pJLL229 | pJH086 carrying $\Delta murAA$ allele, used for generation of CM32 | (2) |
| pCJK218 | E. faecalis allelic exchange vector (Cm ^R); pheS* counterselection | (9) |
| pJLL73 | pCJK218 carrying $\triangle ireB$ (\triangle E6-H84) | (3) |
| pCAM70 | pJH086 carrying $\Delta clpC$ allele, used for generation of CM62 | (10) |
| pCAM133 | pJH086 carrying <i>ireB</i> D50A allele amplified from JG4; used for generation of CM70 and CM71 | This work |

| pJRG9 | E. faecalis expression vector, constitutive P23 _s promoter | (11) |
|--|--|-----------|
| - | (Cm ^R) | |
| pDDJ99 | pJRG9:: <i>murAA</i> -strep | (2) |
| pJLL217 | pJRG9:: <i>murAB</i> -strep | This work |
| pJLL286 | Nitrate-inducible expression vector (Em ^R) | (2) |
| pJLL288 | pJLL286 carrying P _{nisA} ::murAA | (2) |
| pKT25 | E. coli vector used to generate fusions with the C-terminus | Lab stock |
| • | of cya T25 (Kn ^R) | |
| pCAM73 | pKT25::murAB | (10) |
| T25-zip | pKT25::GCN4 leucine zipper | Lab stock |
| pKNT25 | E. coli vector used to generate fusions with the N-terminus | Lab stock |
| | of cya T25 (Kn ^R) | |
| pSLK148 | pKNT25::ireB | (10) |
| pCAM113 | pKNT25::ireB D50A | This work |
| pUT18c | E. coli vector used to generate fusions with the C-terminus | Lab stock |
| | of cya T18 (Amp ^R) | |
| pSLK163 | pUT18c::ireB | (10) |
| pCAM114 | pUT18c::ireB D50A | This work |
| pCAM72 | pUT18c::murAB | (10) |
| T18-zip | pUT18c::GCN4 leucine zipper | Lab stock |
| pET28b | E. coli expression vector (Kn ^R) | Novagen |
| pDV20 | pET28b::murAA-His ₆ | (12) |
| pDV16 | pET28b::murAB-His ₆ | (10) |
| pCJK111 | pET28b::His ₆ -ireK-n | (7) |
| pET28a::His ₆ -smt ₃ | E. coli protein expression vector (Kn ^R) with cleavable His ₆ | (13) |
| | SUMO tag | |
| pCLH194 | pET28a::His ₆ -smt ₃ -ireB | (14) |
| pCAM143 | pET28a::His ₆ -smt ₃ -ireB D50A | This work |
| pCJK205 | Constitutive expression of <i>lacZ</i> (Em ^R) | (15) |

^a MLST, multilocus sequence type

SUPPLEMENTAL REFERENCES

- 50 1. O. G. Gold, H. V. Jordan, J. van Houte, The prevalence of enterococci in the human mouth and their pathogenicity in animal models. *Arch Oral Biol* **20**, 473-477 (1975).
- C. A. Mascari, D. Djorić, J. L. Little, C. J. Kristich, Use of an Interspecies Chimeric Receptor for Inducible Gene Expression Reveals that Metabolic Flux through the Peptidoglycan Biosynthesis Pathway is an Important Driver of Cephalosporin Resistance in *Enterococcus faecalis*. *J Bacteriol* 204, jb.00602-00621 (2022).
- 56 3. B. D. Labbe, C. J. Kristich, Growth- and Stress-Induced PASTA Kinase Phosphorylation in *Enterococcus faecalis*. *J Bacteriol* **199**, e00363-00317 (2017).
- G. M. Dunny, B. L. Brown, D. B. Clewell, Induced cell aggregation and mating in Streptococcus faecalis: evidence for a bacterial sex pheromone. *Proc Natl Acad Sci U S A* 75, 3479-3483 (1978).
- C. L. Hall, M. Tschannen, E. A. Worthey, C. J. Kristich, IreB, a Ser/Thr kinase substrate,
 influences antimicrobial resistance in *Enterococcus faecalis*. *Antimicrob Agents Chemother* 57,
 6179-6186 (2013).
- 6. C. J. Kristich, J. R. Chandler, G. M. Dunny, Development of a host-genotype-independent counterselectable marker and a high-frequency conjugative delivery system and their use in genetic analysis of *Enterococcus faecalis*. *Plasmid* **57**, 131-144 (2007).
- 7. C. J. Kristich, J. L. Little, C. L. Hall, J. S. Hoff, Reciprocal regulation of cephalosporin resistance in *Enterococcus faecalis. mBio* **2**, e00199-00111 (2011).
- S. L. Kellogg, J. L. Little, J. S. Hoff, C. J. Kristich, Requirement of the CroRS Two-Component
 System for Resistance to Cell Wall-Targeting Antimicrobials in *Enterococcus faecium*.
 Antimicrob Agents Chemother 61 (2017).
- D. Vesic, C. J. Kristich, A Rex family transcriptional repressor influences H2O2 accumulation by
 Enterococcus faecalis. *J Bacteriol* 195, 1815-1824 (2013).
- 73 10. C. A. Mascari, J. L. Little, C. J. Kristich, PASTA-kinase-mediated signaling drives accumulation
 74 of the peptidoglycan synthesis protein MurAA to promote cephalosporin resistance in
 75 Enterococcus faecalis. Mol Microbiol 10.1111/mmi.15150 (2023).
- H. Snyder, S. L. Kellogg, L. M. Skarda, J. L. Little, C. J. Kristich, Nutritional control of antibiotic resistance via an interface between the phosphotransferase system and a two-component signaling system. *Antimicrob Agents Chemother* 58, 957-965 (2014).
- D. Vesic, C. J. Kristich, MurAA is required for intrinsic cephalosporin resistance of *Enterococcus* faecalis. Antimicrob Agents Chemother **56**, 2443-2451 (2012).
- N. E. Minton, D. Djorić, J. L. Little, C. J. Kristich, GpsB Promotes PASTA Kinase Signaling and Cephalosporin Resistance in *Enterococcus faecalis*. *J Bacteriol* **204**, e00304-00322 (2022).
- C. L. Hall *et al.*, Structure and Dimerization of IreB, a Negative Regulator of Cephalosporin Resistance in *Enterococcus faecalis*. *J Mol Biol* **429**, 2324-2336 (2017).
- D. Djorić, C. J. Kristich, Extracellular SalB Contributes to Intrinsic Cephalosporin Resistance and Cell Envelope Integrity in Enterococcus faecalis. *J Bacteriol* **199** (2017).

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