SUPPLEMENTARY DATA

for

Pseudomonas aeruginosa directly shunts β-oxidation degradation intermediates into de novo fatty acid biosynthesis

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Supplementary Figure 1

A

Supplementary Figure 1

B

Supplementary Figure 1

C

Supplementary Figure 1

D

Supplementary Figure 1

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Supplementary Figure 1

F

Supplementary Figure 1

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Supplementary Figure 1
Supplementary Figure 1: Mass spectra of FAMEs with natural isotope abundance isolated from *P. aeruginosa* strains. Parent molecular ions ([M]⁺) and select fragment ions are indicated. The gas chromatogram and corresponding mass spectra of FAMEs with the terminal 7 carbons uniformly deuterated are included in the main text (Fig. 2).
Supplementary Figure 2: Synthetic lethal analysis for fabY with KASIII domain orthologs. The pTMT123 (fabH, solid bars) or pTMT124 (ΔfabY, hatched bars) vectors were individually introduced into *P. aeruginosa* ΔPA0999, ΔPA0998, and ΔPA3333. Colony forming units (CFU) were determined after resolving the vector by sucrose counterselection as described in the Materials and Methods section. CFU were recorded after 24 hr or 48 hr (#) of incubation at 37 °C. Selection media and strain background is denoted on the X-axis and data shown is representative of 3 separate experiments.
Supplementary Figure 3: Mass spectra of deuterated FAMEs unique to E. coli expressing PA3286. FAMEs were prepared from the E. coli strain TMT47 [(fabH::camR (pET-PA3286)] grown on LB agar containing 100 µg/mL of perdeuterated decanoate (d_{19}-C10:0; 100 µg/mL) and 10 µg/mL of palmitate. Parent molecular ions ([M]⁺) and select fragment ions are indicated.