SUPPLEMENTARY DATA

for

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

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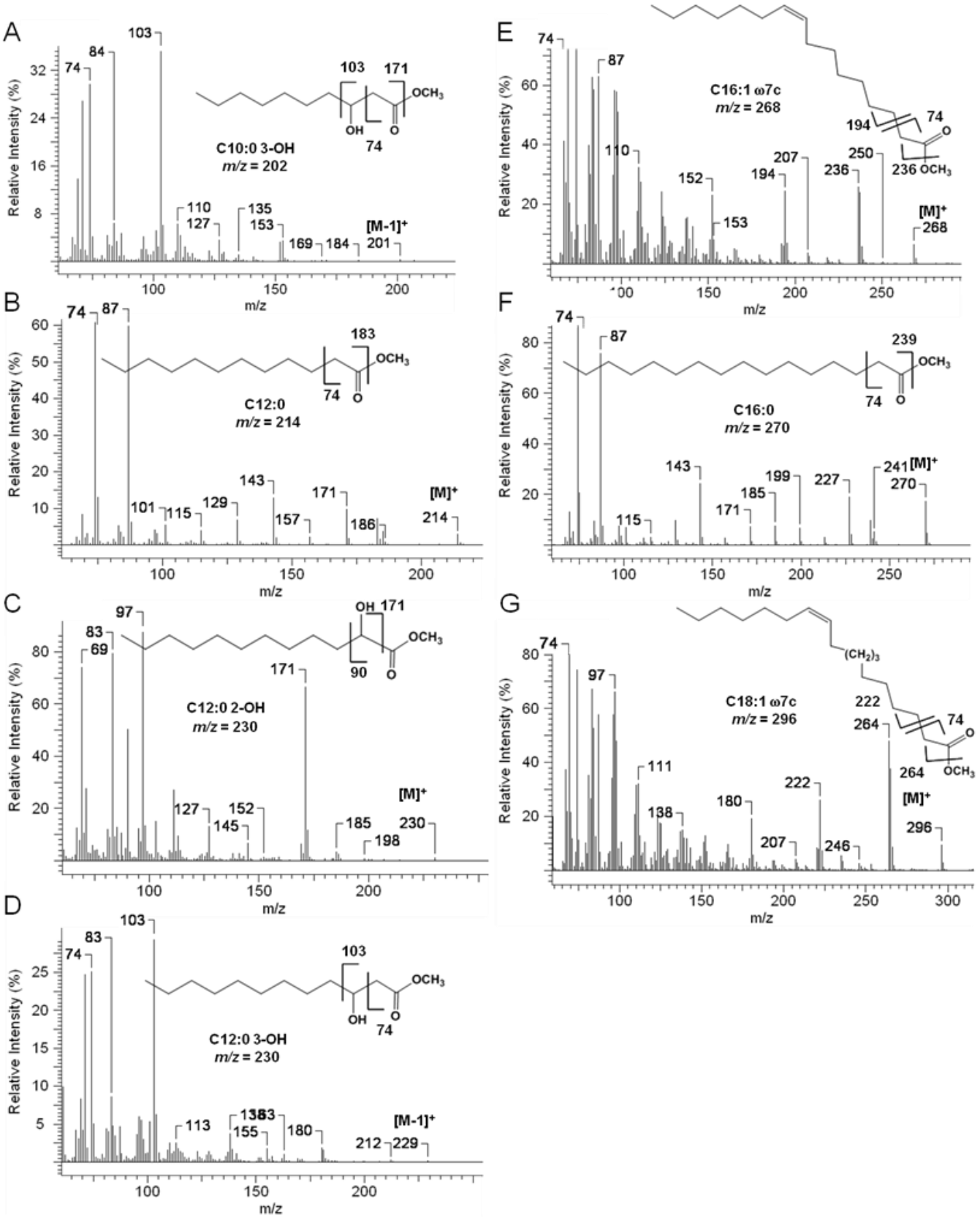
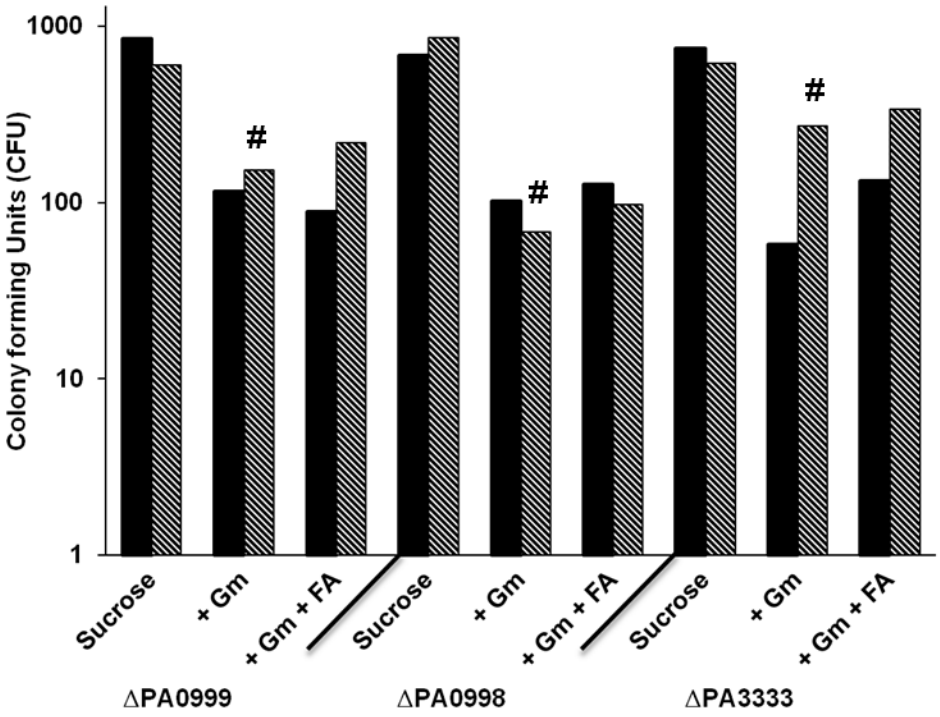
Supplementary Figure 1



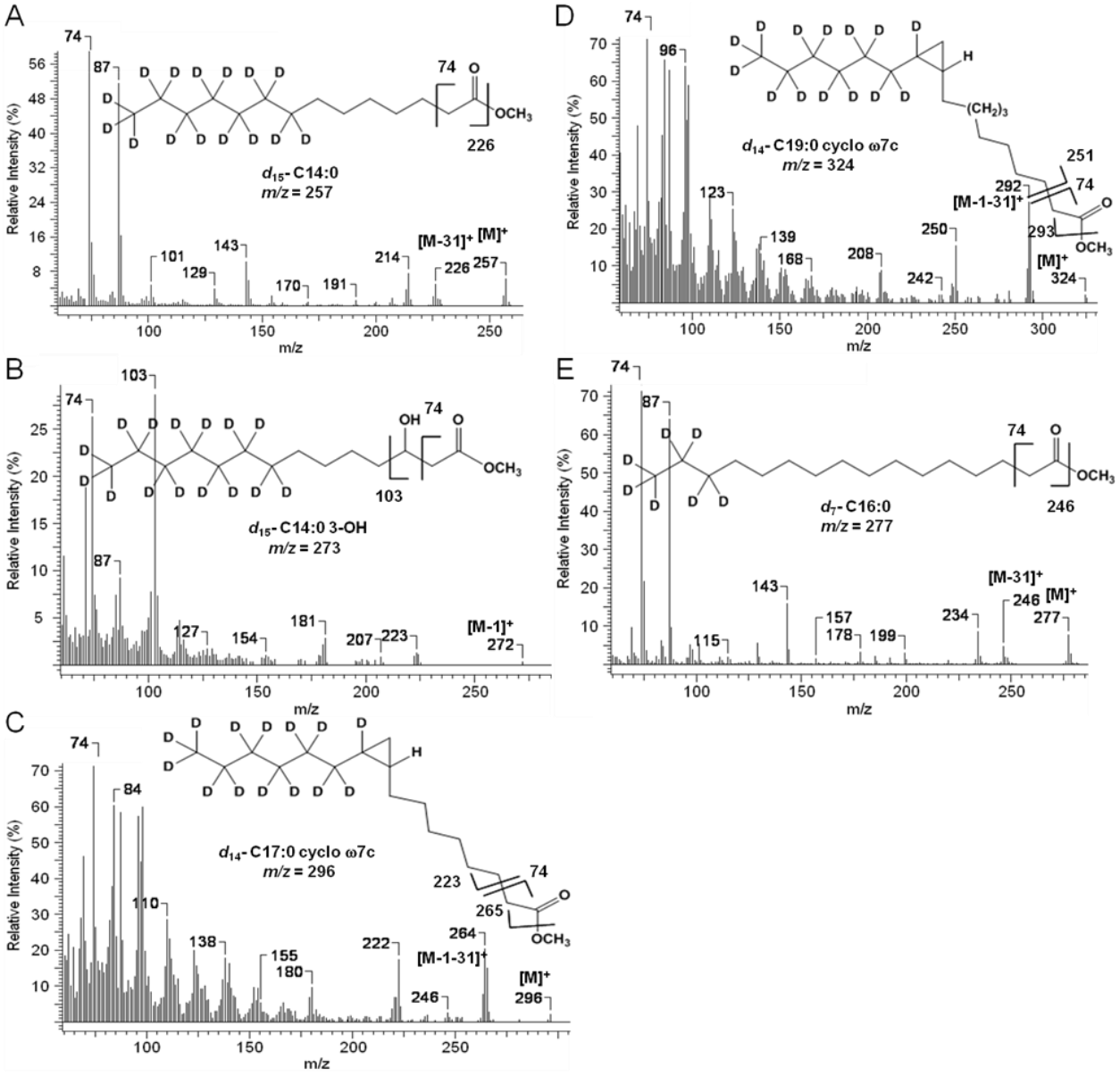
Supplementary Figure 1: Mass spectra of FAMEs with natural isotope abundance isolated from *P. aeruginosa* strains. Parent molecular ions ($[M]^+$) and select fragment ions are indicated. The gas chromatogram and corresponding mass spectra of FAMEs with the terminal 7 carbons uniformly deuterated are included in the main text (Fig. 2).

Supplementary Figure 2



Supplementary Figure 2: Synthetic lethal analysis for *fabY* with KASIII domain orthologs. The pTMT123 (*fabH*$^{-}$, solid bars) or pTMT124 (Δ*fabY*, 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



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.