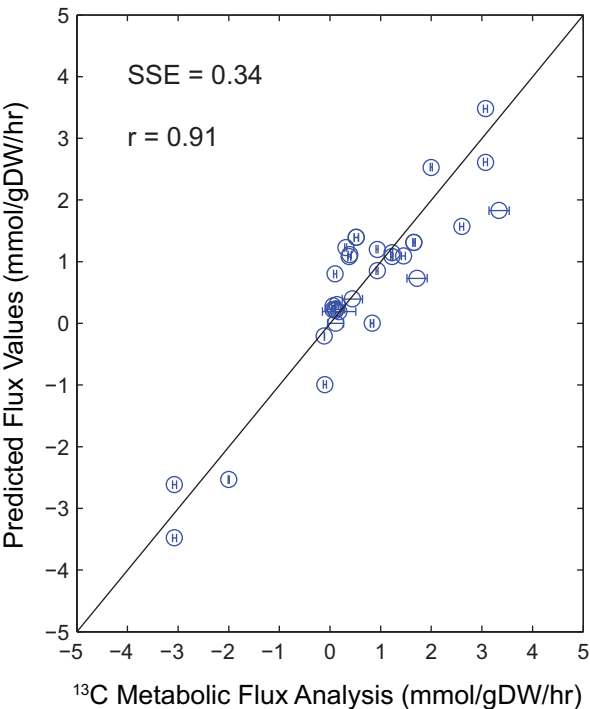
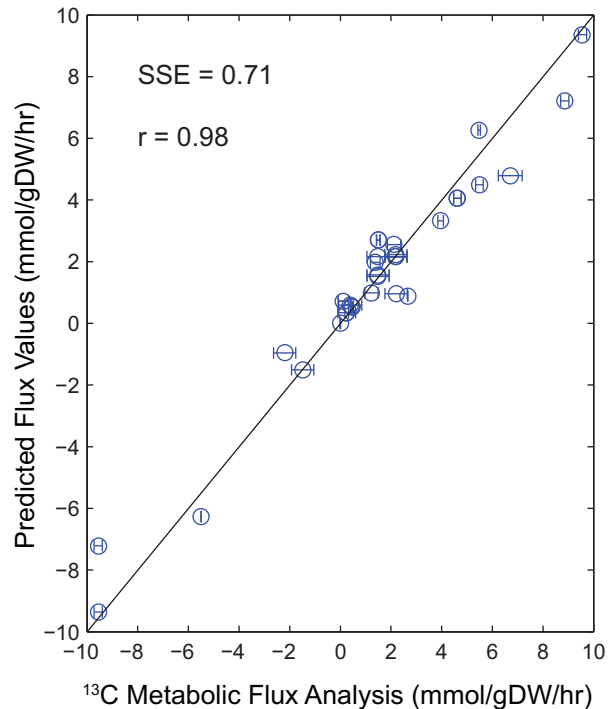


A

Wildtype

**B**

NagC mutant



Supplementary Figure S5. Comparison of ^{13}C MFA estimated fluxes and predictions by RELATCH for (A) wildtype *E. coli* strain and (B) NagC transcription factor knockout *E. coli* strain grown on galactose. The sum of squared errors per flux (SSE) and the Pearson's correlation coefficient (r) are shown for each strain, and the error bars indicate the confidence intervals from ^{13}C MFA.