Electronic Supplementary Material (ESI) for Molecular BioSystems.

Supporting information captions

Figure S1. Measurement bias for mass isotopomer fractions. Experimentally measured MI fractions of the $^{13}C_1{}^{15}N_0$ isotopomer in monitored metabolites from unlabeled cultures (from naturally occuring ^{13}C) is plotted for three replicates. Solid lines mark the theoretical $^{13}C_1{}^{15}N_0$ fraction.

Figure S2. Mass isotopomer distributions at 24h vs 72h. MI fractions from labeled cultures at each time point averaged over three replicates are plotted. Values along line of equality (gray) indicate that steady-state is attained at 24h. Red color marks MI fractions that notably deviate from line of equality, by the criterion of absolute Z-score > 2. Highlighted metabolites are: 6pgc, 6-phosphogluconate; g6p, glucose-6-phosphate; lac, lactate; pro, proline; udpg, uracil diphosphate-glucose.

Figure S3. Mass isotopomer distributions at 24h. All measured and fitted carbon-nitrogen MMIDs at 24h, shown as bar charts. MMIs are grouped by ^{13}C, increasing left to right, while ^{15}C is indicated by bar color within each group (where applicable). Error bars denote standard deviation of triplicates.

Dataset S4. All measured carbon-nitrogen mass isotopomer distributions and fluxes. Please see excel file for documentation.

Dataset S5. Complete metabolic network model with atom mappings. Please see excel file for documentation