Comparison of our kinetic model with other existing models

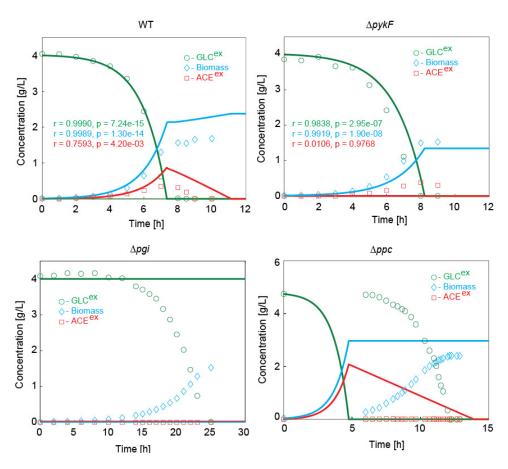


Figure S13: Simulated results by the Matsuoka model [1] for WT, $\Delta pykF$, Δpgi , and Δppc in a batch culture.

The green, blue and red lines represent the simulated results of the extracellular glucose, biomass and acetate, respectively. The corresponding open circles represent the experimental data [2, 3].

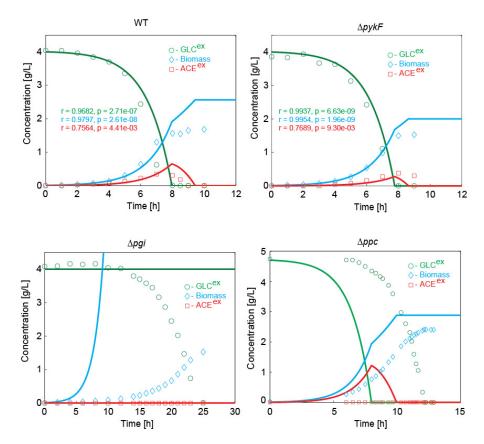


Figure S14: Simulated results by the Kotte model [4] for WT, $\Delta pykF$, Δpgi , and Δppc in a batch culture.

The green, blue and red lines represent the simulated results of the extracellular glucose, biomass and acetate, respectively. The corresponding open circles represent the experimental data [2, 3].

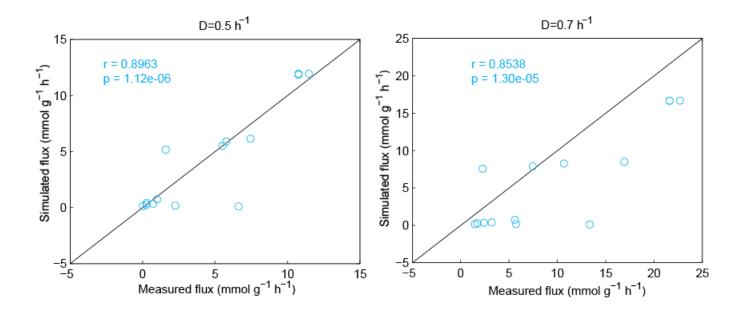


Figure S15: Comparison of the simulated flux by the Chassagnole model [5] with experimental data [6] for WT in a continuous culture.

References

- 1. Matsuoka Y, Shimizu K: Catabolite regulation analysis of *Escherichia coli* for acetate overflow mechanism and co-consumption of multiple sugars based on systems biology approach using computer simulation. *J Biotechnol* 2013, **168:**155-173.
- 2. Toya Y, Ishii N, Nakahigashi K, Hirasawa T, Soga T, Tomita M, Shimizu K: **13C-metabolic flux** analysis for batch culture of *Escherichia coli* and its *Pyk* and *Pgi* gene knockout mutants based on mass isotopomer distribution of intracellular metabolites. *Biotechnol Prog* 2010, **26:**975-992.
- 3. Kadir TA, Mannan AA, Kierzek AM, McFadden J, Shimizu K: **Modeling and simulation of the main metabolism in Escherichia coli and its several single-gene knockout mutants with experimental verification.** *Microb Cell Fact* 2010, **9:**88.
- 4. Kotte O, Zaugg JB, Heinemann M: Bacterial adaptation through distributed sensing of metabolic fluxes. *Mol Syst Biol* 2010, **6:**355
- 5. Chassagnole C, Noisommit-Rizzi N, Schmid JW, Mauch K, Reuss M: **Dynamic modeling of the central carbon metabolism of** *Escherichia coli*. *Biotechnol Bioeng* 2002, **79:**53-73.
- 6. Ishii N, Nakahigashi K, Baba T, Robert M, Soga T, Kanai A, Hirasawa T, Naba M, Hirai K, Hoque A, et al: **Multiple high-throughput analyses monitor the response of** *E. coli* **to perturbations.** *Science* 2007, **316:**593-597.