Supplementary Information for

Enhancement of Lipid Production in *Rhodosporidium toruloides*: Designing Feeding Strategies through Dynamic Flux Balance Analysis.

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S1. Supplementary figures

Figures S1, S2 and S3 show metabolic maps for the WT, KO and DKO strains, respectively. The maps were created with Escher [1].

References

[1] Zachary A. King, Andreas Dräger, Ali Ebrahim, Nikolaus Sonnenschein, Nathan E. Lewis, and Bernhard O. Palsson (2015) Escher: A web application for building, sharing, and embedding data-rich visualizations of biological pathways, *PLOS Computational Biology* 11(8): e1004321. doi:10.1371/journal.pcbi.1004321

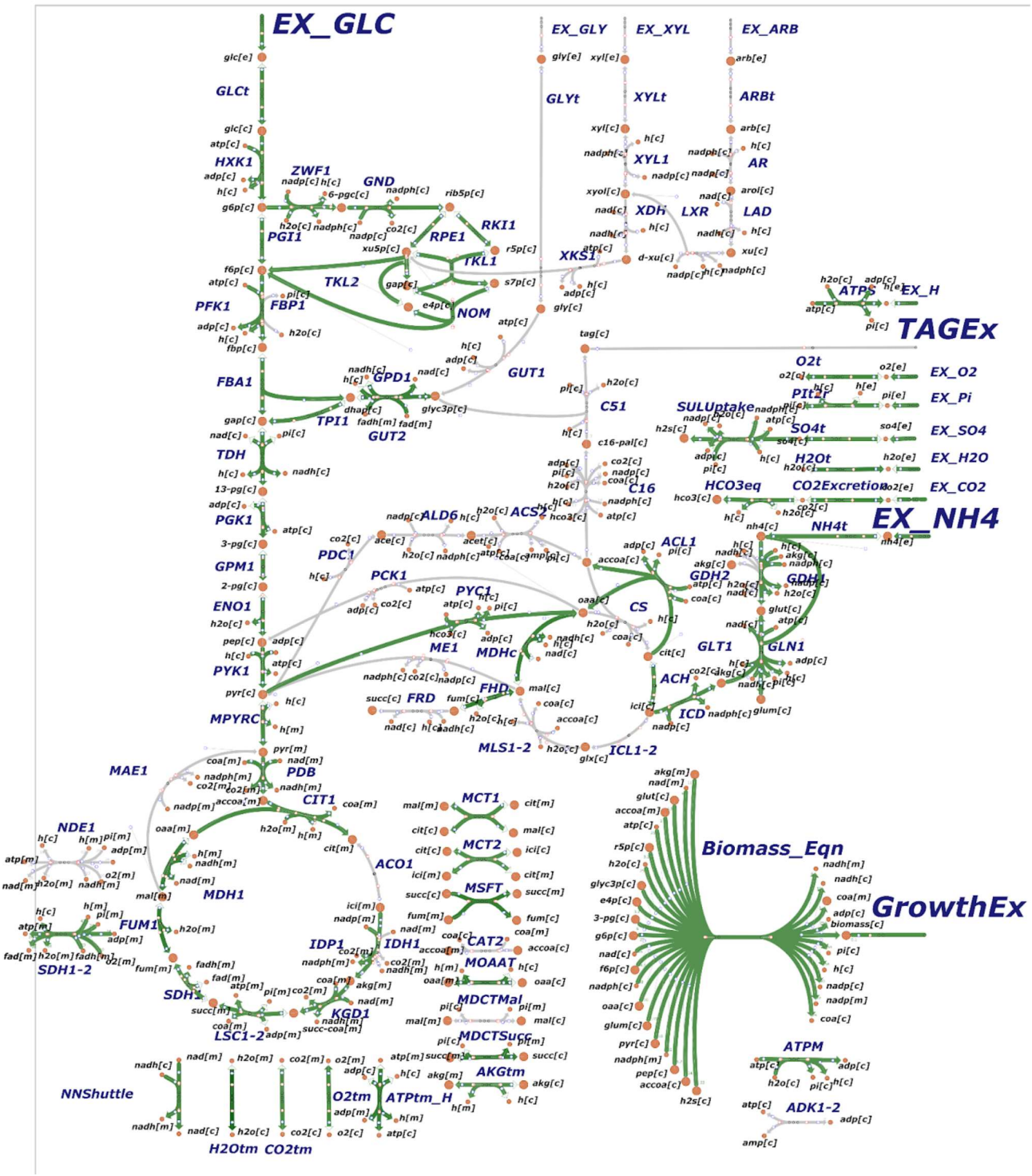


Figure S1: Flux distribution resulting from FBA optimization in the WT strain. Green arrows indicate metabolic reactions with non-zero flux values.

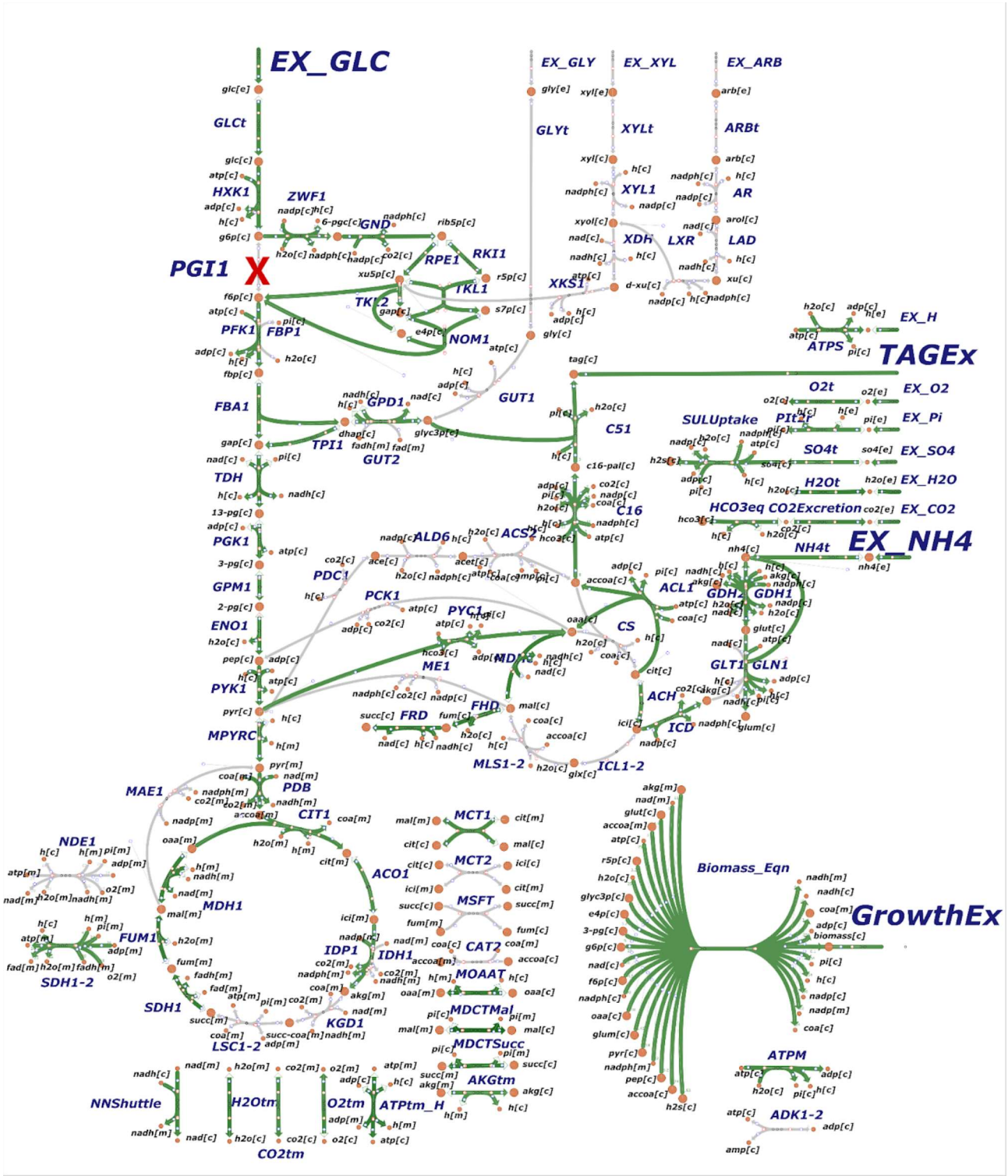


Figure S2: Flux distribution resulting from FBA optimization in the KO strain. Green arrows indicate metabolic reactions with non-zero flux values. The reaction marked with a cross denotes the gene knockout (*PGI1*).

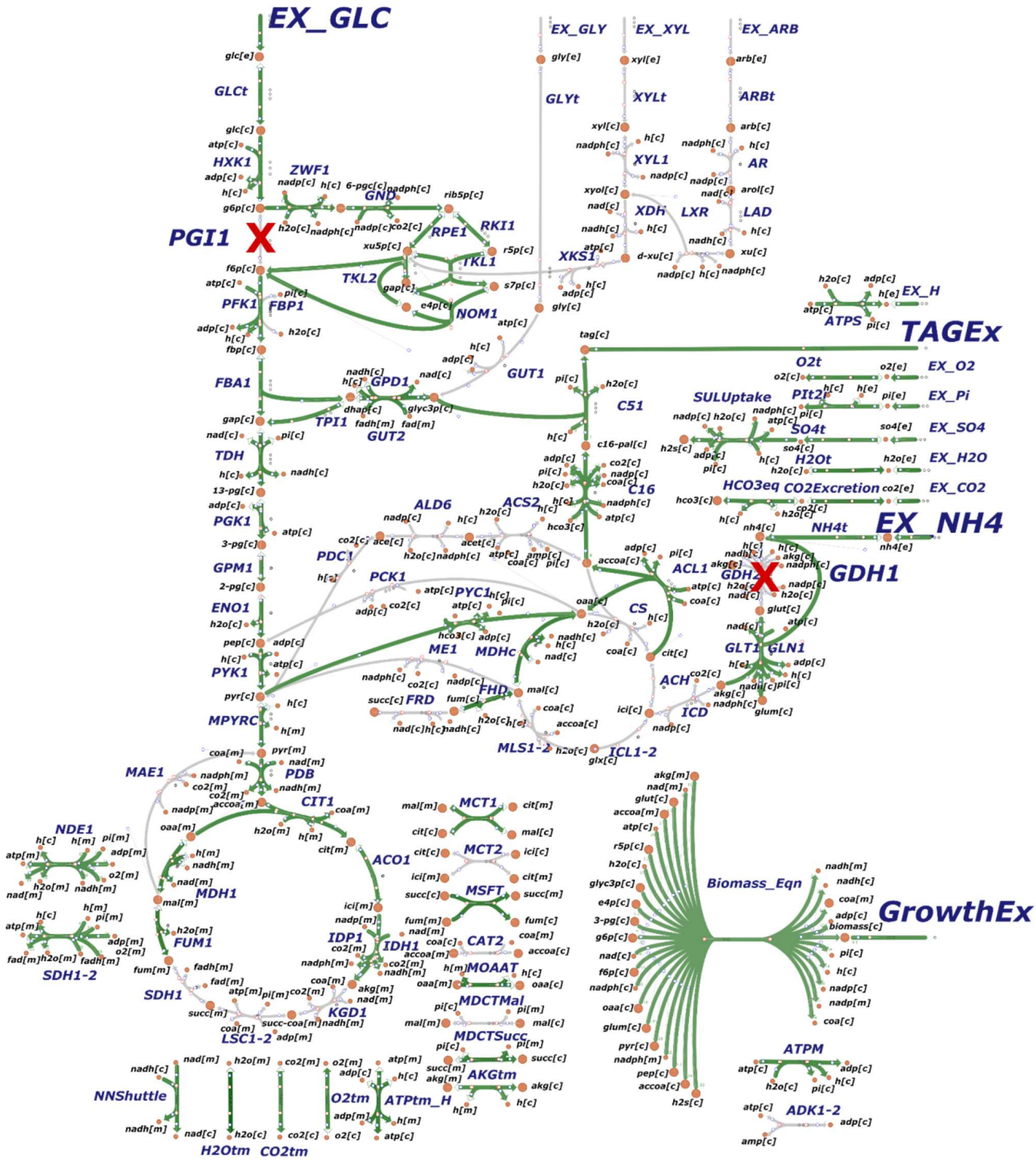


Figure S3: Flux distribution resulting from FBA optimization in the DKO strain. Green arrows indicate metabolic reactions with non-zero flux values. Reactions marked with a cross denote gene knockouts (*PGI1*, *GDH1*).