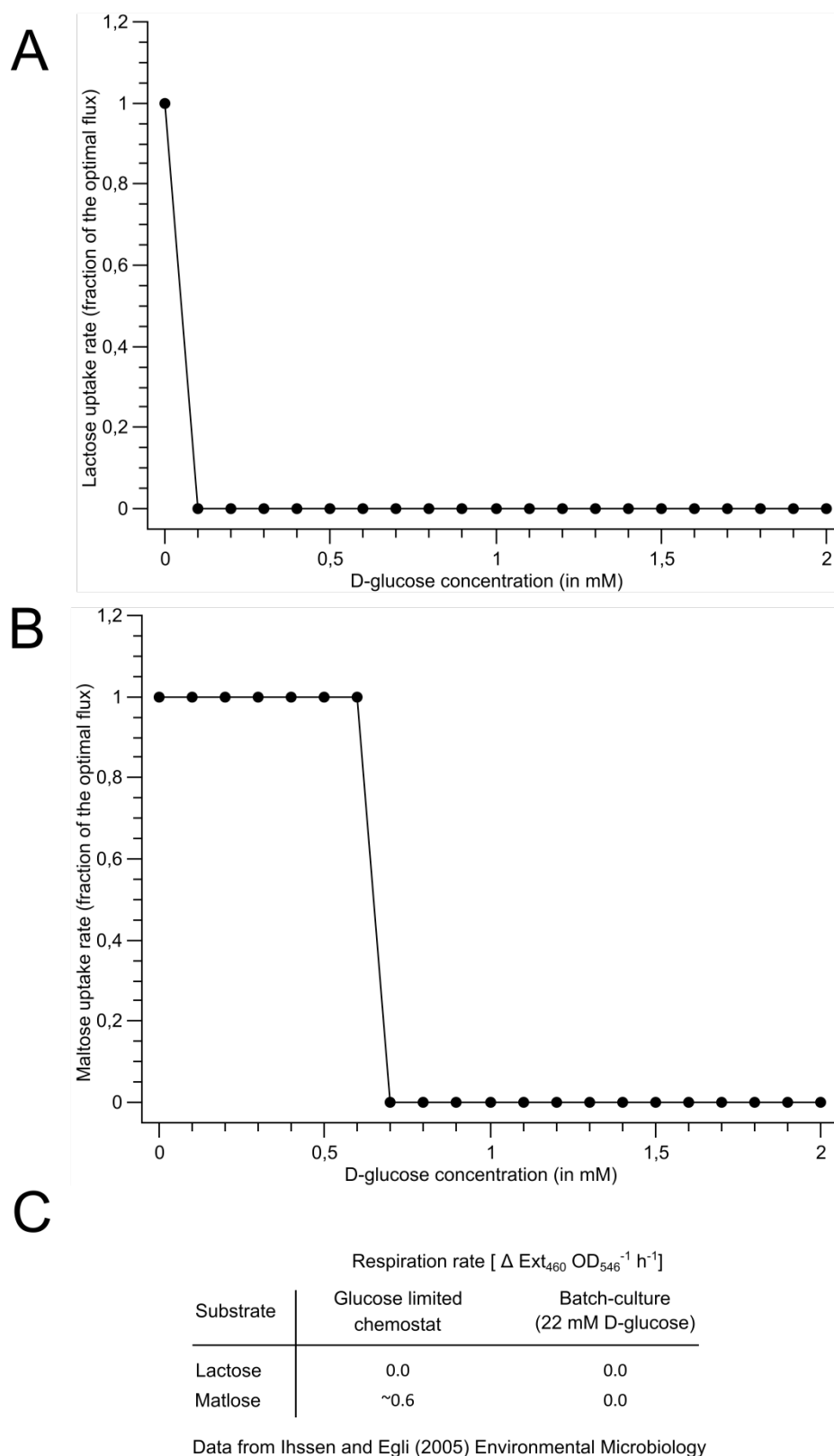


Additional file 6

FlexFlux: combining metabolic flux and regulatory network analyses

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Supplementary Figure 1. Multi-state logical modelling of catabolite repression. Simulation of the *Escherichia coli* lactose uptake rate **(A)** and maltose uptake rate **(B)** depending of the D-glucose concentration in the medium. Simulations were conducted using the genome-scale of *Escherichia coli* (Feist *et al.*, 2007) and the reconstructed regulatory network describing the regulation of the lactose and the maltose operons. The panel **C** displays the

experimental data published by Ihssen and Egli in 2005 in Environmental Microbiology which demonstrate the maltose usage capacity of the *E. coli* cells grown under limited D-glucose concentration, whereas the lactose usage capacity is still repressed.