Organism	Transcriptomics	Fluxoxomics	Other data	Conditions	Reference
E. coli	genome wide	exchange (8)		Batch growth of wild-type and 6 gene deletion mutants under aerobic and anaerobic conditions	Covert et al, 2004
E. coli	central carbon (73) (relative expression)	internal (25)		Batch growth (aerobic) of wild-type and 3 gene deletion mutants	Fong et al, 2006
E. coli	central carbon (85)	internal (42) exchange (9)	proteomics metabolomics	Chemostat growth (aerobic) of wild-type at 5 dilution rates and 24 single gene deletion mutants ($0.2\ h^{-1}$)	Ishii et al, 2007
E. coli	genome wide	internal (25) exchange (2)	metabolomics	Batch growth (aerobic) of wild-type and 2 over expression mutants	Holm et al, 2009
E. coli	genome wide (relative expression)	internal (32) exchange (8)	metabolomics	Chemostat growth ($0.2\ h^{-1}$) of wild-type and arcA mutant (aerobic, anaerobic and nitrate limited)	Toya et al, 2012
Yeast	genome wide	exchange (3)		Chemostat growth ($0.1\ h^{-1}$) using 4 different carbon sources	Lapujade et al, 2004
Yeast	genome wide (relative expression)	internal (83)	metabolomics	Chemostat growth (aerobic, $0.1\ h^{-1}$) of wild-type and gcn4 mutant	Moxley et al, 2009
Yeast	central carbon (41)	exchange (8)	metabolomics	Chemostat growth (anaerobic, $0.03\ h^{-1}$) of 2 yeast strains under glucose and arabinose limited conditions	Wisselink et al, 2010
Yeast	differentially expressed genes (relative expression)	internal (55)	metabolomics	Batch growth (anaerobic) of yeast at different levels of NADPH oxidation	Celton et al, 2012
Yeast	genome wide	exchange (7)		Chemostat growth (aerobic) at 75% and 85% of maximum growth rate	Lee et al, 2012
Yeast	genome wide	internal (28) exchange (4)	proteomics metabolomics	Chemostat growth ($0.1\ h^{-1}$) of yeast at different oxygen levels	Wiebe et al, 2007; Jouhten et al, 2008; Rintala et al, 2009

Covert MW, Knight EM, Reed JL, Herrgard MJ, Palsson BO (2004) Integrating high-throughput and computational data elucidates bacterial networks. Nature 429: 92–96.

Fong SS, Nanchen A, Palsson BO, Sauer U (2006) Latent pathway activation and increased pathway capacity enable Escherichia coli adaptation to loss of key metabolic enzymes. Journal of Biological Chemistry 281: 8024–8033.

Ishii N, Nakahigashi K, Baba T, Robert M, Soga T, et al. (2007) Multiple high-throughput analyses monitor the response of E. coli to perturbations. Science Signalling 316: 593.

Holm AK, Blank LM, Oldiges M, Schmid A, Solem C, et al. (2010) Metabolic and transcriptional response to cofactor perturbations in Escherichia coli. Journal of Biological Chemistry 285: 17498– 17506.

Toya Y, Nakahigashi K, Tomita M, Shimizu K (2012) Metabolic regulation analysis of wild-type and arcA mutant Escherichia coli under nitrate conditions using different levels of omics data. Molecular BioSystems 8: 2593–2604.

Daran-Lapujade P, Jansen ML, Daran JM, van Gulik W, de Winde JH, et al. (2004) Role of Transcriptional Regulation in Controlling Fluxes in Central Carbon Metabolism of Saccharomyces cerevisiae, a Chemostat Culture Study. Journal of Biological Chemistry 279: 9125–9138.

Moxley J, Jewett M, Antoniewicz M, Villas-Boas S, Alper H, et al. (2009) Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. Proceedings of the National Academy of Sciences 106: 6477–6482.

Wisselink HW, Cipollina C, Oud B, Crimi B, Heijnen JJ, et al. (2010) Metabolome, transcriptome and metabolic flux analysis of arabinose fermentation by engineered Saccharomyces cerevisiae. Metabolic Engineering 12: 537–551.

Celton M, Sanchez I, Goelzer A, Fromion V, Camarasa C, et al. (2012) A comparative transcrip- tomic, fluxomic and metabolomic analysis of the response of Saccharomyces cerevisiae to increases in NADPH oxidation. BMC Genomics 13: 317.

Lee D, Smallbone K, Dunn W, Murabito E, Winder C, et al. (2012) Improving metabolic flux predictions using absolute gene expression data. BMC Systems Biology 6: 73.

Wiebe MG, Rintala E, Tamminen A, Simolin H, Salusjarvi L, et al. (2008) Central carbon metabolism of Saccharomyces cerevisiae in anaerobic, oxygen-limited and fully aerobic steady- state conditions and following a shift to anaerobic conditions. FEMS Yeast Research 8: 140–154.

Jouhten P, Rintala E, Huuskonen A, Tamminen A, Toivari M, et al. (2008) Oxygen dependence of metabolic fluxes and energy generation of Saccharomyces cerevisiae CEN. PK113-1A. BMC Systems Biology 2: 60.

Rintala E, Toivari M, Pitkanen JP, Wiebe MG, Ruohonen L, et al. (2009) Low oxygen levels as a trigger for enhancement of respiratory metabolism in Saccharomyces cerevisiae. BMC Genomics 10: 461.