



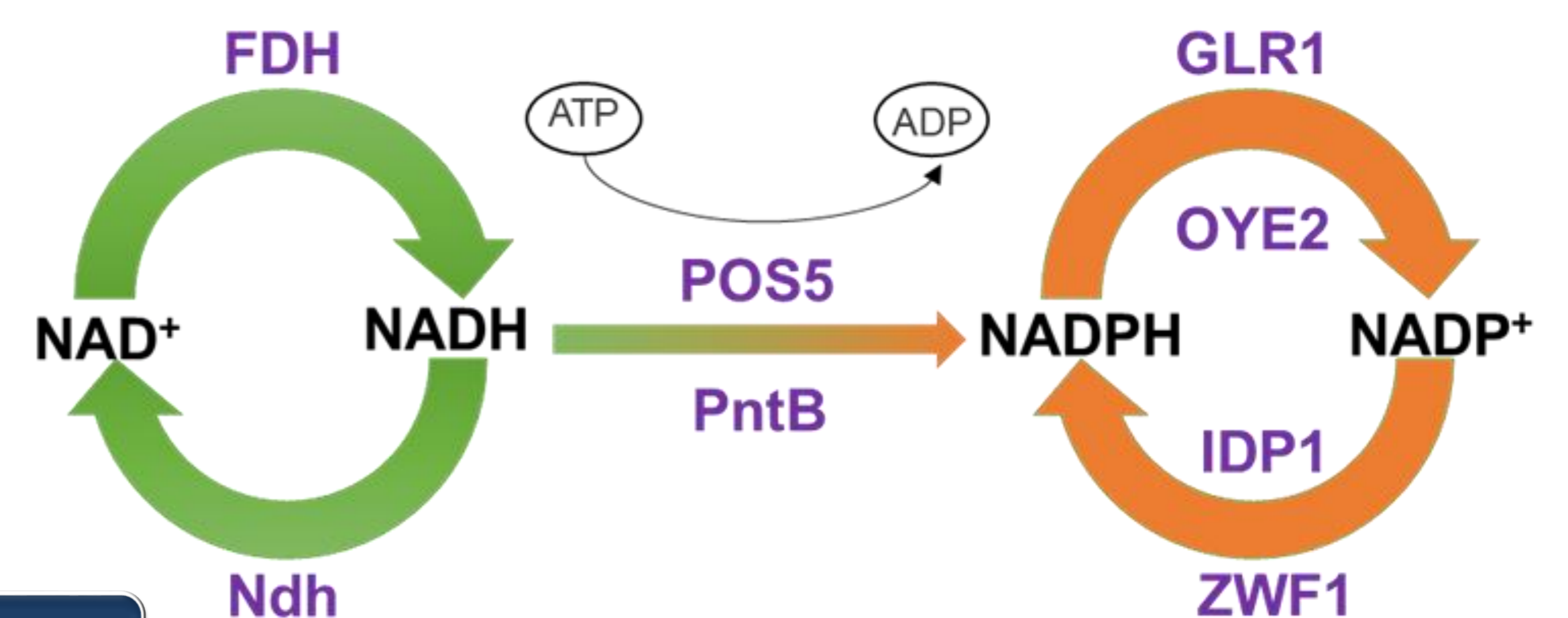
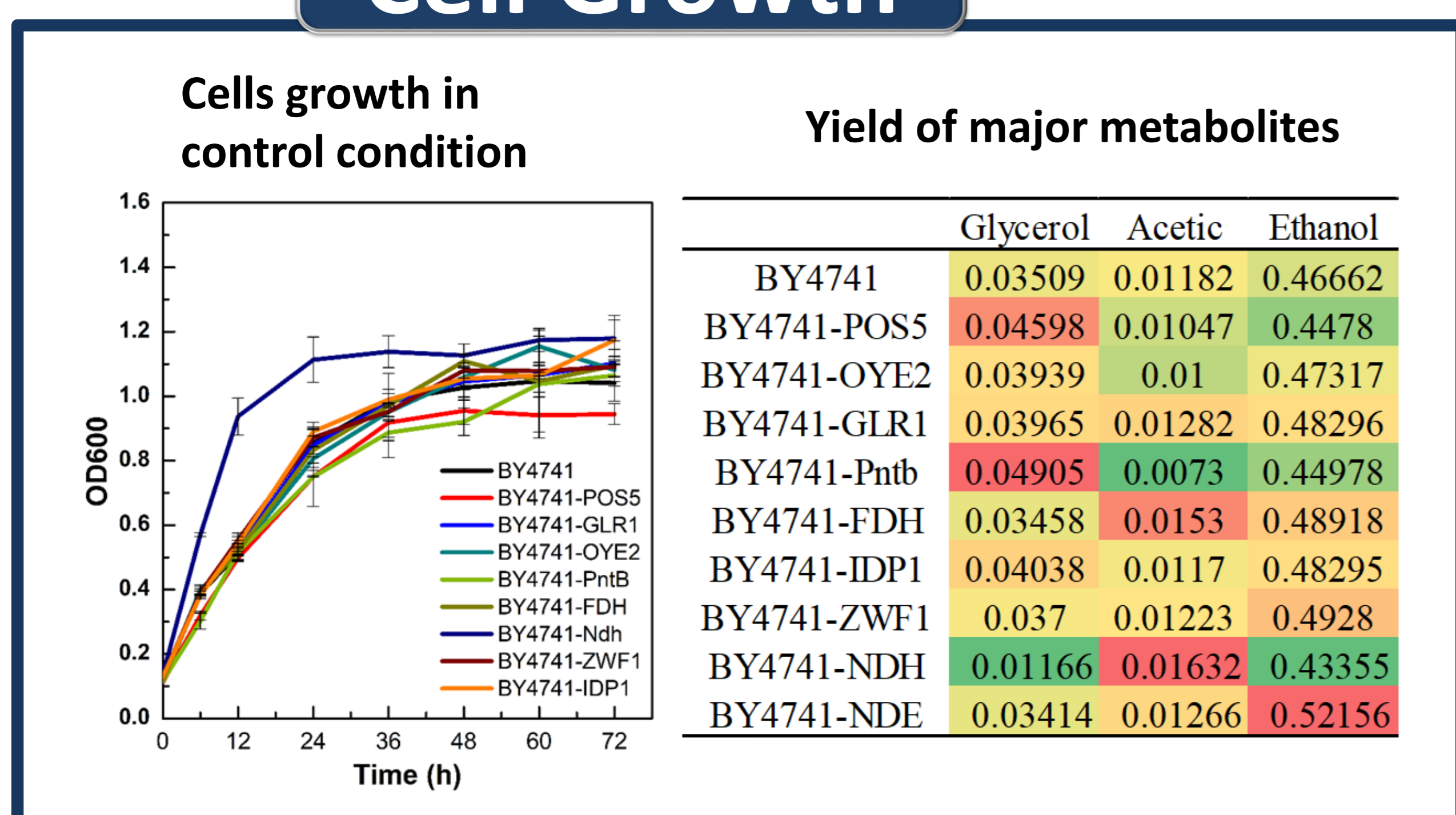
Intracellular redox perturbation in *Saccharomyces cerevisiae* for improvement of furfural tolerance

Kai Li, Chen-Guang Liu*, Feng-Wu Bai

Email: likai.sjtu@sjtu.edu.cn

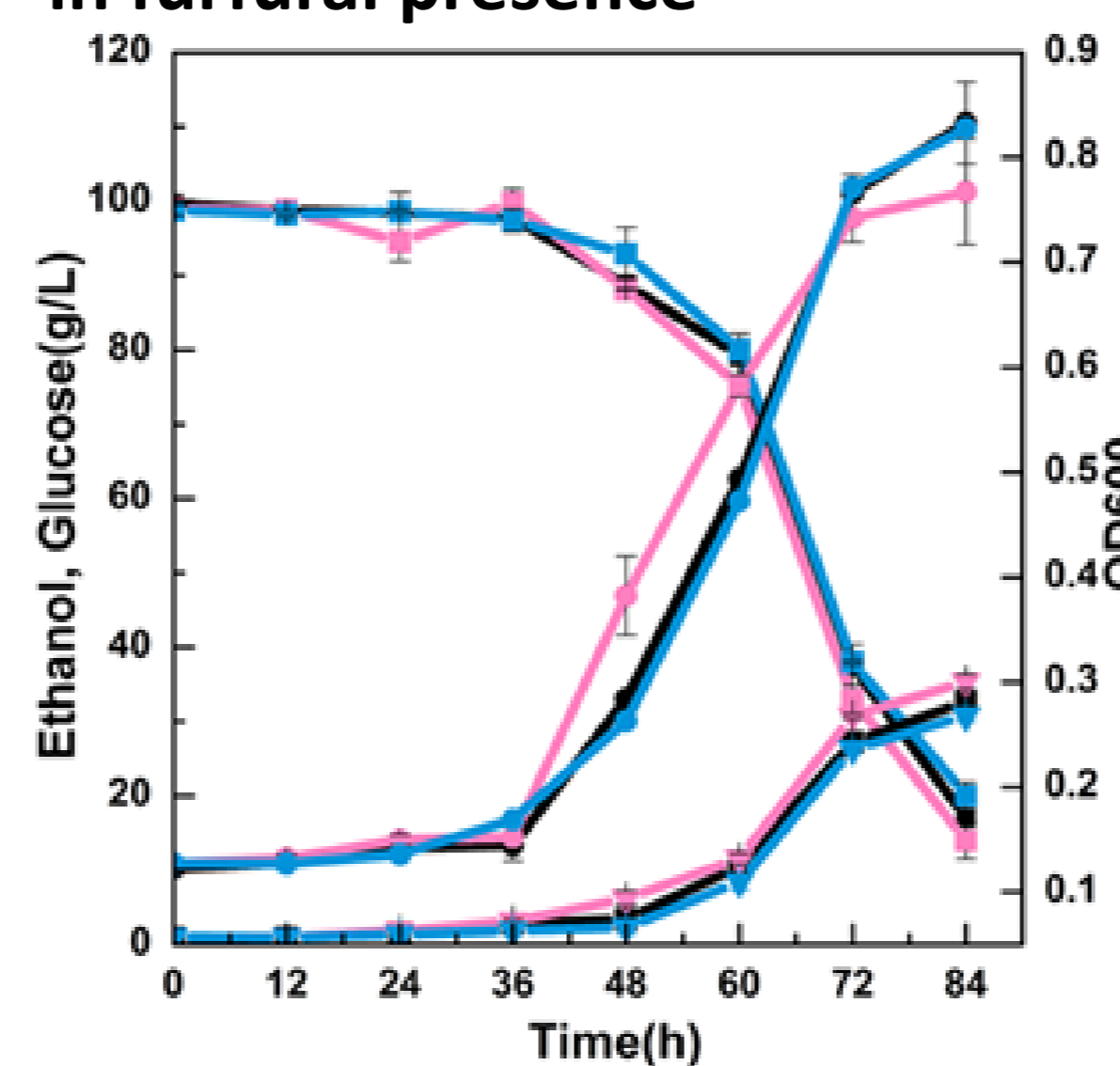
Introduction: Furfural is one of the key inhibitors present in the hydrolysate of lignocellulosic biomass, which compromises growth and ethanol fermentation of *Saccharomyces cerevisiae*. Cofactors NADH/NAD⁺, and NADPH/NADP⁺ are essential electron shuttles to a majority of oxidoreduced reaction in cell metabolism. Cofactor engineering aiming to regulate the availability of cofactors has proved its advantages in modulating metabolic networks, signal transduction, material transport, and then physiological function. Therefore, changes of intracellular redox levels propose a theoretical solution to enhance the yeast cell tolerance to furfural.

Cell Growth

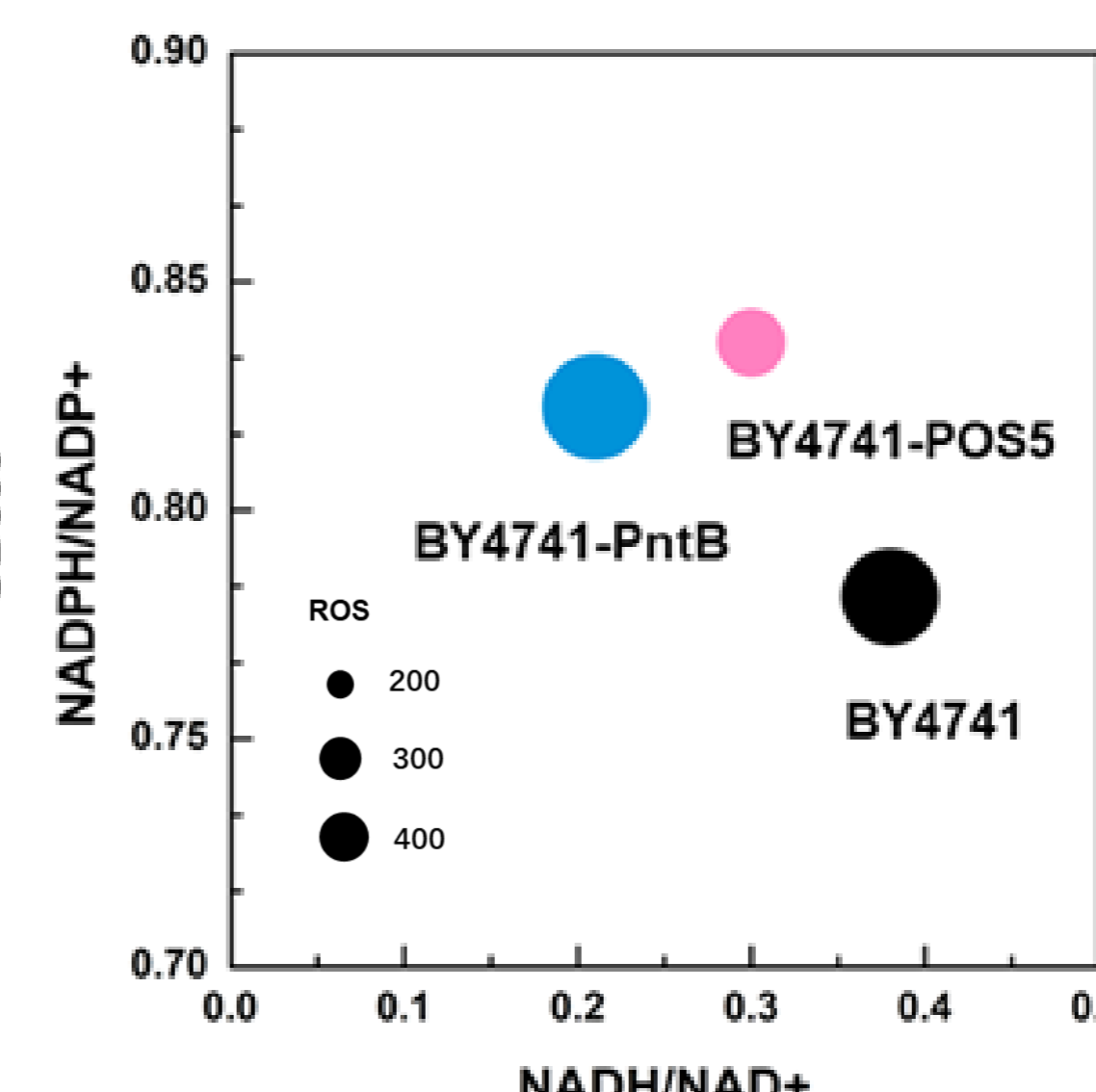


NADH-NADPH

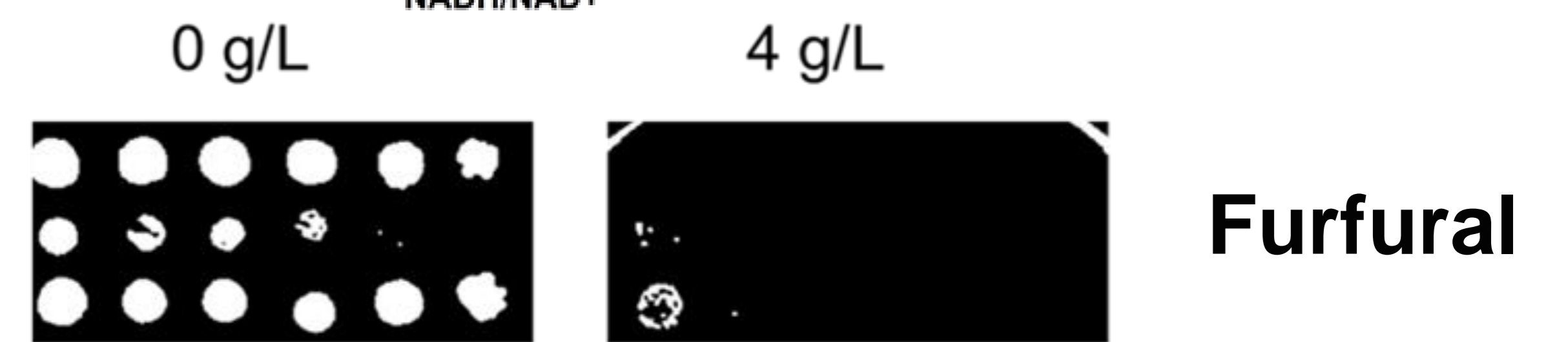
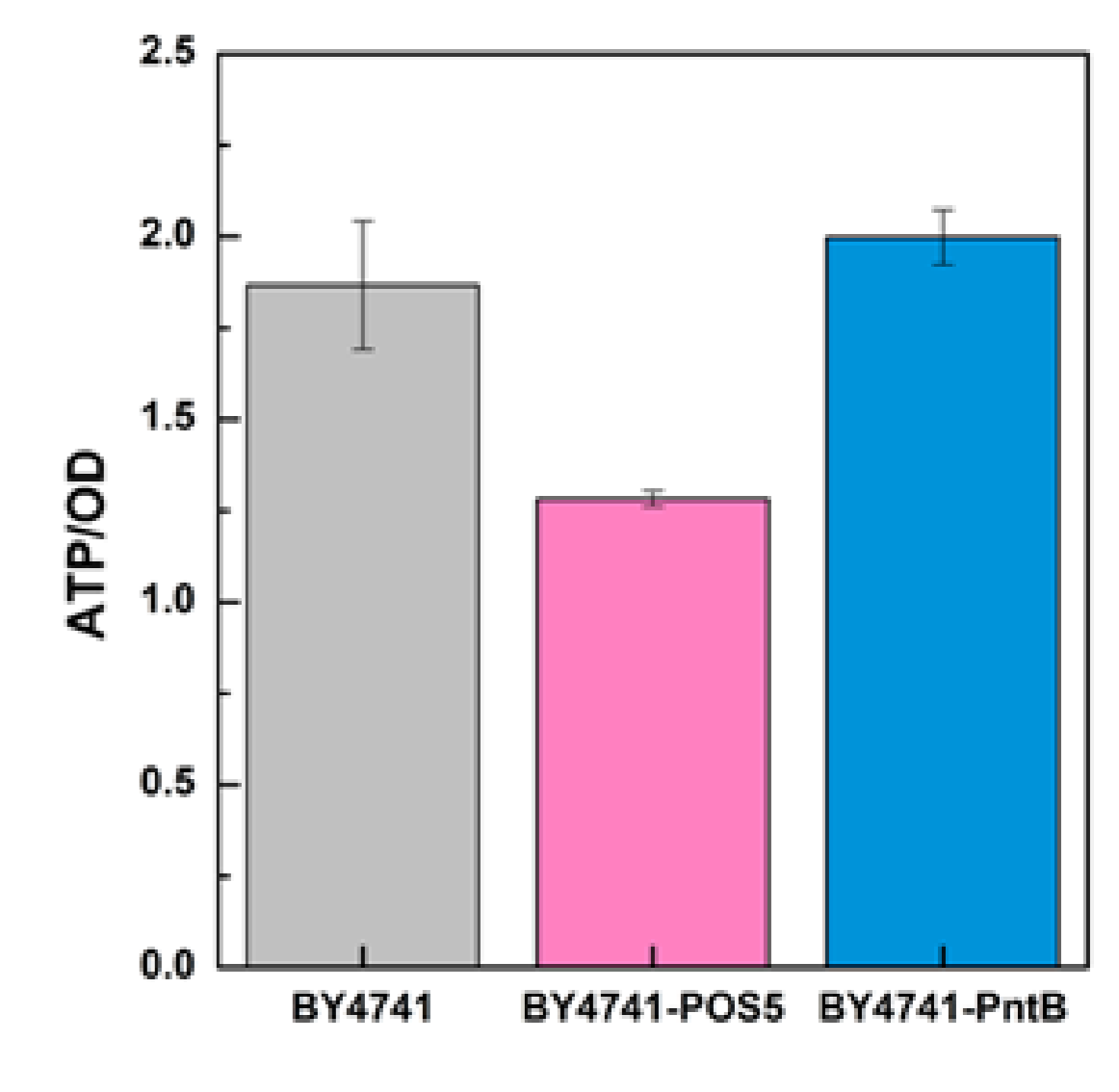
Yeast growth with NADH-NADPH related gene expression in furfural presence



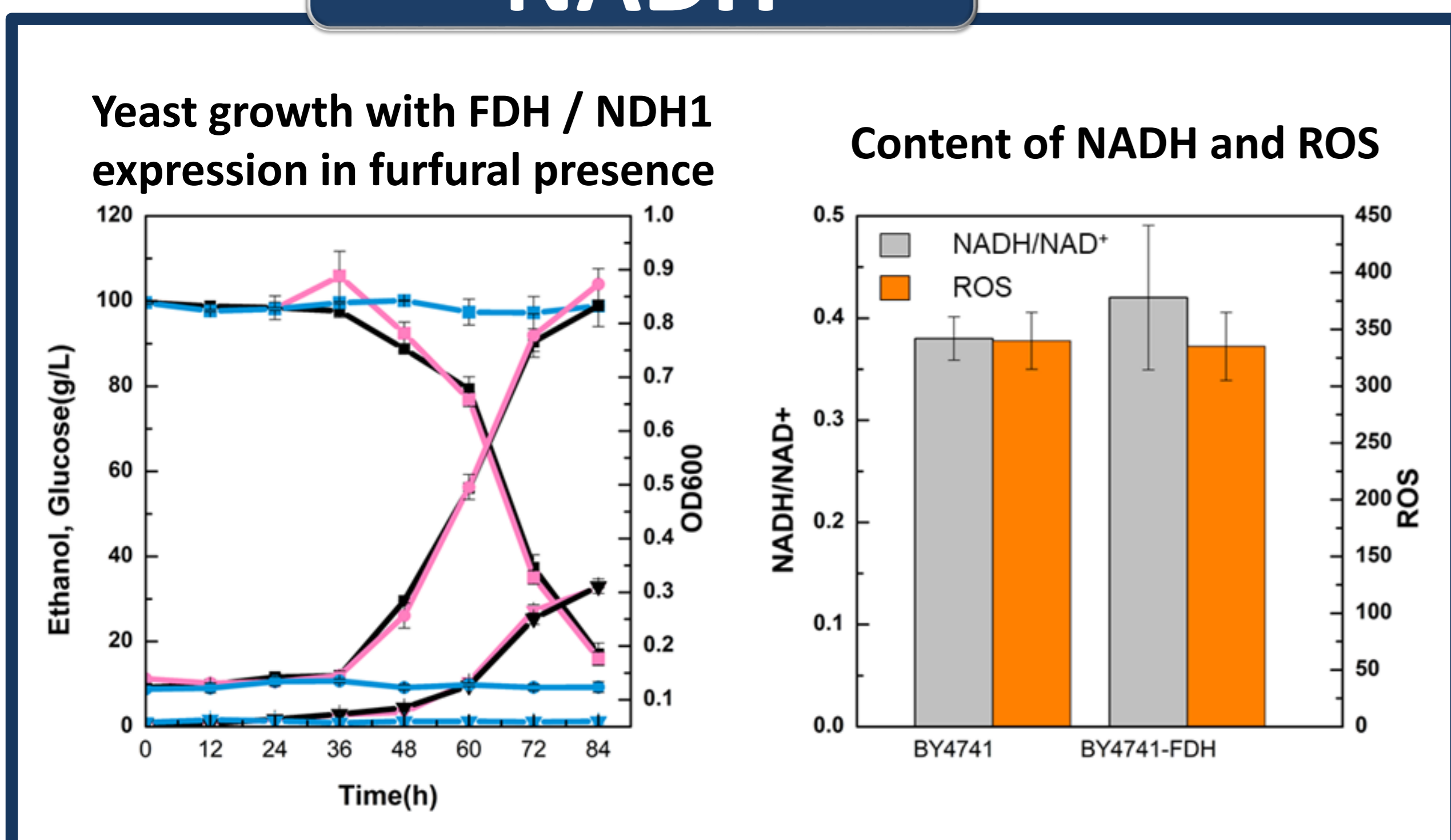
Content of NADPH, NADH, and ROS



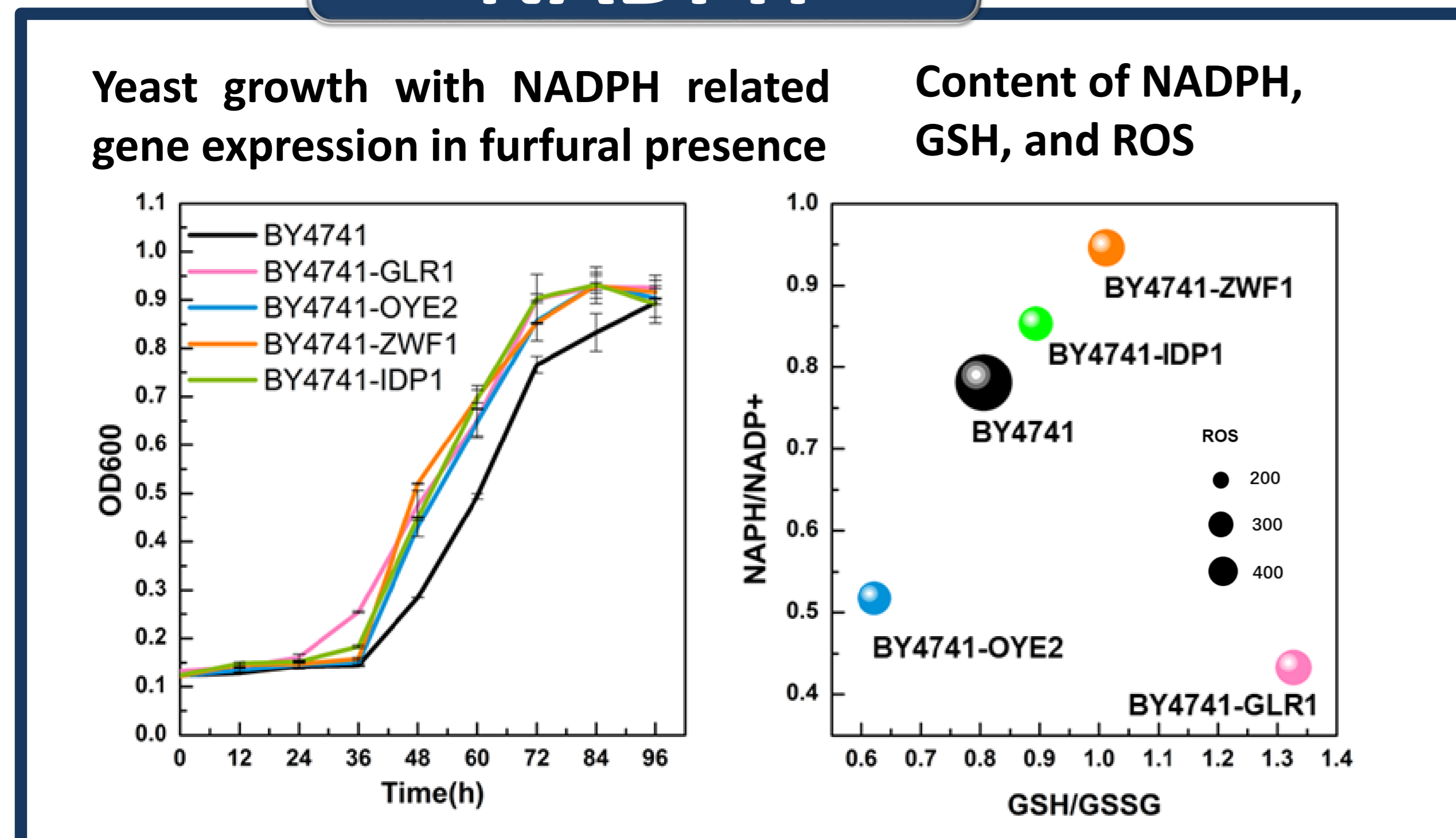
Content of ATP



NADH

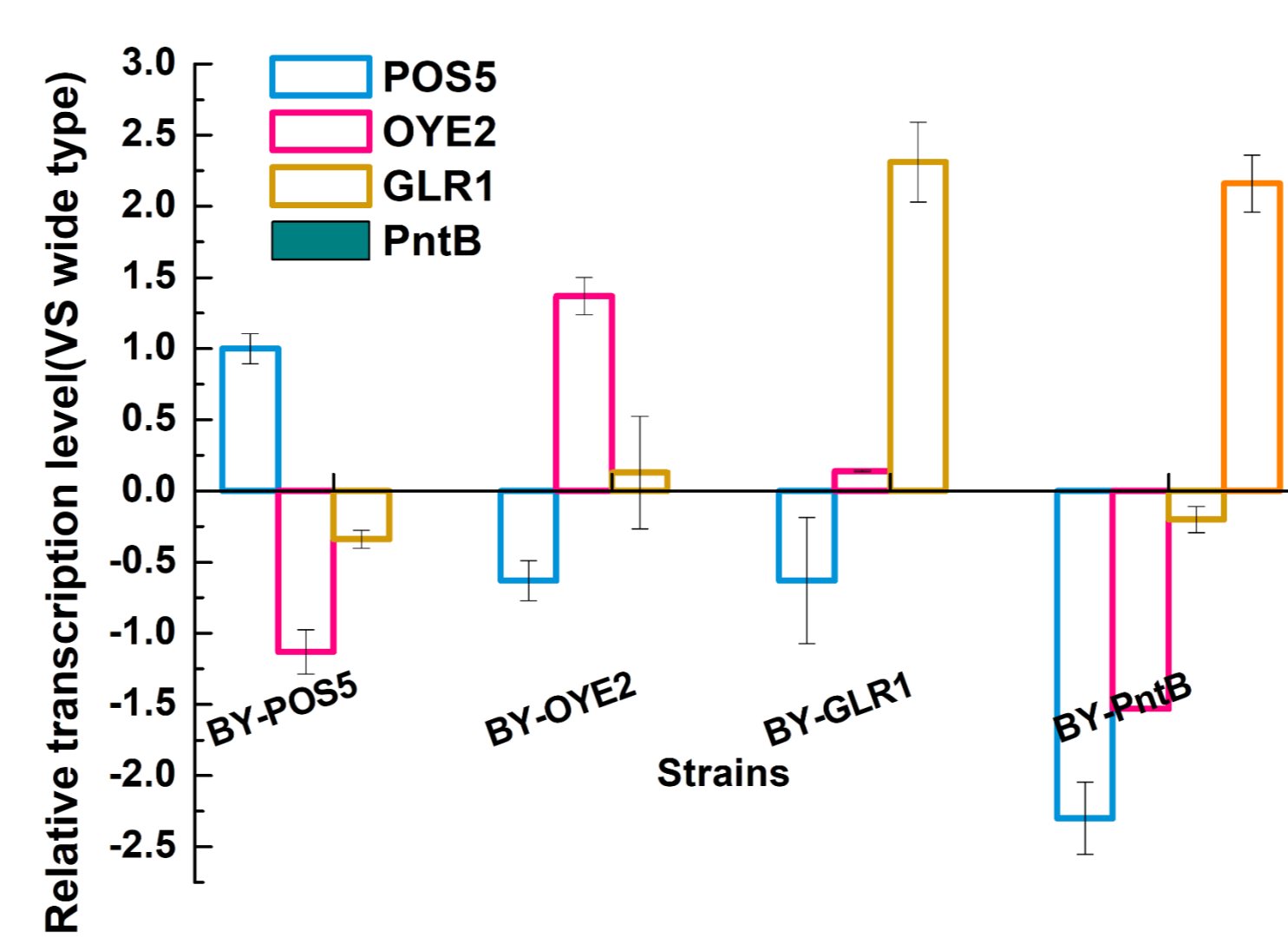


NADPH



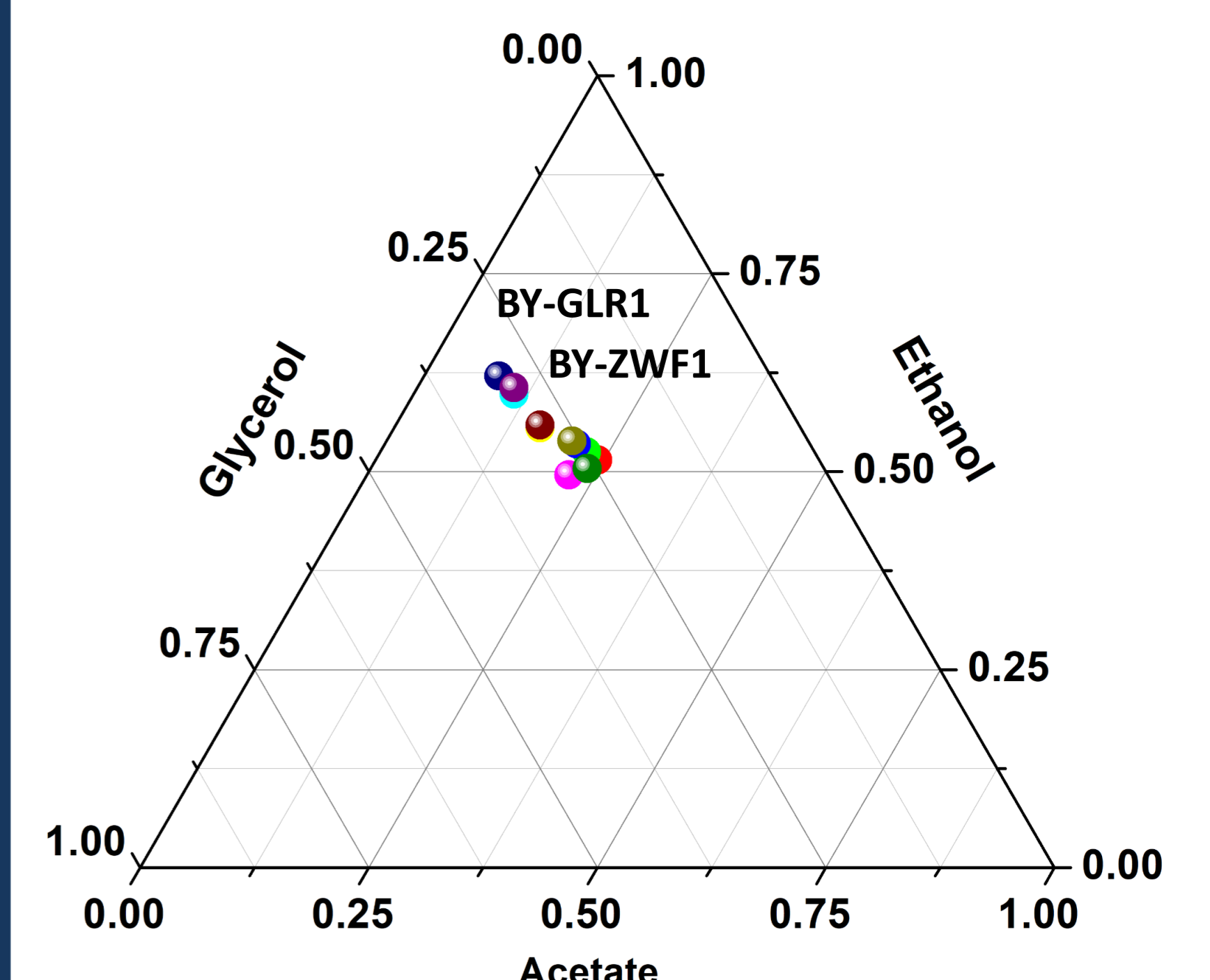
Transcription

Relative transcription level of genes related to NADH and NADPH



Ternary Plot

Main metabolites in the presence of furfural



Conclusion

- Cofactor-related gene expression disturbs intracellular metabolic flow.
- NADPH-related genes expression enhance yeast tolerance to furfural.
- NAD⁺ transhydrogenase or kinase expression weaken cells growth but enhance yeast tolerance to furfural.