

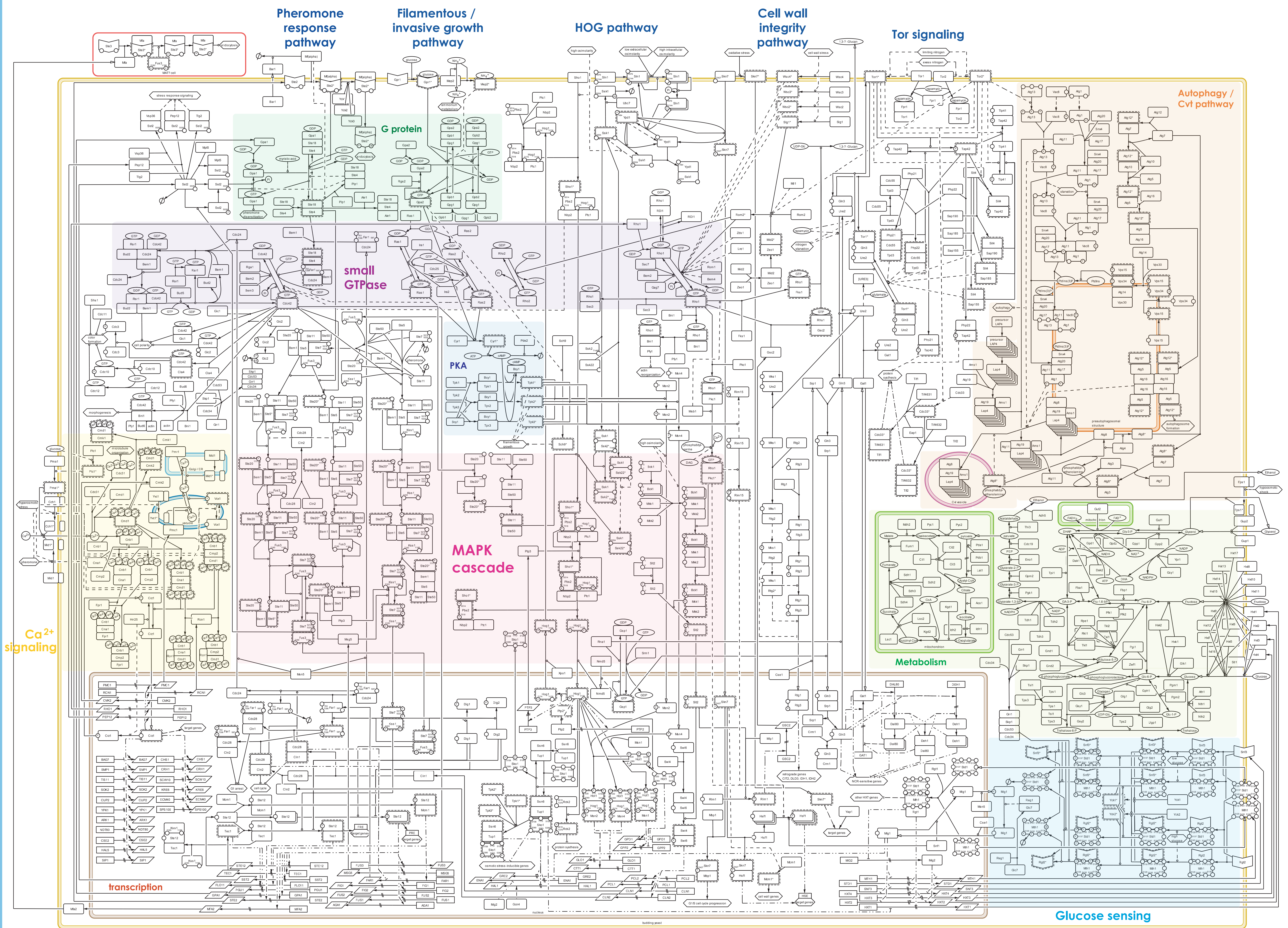
The draft version of the Budding Yeast Molecular Interaction Map includes signal transduction and carbohydrate metabolic pathways, as well as cell cycle net work. 'Signal Transduction and Carbohydrate Metabolic Pathways' includes five major signal transduction and other related pathways: the pheromone response pathway, the filamentous/ invasive growth pathway, the high osmolarity glycerol (HOG) pathway, the cell wall integrity pathway, the Tor signaling pathway, the autophagy/ Cvt pathway, the glucose sensing pathway, the cell wall integrity pathway, the Tor signaling, the autophagy/ Cvt pathway, the carbohydrate metabolism, and the glucose sensing pathway. Modules, such as MAPK cascade, are highlighted within color boxes. 'Cell Division Cycle' includes core regulatory processes which regulate cyclin-dependent kinase

activities. G1 cyclins and B-type cyclins are surrounded with green and red lines respectively. Our long term goal is to successively enhance the map to cover each and every interaction in budding yeast within the next decade.

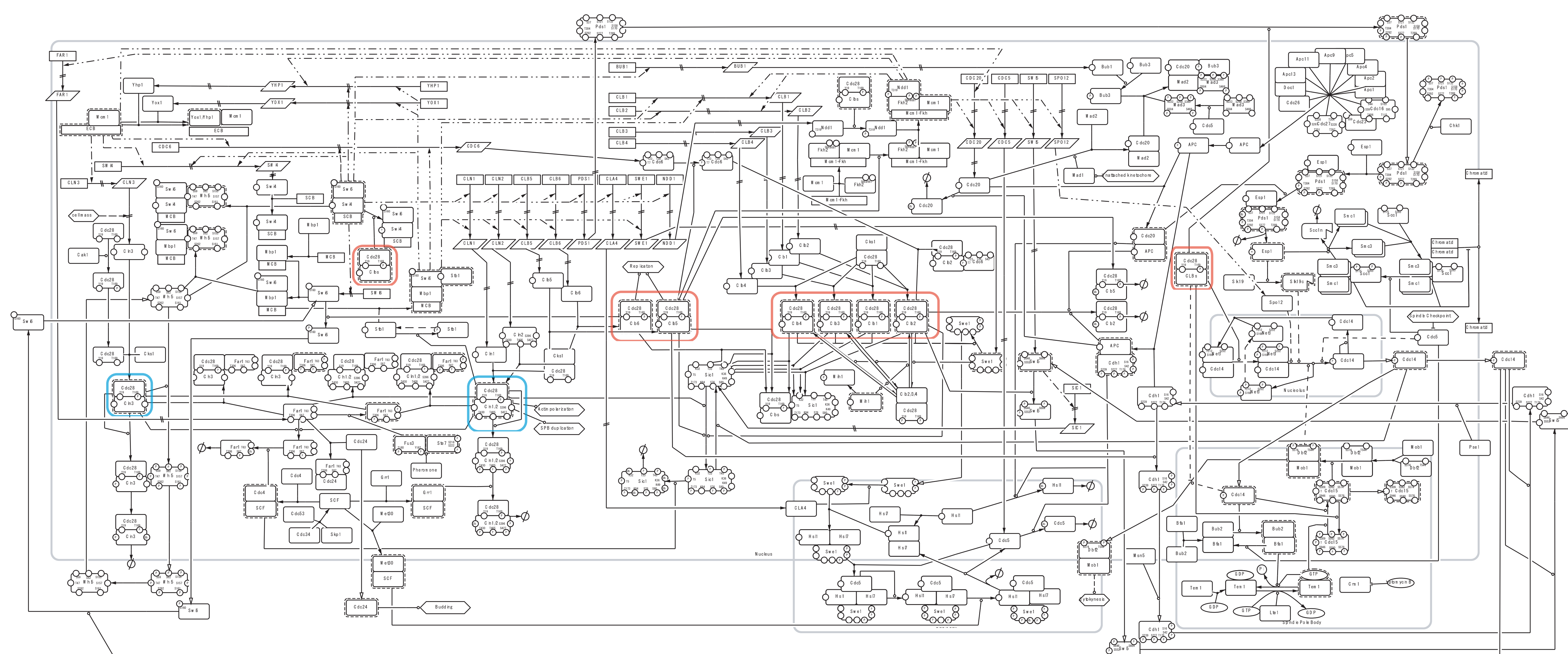
The success of the Yeast Interaction Map project will results in a precise and exhaustive interaction map of yeast which will be an invaluable resource to the community. But, this requires extensive feedback and kind collaboration from the yeast community.

Please provide us your comments on the map and possible contribution to: yeast_map@sbi.jp

Signal Transduction and Carbohydrate Metabolic Pathways (K.Oda)



Cell Division Cycle (H.Moriya)



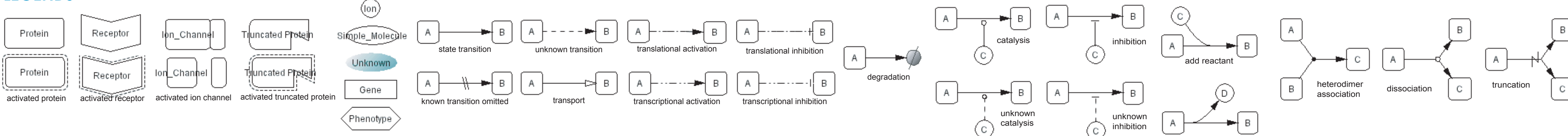
maps stats

produced by CellDesigner ver2.2
+ Adobe Illustrator

Signal Transduction
- 864 Species
- 360 proteins
- 528 reactions

Cell Division Cycle
- 264 Species
- 90 proteins
- 199 reactions

LEGENDS



maps

These maps are created using **CellDesigner ver.2.2**, a structured diagram editor for drawing gene-regulatory and biochemical networks. Networks are drawn based on the process diagram with graphical notation system proposed by Kitano (Kitano et al. Nat. Biotech. Aug. 2005), and are stored using the **Systems Biology Markup Language (SBML)**, a standard for representing models of biochemical and gene-regulatory networks. Each gene or protein node can directly link to the database such as **Saccharomyces Genome Database (SGD)**. CellDesigner is also a **Systems Biology Workbench (SBW)**-enabled application and can integrate with all SBW-enabled modules, including simulation and other analysis packages.



<http://sbml.org>



<http://sbn.org>

This is a part of activities in **Yeast Systems Biology Network (YSBN)**.



www.ysbn.org

downloads

The maps

SBML or PDF files can be downloaded from <http://www.systems-biology.org/001/>

CellDesigner

is available from <http://celldesigner.org/>