

Towards a yeast reference interactome

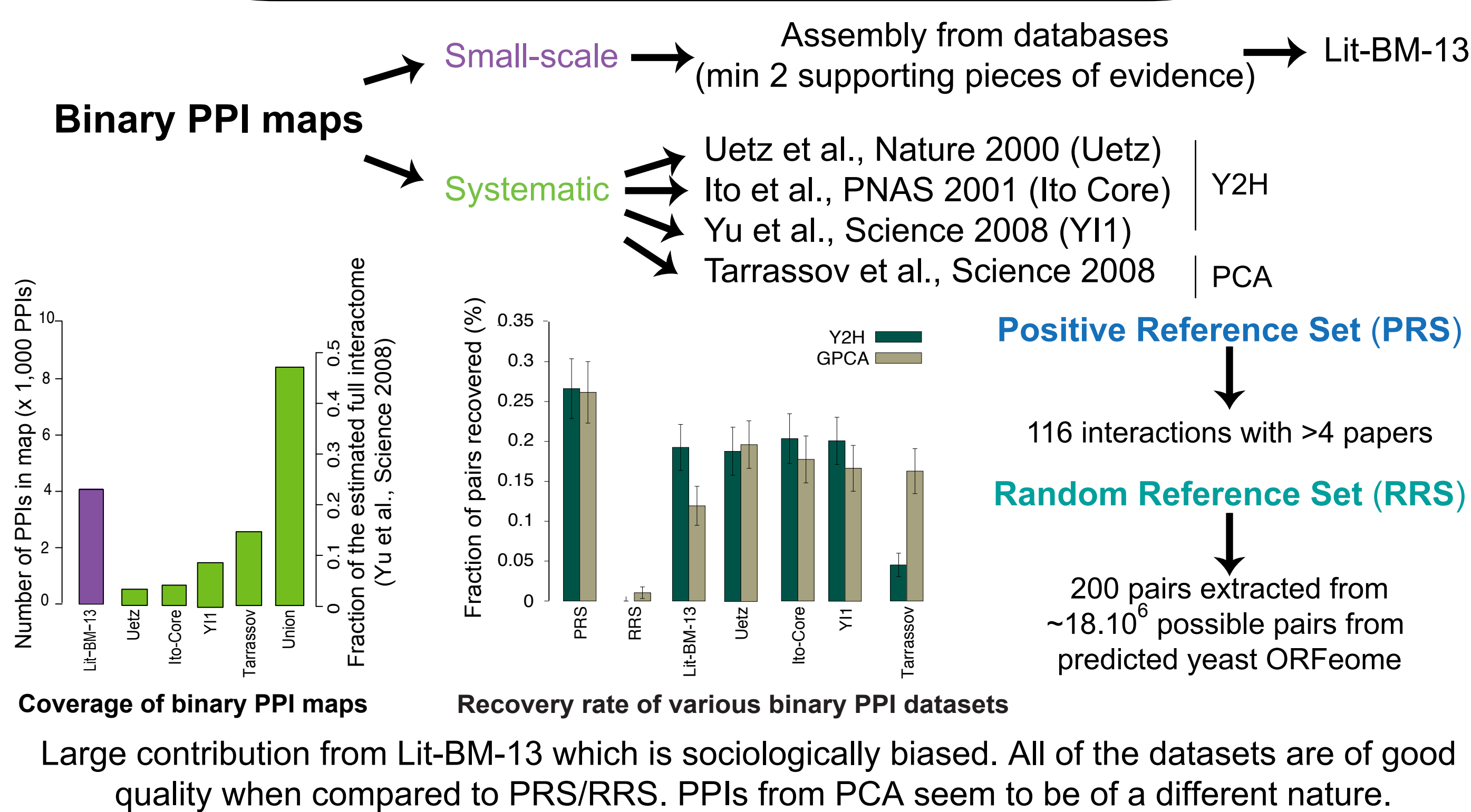
Alice Desbuleux^{1,2}, Tiziana Cafarelli¹, Yang Wang¹, Thomas Rolland¹, Noor Jaikhani¹, Yun Shen¹, Katja Luck¹, Kerstin Spirohn¹, Sudharshan Rangarajan¹, Charles Ogagan Jr.¹, Jean-Claude Twizere², Mike Calderwood¹, Tong Hao¹, Yves Jacob^{1,3}, David Hill¹, Quan Zhong^{1,4}, Marc Vidal¹, Benoit Charlotteaux¹

¹DFCI Center for Cancer Systems Biology (CCSB) and Department of Cancer Biology, and Harvard Medical School, Department of Genetics, Boston, MA, ²University of Liege, GIGA-R, Liege, Belgium, ³Pasteur Institute, Department of Genetics, Paris, France, ⁴Wright State University, Dayton, OH

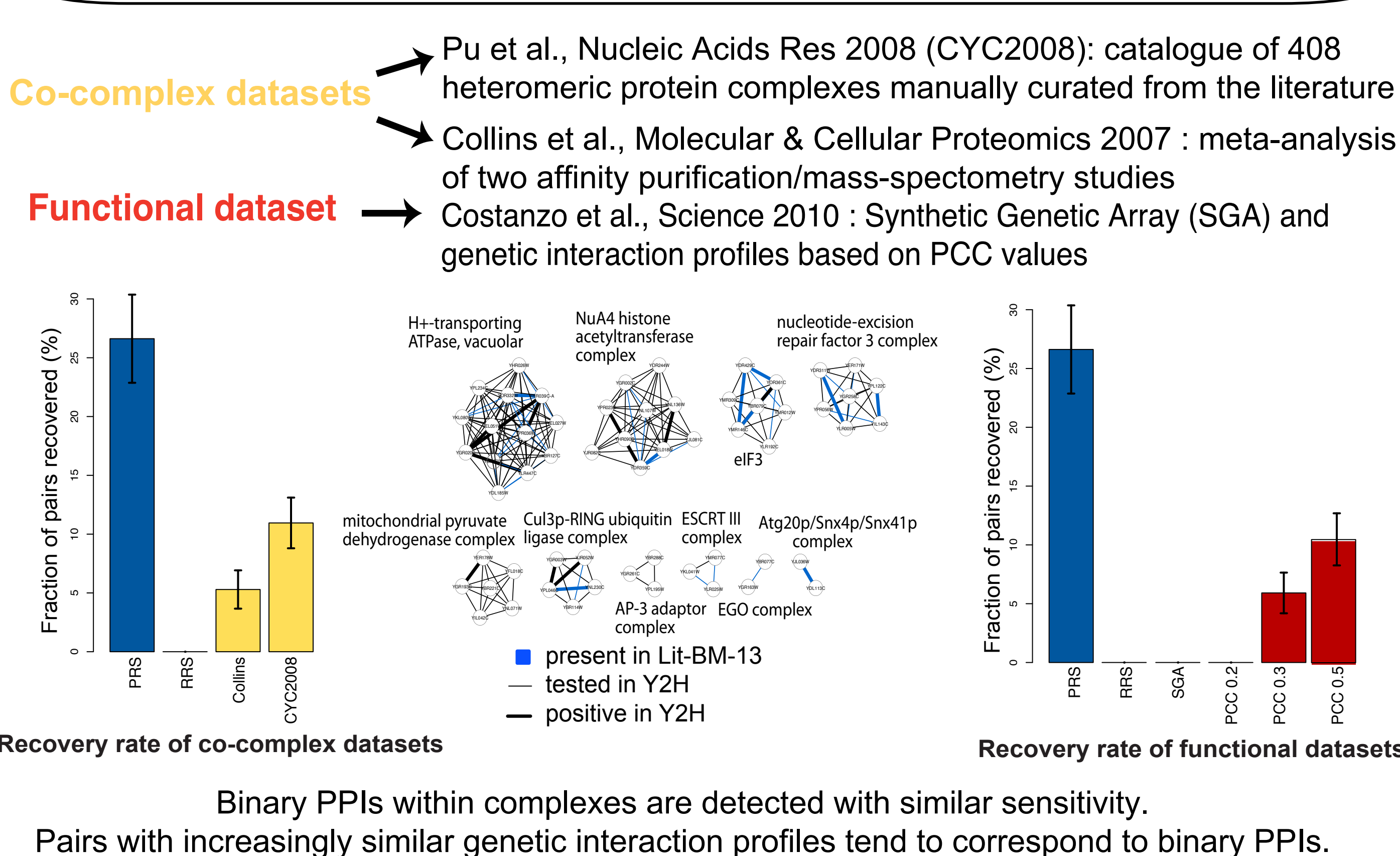
Motivation

Despite an increasing number of interactomic datasets already available for model organisms and humans, many aspects remain contradictory, debatable or unclear due to the lack of complete high-quality networks. For example, does macromolecule connectivity in interactome maps reflect functional importance or sociological biases? Do biophysical interactions always reflect functional relationships? Here we propose to build a new, alternative view of an interactome map for *S. cerevisiae* for which a lot of genome-wide datasets, protein-protein interaction (PPI) maps and functional maps based for instance on expression or genetic interactions, are already available.

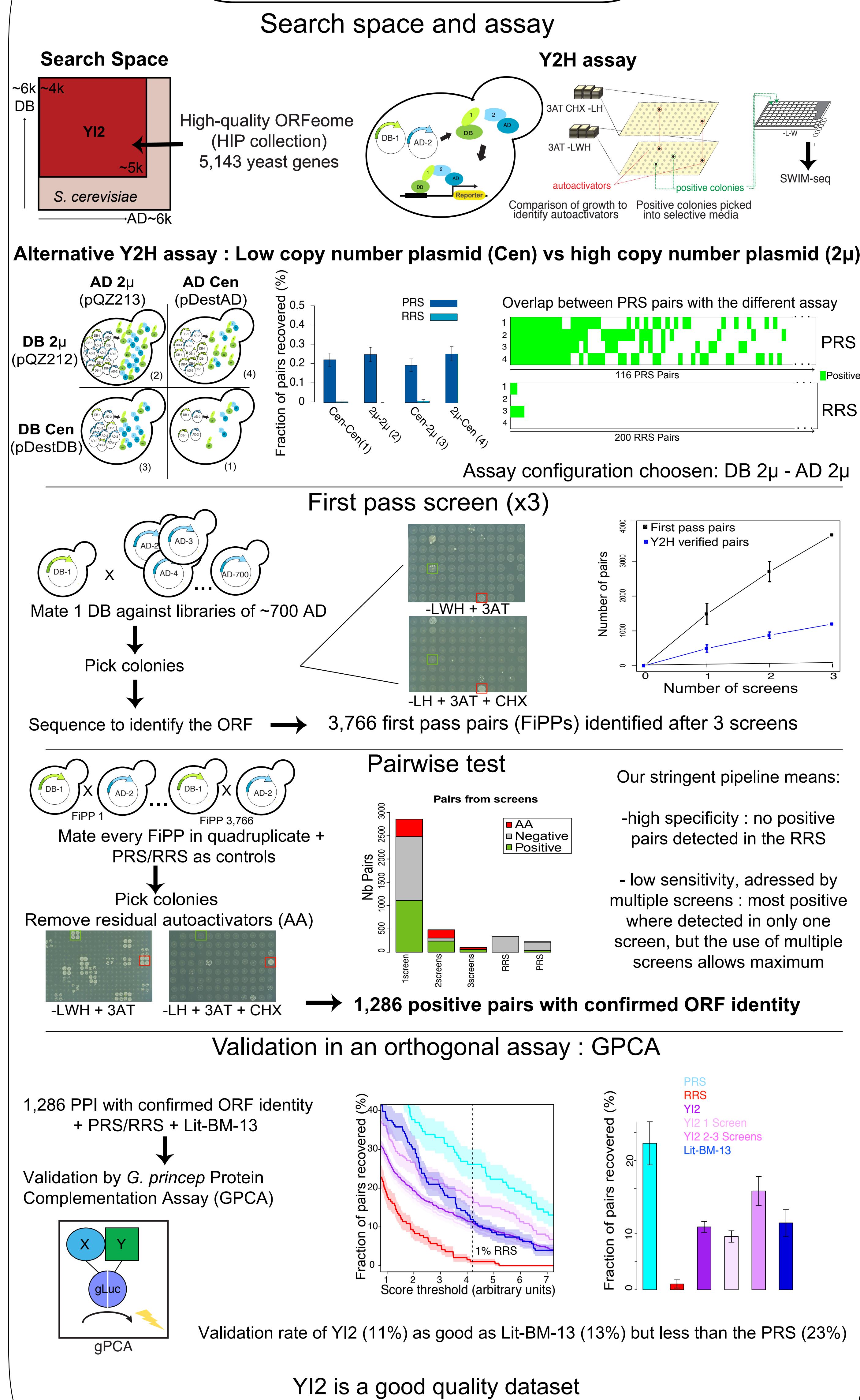
Less than half of the yeast interactome covered



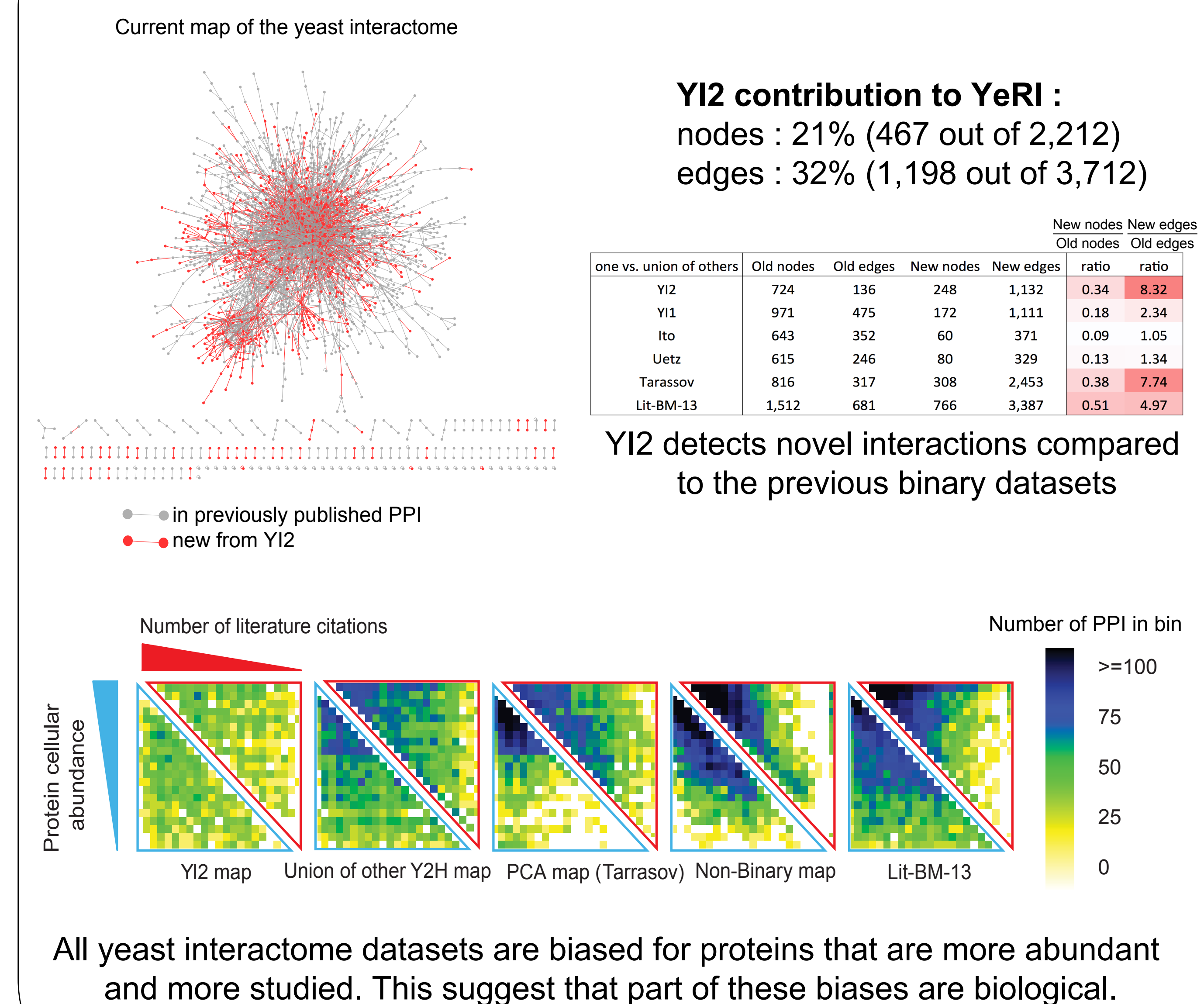
Recovery of binary PPI in protein complexes and functional datasets



Approach to build a reference map



Preliminary results



Future plans

- Validate the Y12 dataset with another orthogonal assay to further assess the quality of our dataset
- Expand the screens to the complete search space for *S. cerevisiae*, including candidate proto-genes (~1,139 genes) (Carvunis et al., Nature 2012)
- Perform additional screens of the complete search space to generate a first Yeast Reference Interactome map (YeRI)