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FANCY metabolomics

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In the January [Nature Biotechnology](#), Raamsdonk *et al.* find that, even when mutation of a gene causes no obvious phenotype, metabolite profiling can still give clues to gene function (*Nat Biotechnol* 2001, **19**:45-50). Their test case involves two yeast strains deleted for either one of the two redundant genes for 6-phosphofructo-2-kinase (6-PF-2-K). These deletion strains fail to show a growth defect, even in chemostat competition experiments, but an analysis of specific metabolites clearly sets them apart from wild-type yeast. Raamsdonk *et al.* then test a more general method, in which the extracts from the two deletion strains and several other metabolic mutants are analyzed by ¹H-NMR spectroscopy. Even without identifying the individual metabolites whose concentrations have changed, the two 6-PF-2-K mutants can be clustered together based on the similar changes in particular peaks. This method, dubbed functional analysis by co-responses in yeast (FANCY), is now being applied to a [collection](#) of yeast deletion mutants.

References

1. *Nature Biotechnology*, [<http://www.nature.com/nbt/>]
2. Functional characterization of the *S. cerevisiae* genome by gene deletion and parallel analysis.