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A list of lists for yeast

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The function of an uncharacterized gene can sometimes be determined by mutating the gene and using a [phenotypic assay](#). But sometimes a convenient phenotype does not exist for a given cellular function. Hughes *et al.* suggest in the July 7 [Cell](#) that expression profiles can be used instead (*Cell* 2000, **102**:109-126). Rather than measuring expression profiles as conditions change (e.g., at different points in the [cell cycle](#), Hughes *et al.* keep the culture conditions constant and measure the profiles of 276 deletion mutants, 11 conditional lethal mutants, and wildtype cells after each of 13 different chemical treatments. The resultant expression profiles are clustered and used to assign functions to 8 previously uncharacterized genes and to determine the target of a commonly used anesthetic. Many important correlated expression changes are small (1.5-fold or less), suggesting that data sets need to be highly internally consistent, and large.

References

1. Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular bar-coding strategy.
2. Cell Online, [<http://www.cell.com/>]
3. A genome-wide transcriptional analysis of the mitotic cell cycle.