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Watch out for aneuploidy

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In an analysis of both new and old microarray data in the July [Nature Genetics](#), Hughes *et al.* find that results are frequently skewed by aneuploidy (*Nat. Gen.* 2000, **25**:333-337). Their first clue was an unexpected transcript profile similarity between two unrelated yeast mutants; the cause turned out to be an extra copy of an entire chromosome. Approximately 8% of the yeast mutants examined had chromosome-wide expression biases, even though most of these mutants are not known to have chromosome transmission defects. In five cases a gained chromosome had a close homologue of the deleted gene, and in two cases a growth advantage was demonstrated.

References

1. Nature genetics, [<http://www.nature.com/ng/>]