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Splicing chips

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The process of RNA splicing by the spliceosome helps to generate molecular diversity beyond the genome sequence. In the May 3 Science, Tyson Clark and colleagues at the University of California, Santa Cruz describe a genome-wide study of splicing in yeast (*Science* 2002, **296**:907-910). They designed custom microarrays with oligonucleotides capable of distinguishing between spliced and unspliced RNAs, and demonstrated the specificity of this splicing-specific microarray by analysing RNA from *Saccharomyces cerevisiae* with a mutation in the prp4-1gene, which encodes a component of the spliceosome. Clark *et al.* studied 18 mutant yeast strains lacking non-essential genes linked to RNA processing and found several examples of increased accumulation of introns and loss of spliced junction sequences. They also found that different mutations had distinct effects on spliced and unspliced RNA. This strategy will could be applied to the human genome in which as many as 60% of transcript may undergo alternative splicing.

References

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