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Cycling surprises

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Array analysis of dividing cells has been tackled for yeast, but in the January *Nature Genetics* Cho *et al.* present the first large-scale analysis in human cells (*Nat Genet* 2001, **27**:48-54). They identify 731 of 40,000 human genes and expressed sequence tags (ESTs) as being cell cycle regulated in primary fibroblasts, and use a functional classification system to identify coordinate regulation of pathways. Notable surprises include upregulation of motility-related genes in G2 (perhaps to prepare daughter cells for migration away from each other), and of extracellular matrix-associated genes in M (possibly to enhance the re-establishment of cell-cell contact and communication after mitosis).

References

1. Expression monitoring by hybridization to high-density oligonucleotide arrays.
2. A genome-wide transcriptional analysis of the mitotic cell cycle.
3. *Nature Genetics*, [<http://www.nature.com/ng/>]
4. Supplementary data to *Nat Genet* 2000, 27:48-54, [<http://www.salk.edu/LABS/chipdata/>]