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In the April 10 Sciencexpress Scherer *et al.* report completion of the sequencing and annotation of human chromosome 7 (*Sciencexpress*, DOI:10.1126/science.1083423, April 10, 2003). The sequence is 158 megabases long, most of which comes from the Celera whole-genome scaffolds, combined with the publicly funded clone-based sequence. The authors integrated the chromosome 7 sequence with data from a number of database resources, particularly those related to human disease. Comparative analysis revealed a relatively small number of discrepancies with the NCBI chromosome 7 assembly. Comparison with the Celera mouse genome sequence led to the identification of around 22,000 syntenic anchor points. Scherer *et al.* identified 1,917 gene structures, almost half of which correspond to known genes; the average gene size is around 70 kb, and there are 99 overlapping genes and 38 sense-antisense gene pairs. There is evidence for extensive intra-chromosomal duplications, some of which coincide with mouse synteny breaks or with human diseases. Scherer *et al.* report that several human disorders, including susceptibility to autism and Williams-Beuren syndrome, may map to inversion breakpoints.

References

1. *Sciencexpress*, [http://www.sciencexpress.org]

2. Celera , [http://www.celera.com]

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