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Synteny on chromosome 21

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Conservation of genomic sequences between species indicates regions of functional importance, containing protein-coding genes, non-coding genes or [regulatory elements](#). In the December 5 [Nature](#) Dermitzakis *et al.* describe a thorough analysis of syntenic regions of [human chromosome 21](#) (*Nature* 2002, **420**:578-582). The 33.5 Mb of chromosome 21 was compared to sequences from mouse chromosomes 16, 17 and 10. There were 3,491 blocks that are over 100 bp long and have at least 70% sequence identity; around two thirds of these correspond to regions with unknown function. Only a small number of these regions appear to represent potential unknown genes, and most are probably not transcribed. A three-way species analysis (human, mouse and rabbit) provided evidence for broad conservation of these sequence blocks, supporting their functional significance. This study provides an example of the power of combined computational, experimental and evolutionary analysis. The conserved, non-genic regions that have been identified probably contain regulatory features and will require specific functional genomic strategies to figure out what they do.

References

1. Conserved noncoding sequences are reliable guides to regulatory elements.
2. *Nature*, [<http://www.nature.com>]
3. The DNA sequence of human chromosome 21.