

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

## Mouse map

ArticleInfo		
ArticleID	:	4548
ArticleDOI	:	10.1186/gb-spotlight-20020806-01
ArticleCitationID	:	spotlight-20020806-01
ArticleSequenceNumber	:	214
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2002-8-6 OnlineDate : 2002-8-6
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

---

Comparative analysis of complete genome sequences for several mammals is predicted to provide greater understanding of biological processes and to have huge impact on human health. In an Advanced Early Publication in *Nature*, an international consortium led by David Bentley at [The Wellcome Trust Sanger Institute](#), UK, brings that goal one step closer with the report of a completed physical map of the mouse genome (*Nature*, 31 July 2002, doi:10.1038/nature00957). The consortium constructed a clone map in two phases: they analysed restriction digest pattern 'fingerprints' and boundary sequences of over 300,000 bacterial artificial chromosomes (BAC) clones to construct a human-mouse homology clone map; and then they used thousands of independently mapped mouse markers to generate a [final map](#) containing around 300 contigs (representing 98% coverage of the genome). The consortium found over 50,000 homologous sections between the mouse and human genomes (many in introns and intergenic regions). They document extensive [conserved synteny](#), finding hundreds of regions where the chromosomal location of multiple blocks of genes is conserved. This study highlights how completed genome data will help to speed up the mapping of genomes of related organisms, and will provide an essential framework for the generation of complete sequence and subsequent annotation of the mouse genome.

## References

1. *Nature*, [<http://www.nature.com>]
2. The Wellcome Trust Sanger Institute , [<http://www.sanger.ac.uk>]
3. Mouse genome resources, [<http://www.ncbi.nlm.nih.gov/genome/guide/mouse>]
4. Human sytenyview, [[http://www.ensembl.org/Homo\\_sapiens/sytenyview](http://www.ensembl.org/Homo_sapiens/sytenyview)]