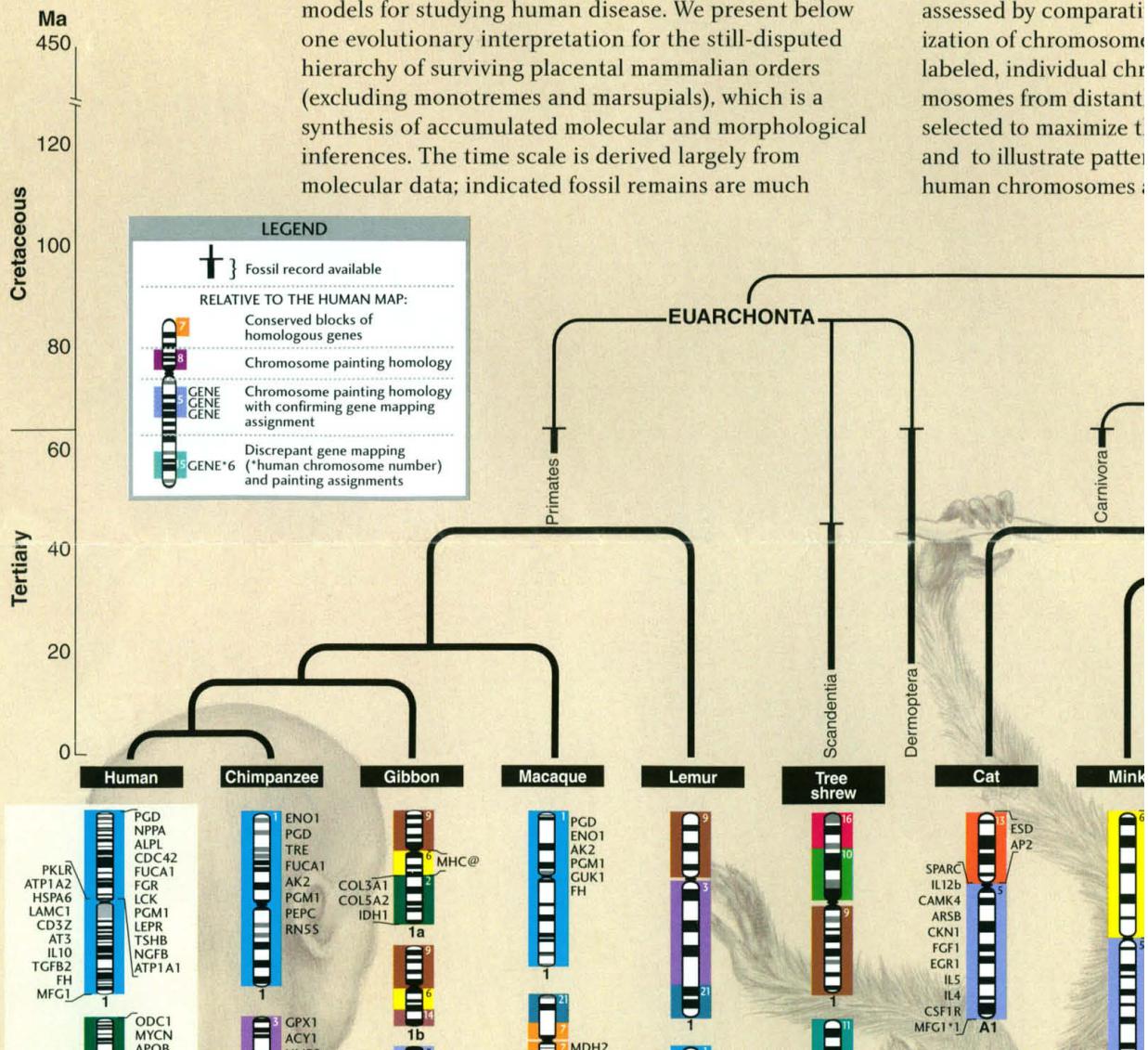


Science

Comparative MAMMAL GENOMICS

Traces of evolutionary history appear in functional morphology and DNA sequences of living and extinct species. These remnants of the past can lead to insights into the relationships among extant groups of animals, the forces driving evolution, and the utility of animal models for studying human disease. We present below one evolutionary interpretation for the still-disputed hierarchy of surviving placental mammalian orders (excluding monotremes and marsupials), which is a synthesis of accumulated molecular and morphological inferences. The time scale is derived largely from molecular data; indicated fossil remains are much

younger, raising controversial issues about the timing of mammal ancestors. The figure depicts genomes for 21 orders, which are labeled by their names. Examples show genomic regions assessed by comparative analysis of chromosome painting homology. Labeled, individual chromosomes from distant species are selected to maximize the contrast and to illustrate patterns of human chromosomes.



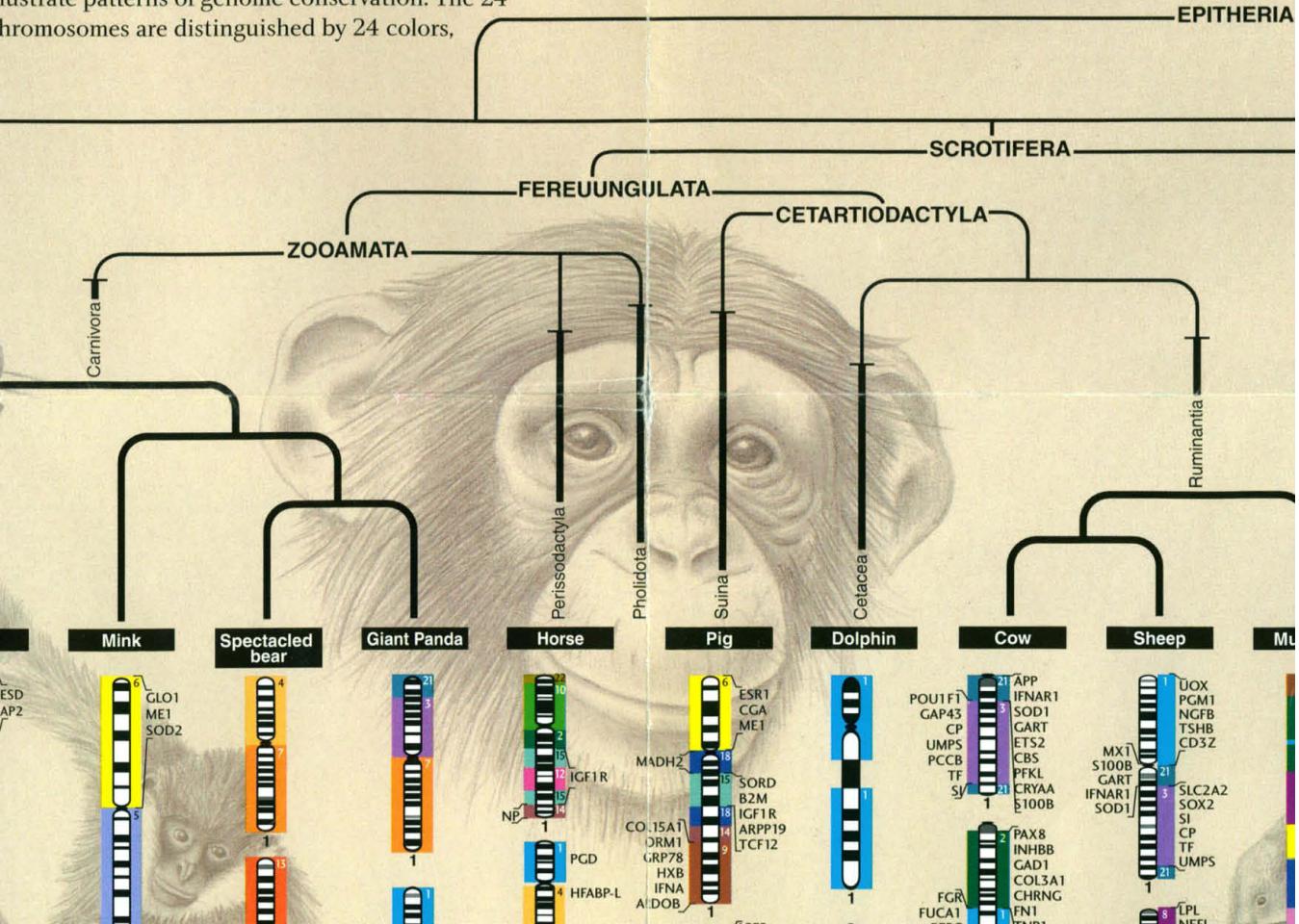
Comparative Genomic Radiation

raising controversies around the precise age of our ancestors. The tips of the phylogenetic tree show genome-wide homology alignments for 21 representative species from 11 orders, which are labeled on the vertical lines. These alignments show genome-wide homology alignments determined by comparative gene mapping or direct visualization of chromosome painting, in which fluorescently labeled individual chromosomes are hybridized to chromosomes from distantly related species. Species were chosen to maximize the number of orders represented and to illustrate patterns of genome conservation. The 24 chromosomes are distinguished by 24 colors,

and regions of human chromosome homology in other species are indicated by color and human chromosome number (for example, cat chromosome A1 contains gene stretches homologous to human chromosomes 5 and 13). Selected gene homologs in each species represent a subset of extensive comparative gene mapping data; thus genes listed may not reflect the extreme borders of the conserved segments. Gene orders have been determined in human, cat, pig, sheep, rat, mouse, and zebrafish; in other species the genes are listed in the order in which

they appear in linkage groups. This figure is present to serve for discussion of what can be found associated with a feature/disease.

EPITHERIA



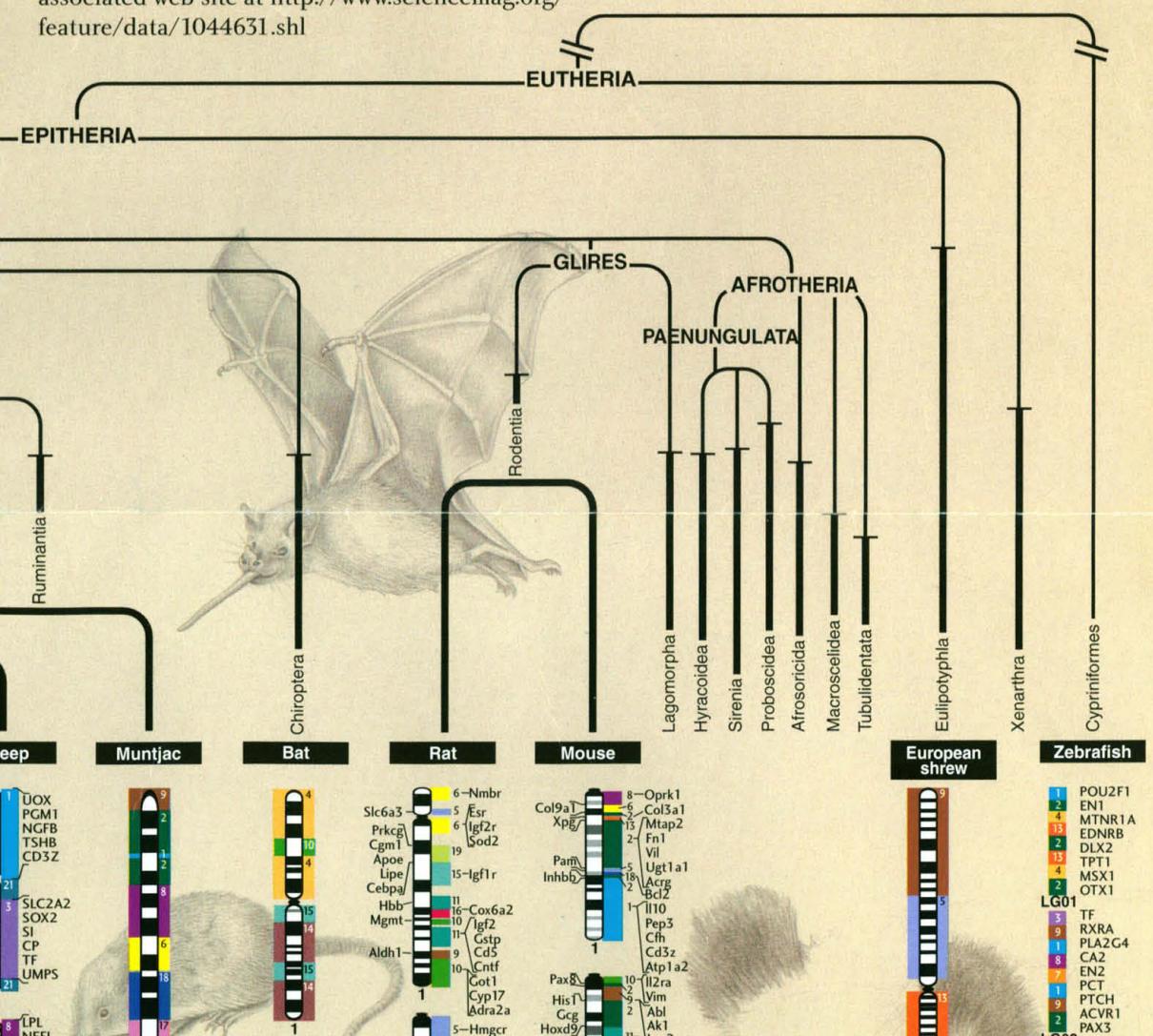
genomics

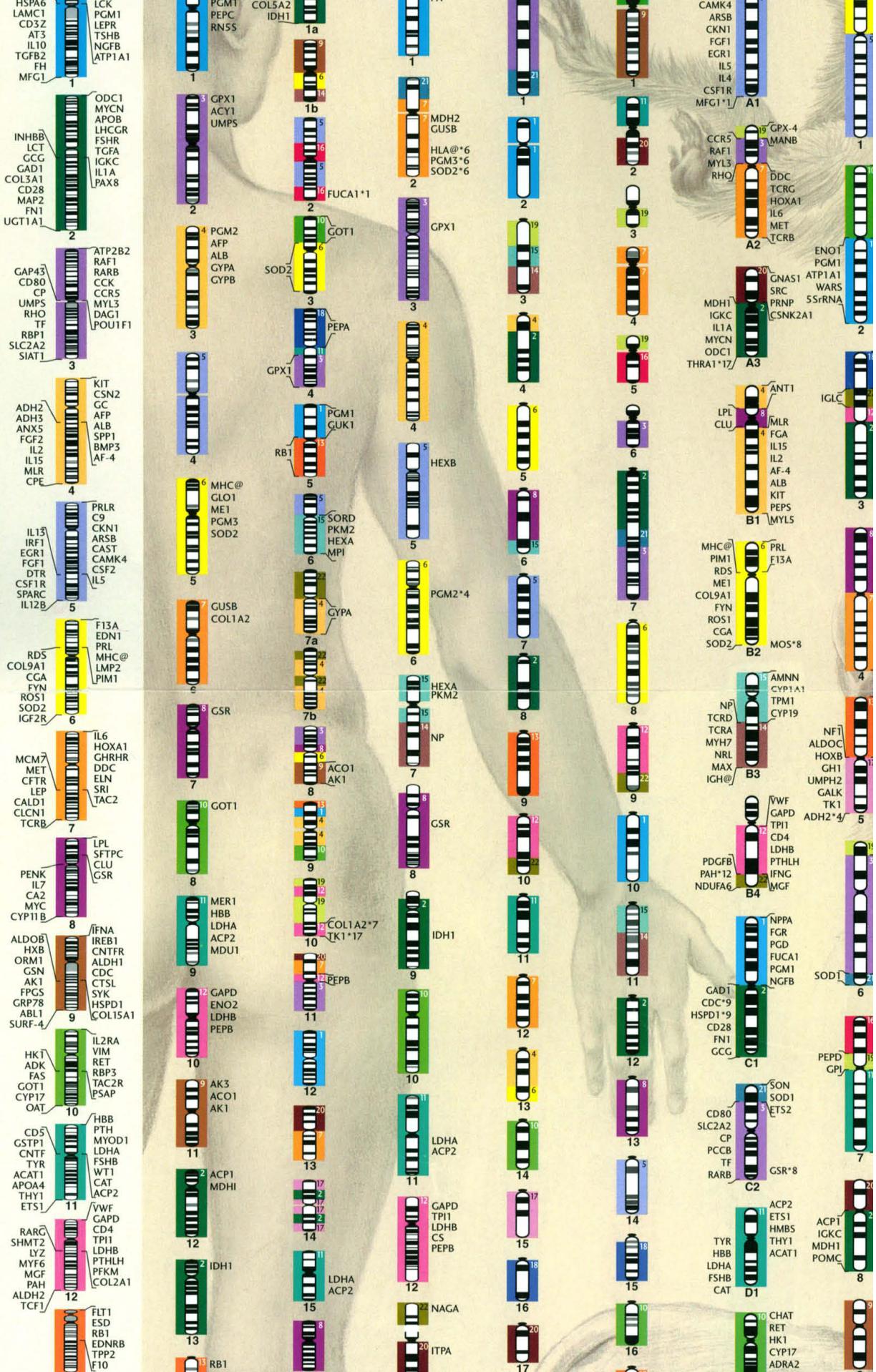
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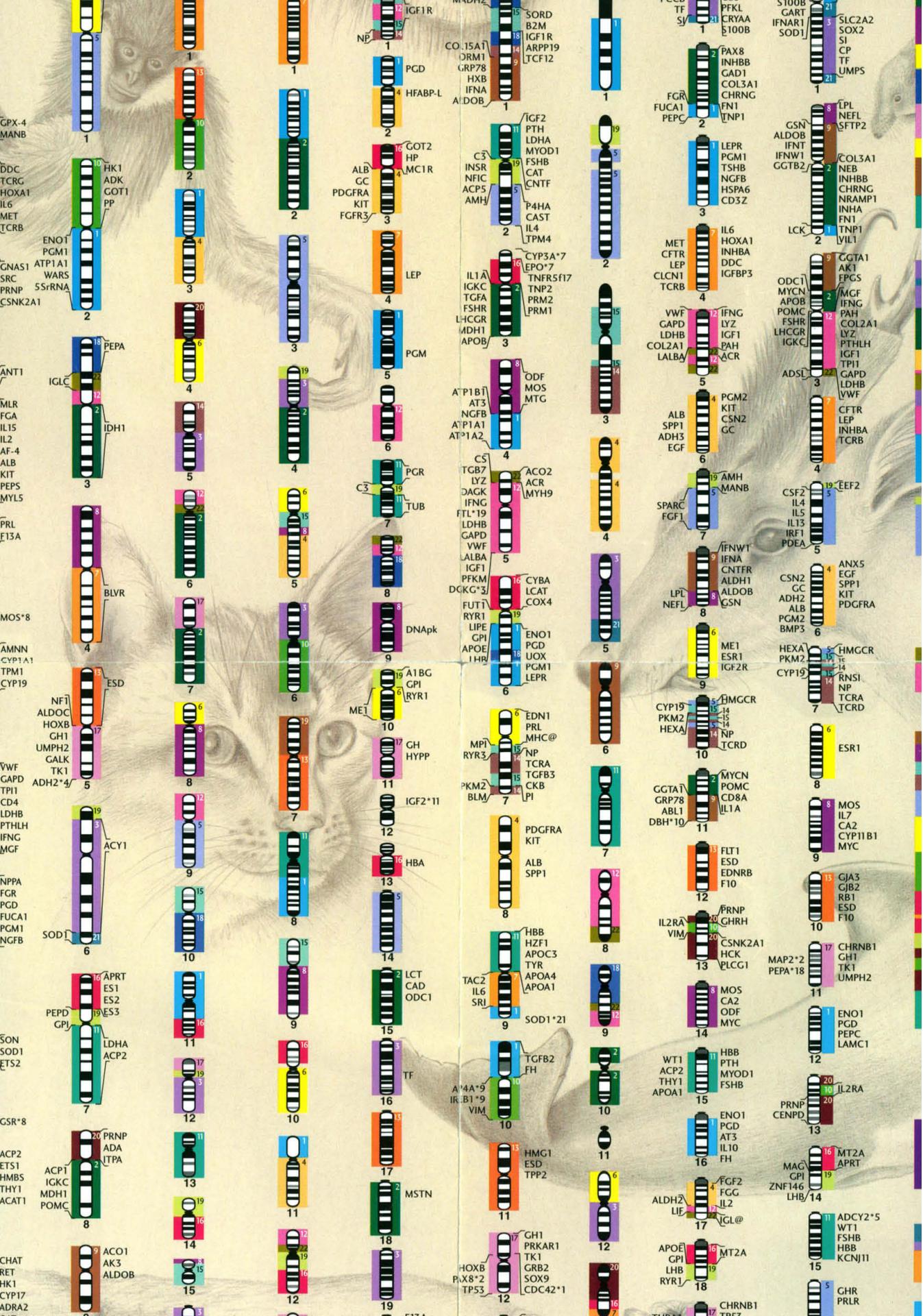


Genome
Maps Ten

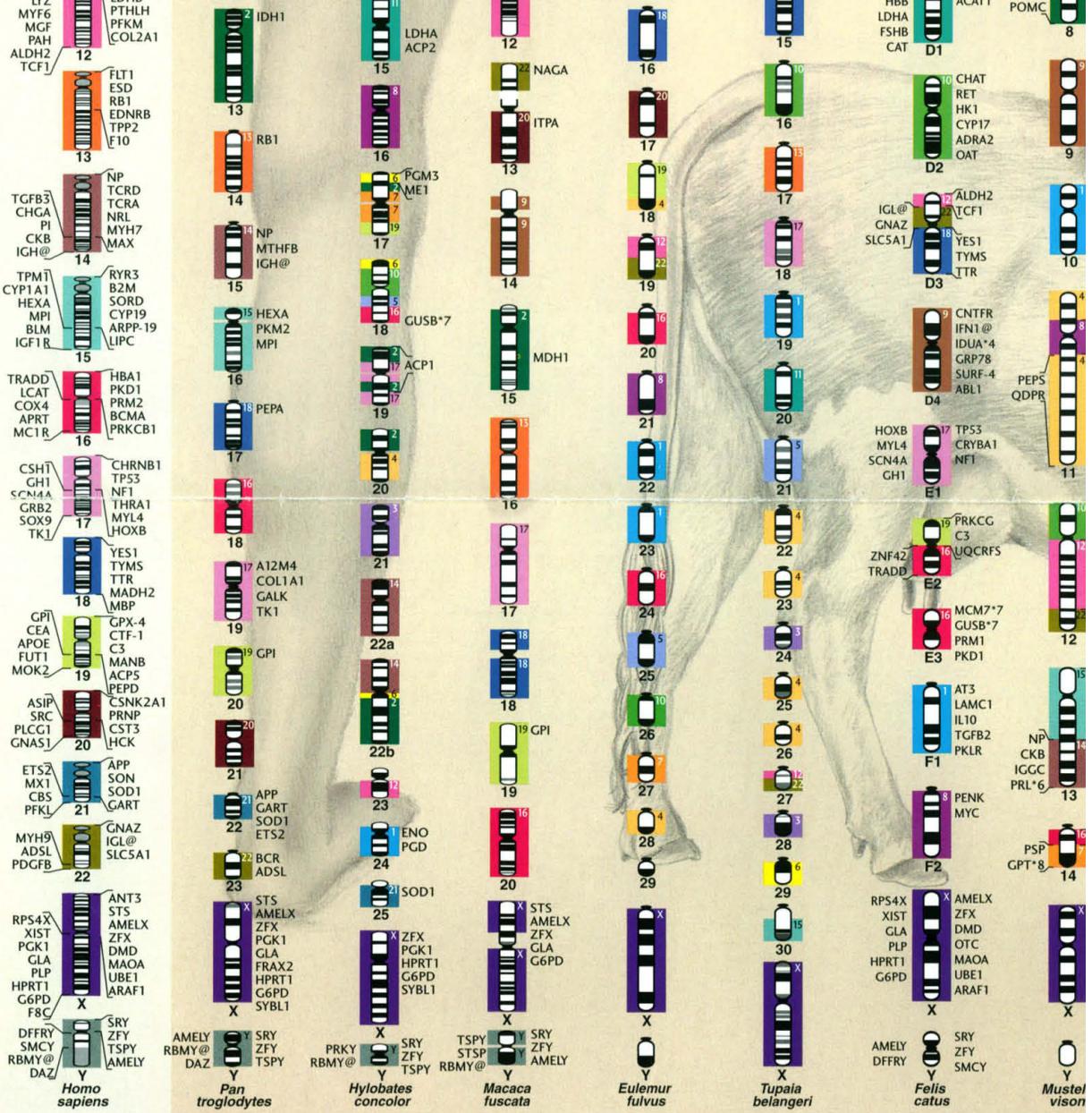
they appear in humans. The zebrafish map, including 25 linkage groups not yet assigned to the 25 chromosomes, is presented to illustrate the array of gene segments conserved for 450 million years. Further information and discussion of dissenting views of mammalian evolution can be found in the 15 October 1999 issue of *Science* and the associated web site at <http://www.sciencemag.org/feature/data/1044631.shtml>











HUMAN CHROMOSOME COLOR KEY

1	2	3	4	5	6	7	8
9	10	11	12	13	14	15	16
17	18	19	20	21	22	X	Y

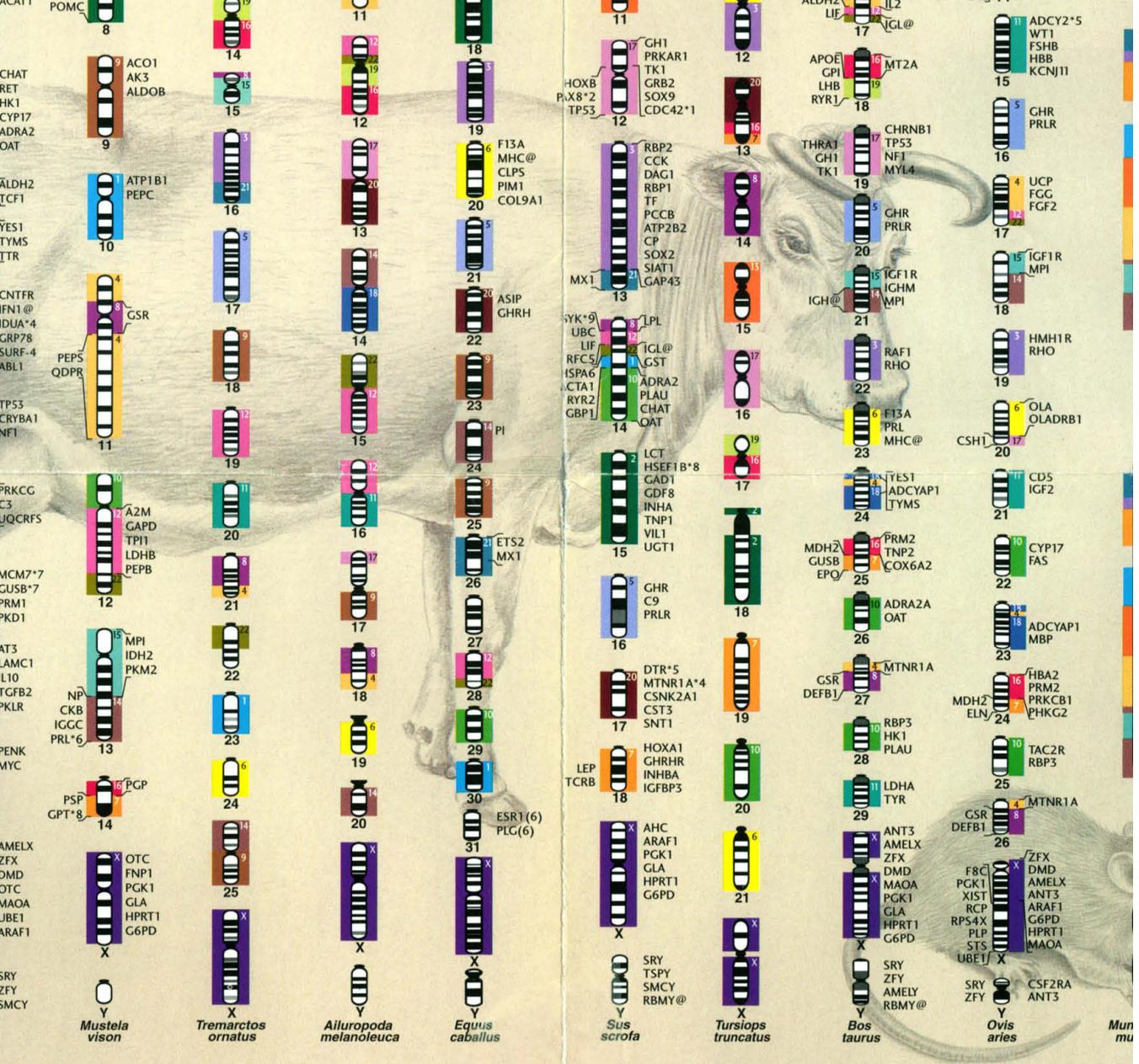
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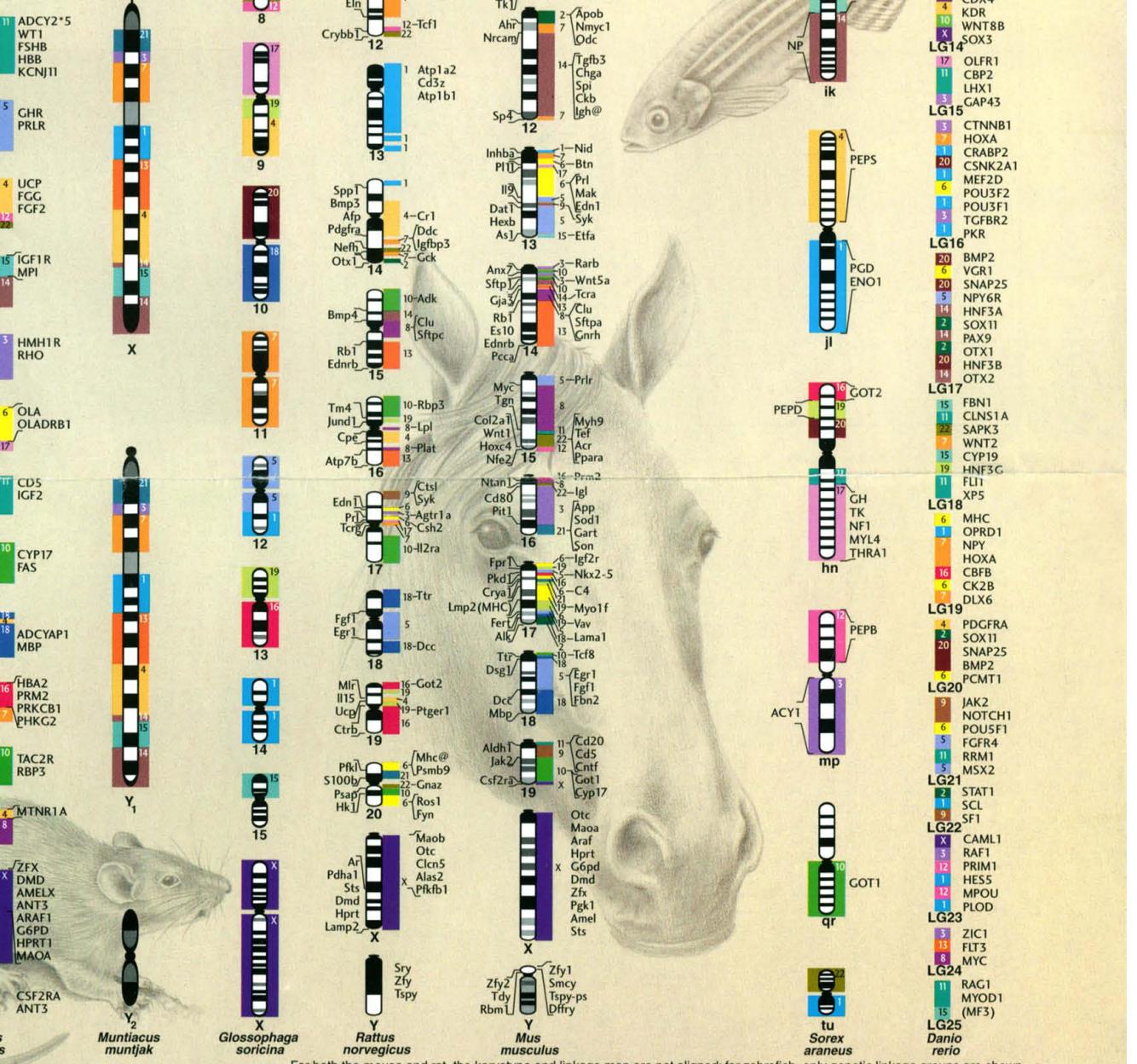
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For both the mouse and rat, the karyotype and linkage map are not aligned; for zebrafish, only genetic linkage groups are shown.

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