

Legends to Figures

Figure 1. Establishment of a gene model based on genomic resources and prediction programs.

The centromere is to the left and the telomere to the right. The upper line represents a segment of the chromosome 14 sequence, masked against repeats. The gene model is in the reverse orientation. Homology hits using biological and predictive data (vertical bars) are presented on the bottom. Solid lines represent *in silico* models (green: FGENESH; red: GENSCAN). Open boxes above represent partial transcripts reconstituted essentially from 2 human and 7 mouse spliced ESTs, and the proposed model lying between positions 70,914,475 and 71,091,684 (see text). Vertical bars inside the partial transcripts and the proposed model symbolize exons. Note the presence of a CpG island at the annotated 5' end of this gene.

Figure 2. Dot plot of sequence alignments of human chromosome 14 versus homologous mouse regions.

Each dot represents a MUMer alignment (see Methods) of sequence from human chromosome 14 versus syntenic regions from mouse chromosome 12 (blue dots) and mouse chromosome 14 (red dots).