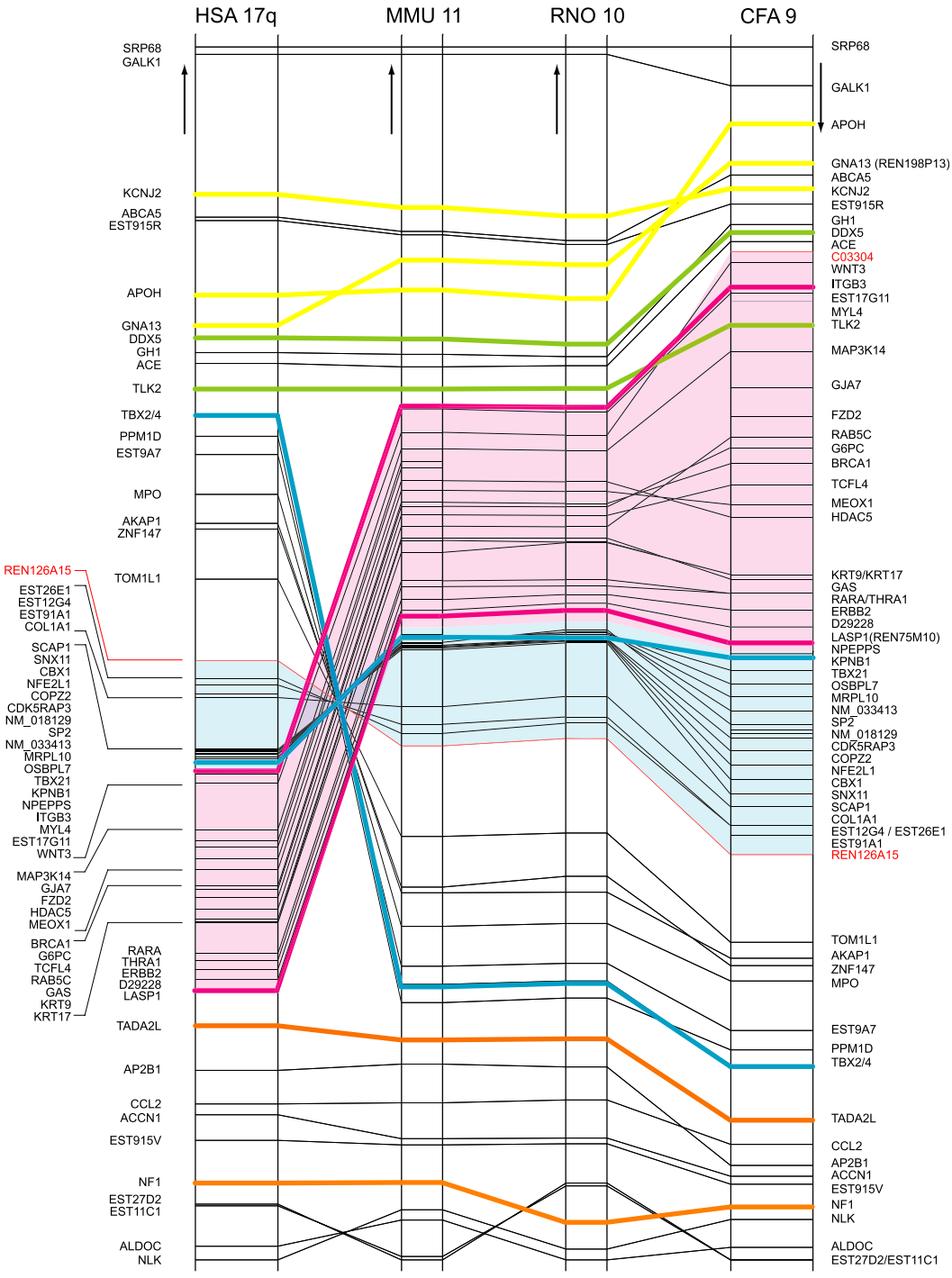


Fig. 2. Horizontal axis: human chromosome 17q (HSA17q) and its syntenic regions on mouse chromosome 11 (MMU11), rat chromosome 10 (RNO10), and dog chromosome 9 (CFA9). Vertical axis: Chromosomal positions of genes, with largest distances in individual species equalized to each other. Positions are drawn to scale. Arrows denote directionality from centromere to telomere. The recombinant markers for the *ctvm* interval, *C03304* and *REN126A15*, are labeled by red lettering in the right-hand column. Yellow, green, blue, purple, and orange lines facilitate the identification of genes involved in important rearrangement events. Pink and blue overlays identify human chromosomal segments that undergo macroreversals in the Multiple Genome Rearrangement scenario. Brackets group genes in densely mapped areas in respective order.

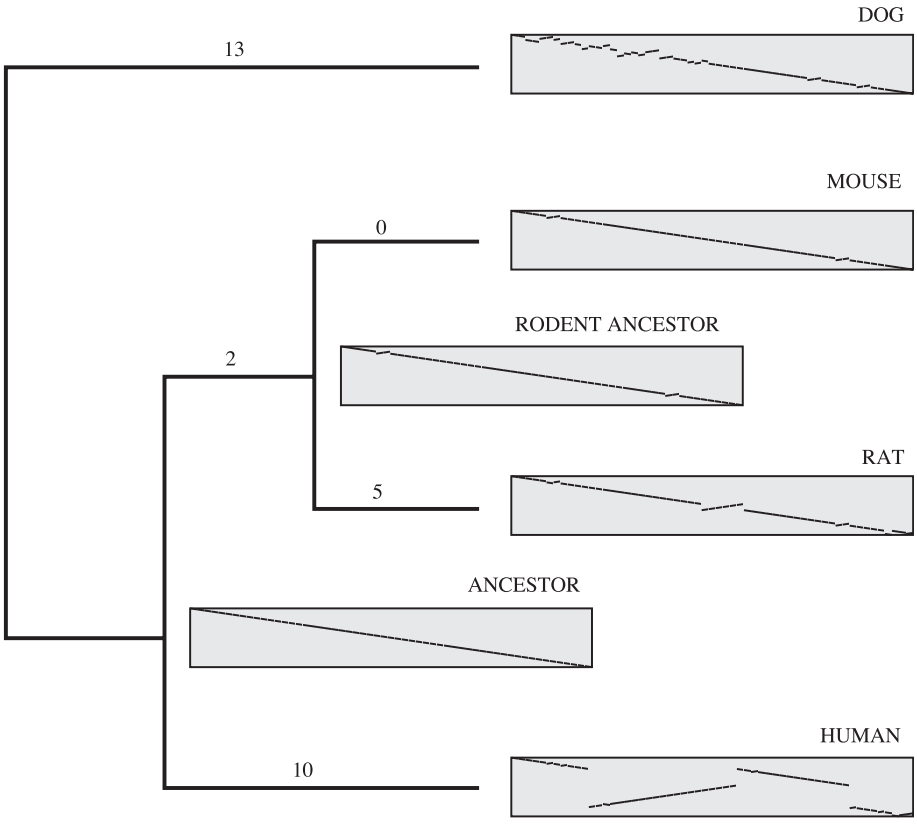


Fig. 3. Schematic representation of the recovered unrooted phylogenetic tree. The number of rearrangements that occurred on each edge is shown. The 57 markers common to all genomes are represented and combined into shaded rectangles. In these rectangles, each marker corresponds to a small segment, not drawn to scale, and is traversed by a diagonal line to provide a visual indication of the gene order and of the positions of rearrangements. These diagonal lines are drawn such that the common putative ancestor is traversed from top left to bottom right.