HORSE GENE MAP

A FIRST GENERATION RADIATION HYBRID MAP AND A HORSE-HUMAN-MOUSE COMPARATIVE MAP

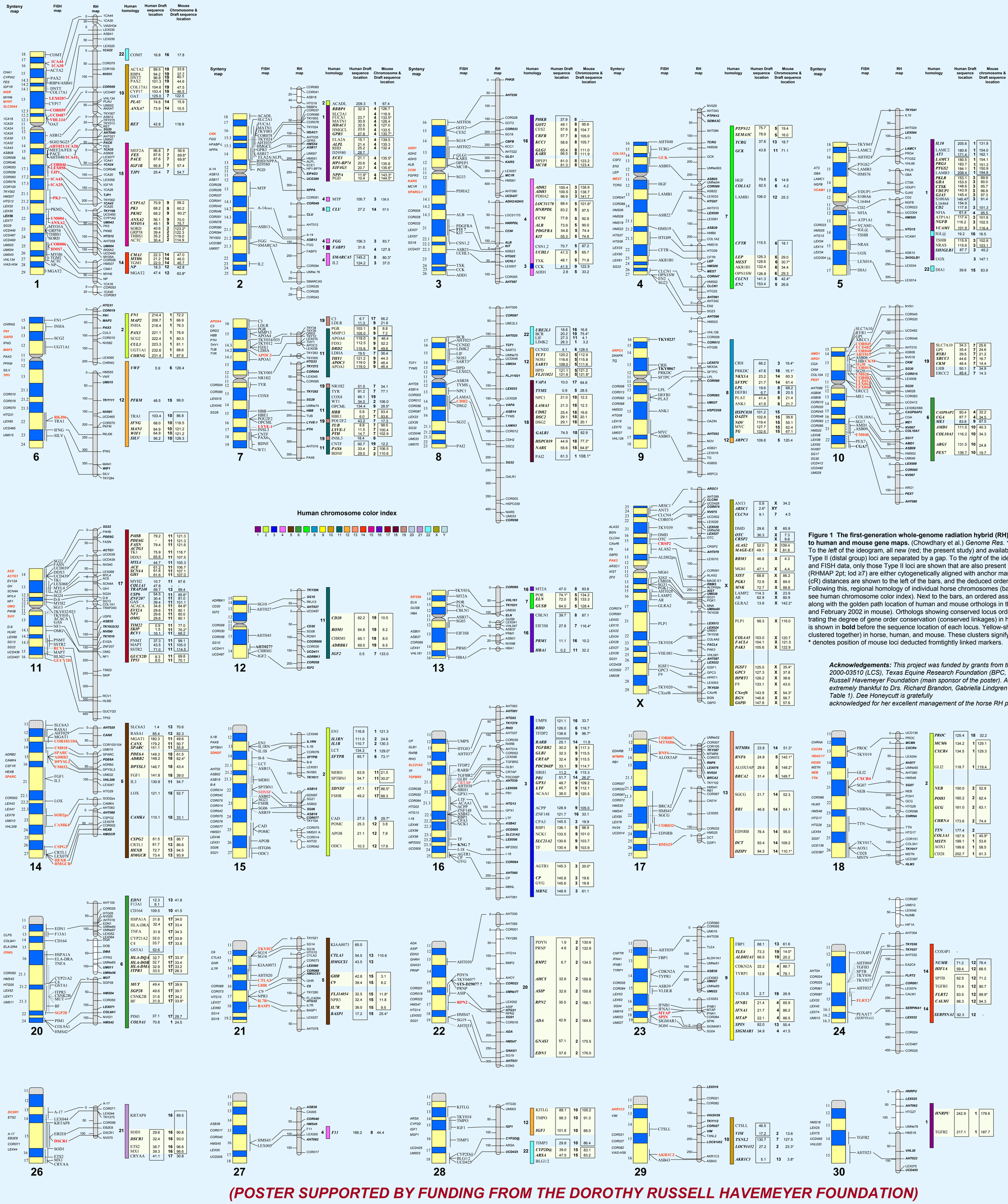

Figure 1 The first-generation whole-genome radiation hybrid (RH) map in the horse along with a comparative overview of the map in relation to human and mouse gene maps. (Chowdhary et al.) *Genome Res.* **13** (4). Each diagram of a chromosome shows a G-banded ideogram (ISCNH 1997). To the *left* of the ideogram, all new (red; the present study) and available synteny data are shown. Alphabetically arranged Type I (proximal group) and Type II (distal group) loci are separated by a gap. To the *right* of the ideogram, all new (red; this study) and available FISH data are shown. For both synteny and FISH data, only those Type II loci are shown that are also present on the RH map. The vertical rounded bars in the RH map represent RH groups (RHMAP 2pt; lod ≥7) are either cytogenetically aligned with anchor markers (shaded) or placed according to available meiotic map results (white). CentiRay (cR) distances are shown to the left of the bars, and the deduced order of mapped loci is to the right. Framework markers are depicted in ***bold italics***. Following this, regional homology of individual horse chromosomes (based on mapped Type I loci) with the human genome is shown (colored vertical bars; see human chromosome color index). Next to the bars, an ordered assembly of *all* RH (***bold italics***) and FISH-mappedType I loci in the horse is shown, along with the golden path location of human and mouse orthologs in the respective draft sequences (http://genome.ucsc.edu; version June 2002 in human and February 2002 in mouse). Orthologs showing conserved locus order compared to the derived order of equine genes are grouped in boxes demonstrating the degree of gene order conservation (conserved linkages) in human and mouse compared to that seen in the horse. Mouse chromosome number is shown in **bold** before the sequence location of each locus. Yellow-shaded horizontal regions represent loci that have preserved gene order (or are clustered together) in horse, human, and mouse. These clusters signify core ancestral segments. A **?** denotes loci with controversial cytogenetic location; * denotes position of mouse loci deducted frontightly linked markers.

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