

The Zebrafish Gene Map Defines Ancestral Vertebrate Chromosomes

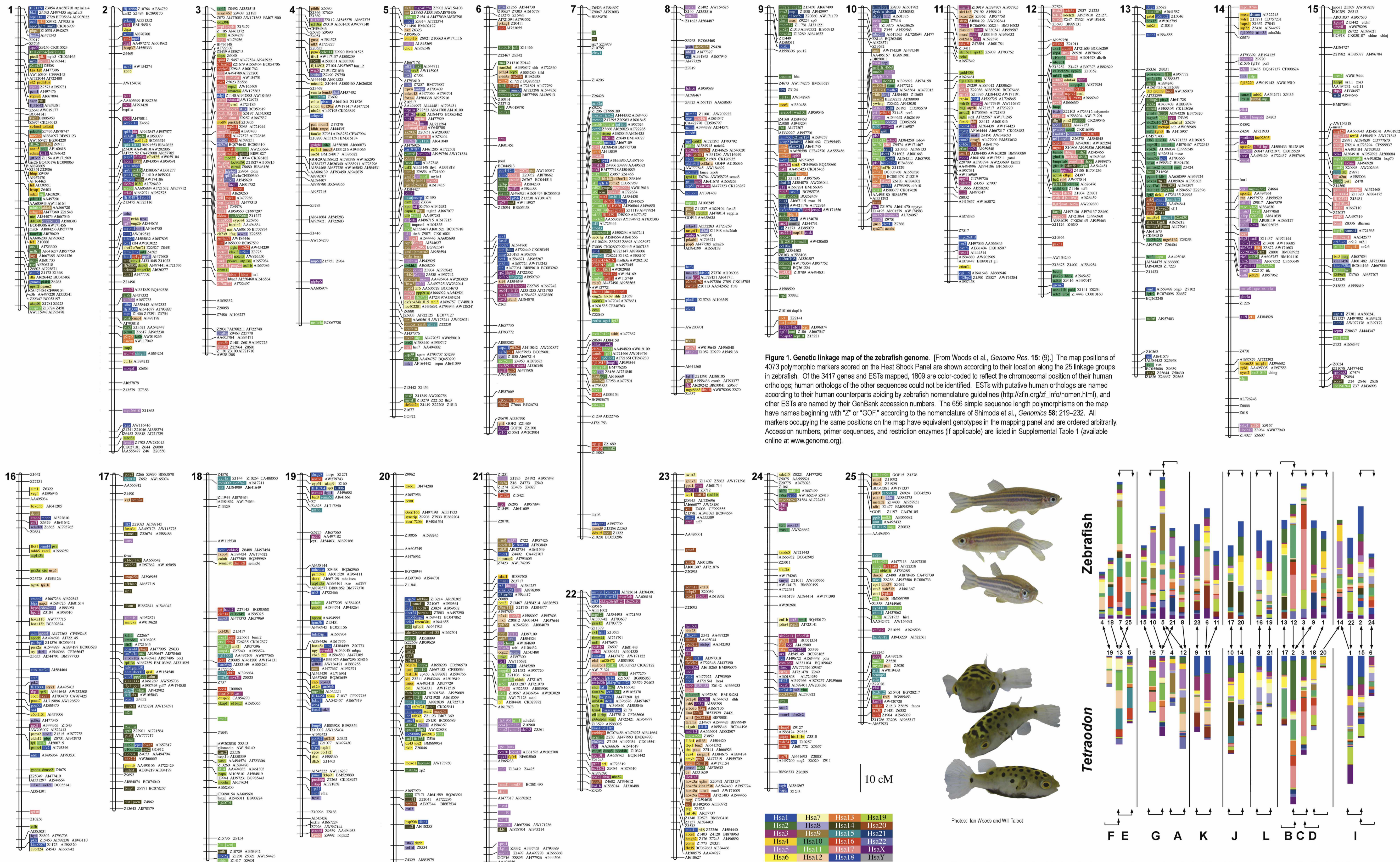


Figure 1. Genetic linkage map of the zebrafish genome. [From Woods et al., *Genome Res.* 15: (9).] The map positions of 4073 polymorphic markers scored on the Heat Shock Panel are shown according to their location along the 25 linkage groups in zebrafish. Of the 3417 genes and ESTs mapped, 1809 are color-coded to reflect the chromosomal position of their human orthologs; human orthologs of the other sequences could not be identified. ESTs with putative human orthologs are named according to their human counterparts by zebrafish nomenclature guidelines (http://zfin.org/zfin_info/nomen.html), and other ESTs are named by their GenBank accession numbers. The 656 simple sequence length polymorphisms on the map have names beginning with "Z" or "GOF," according to the nomenclature of Shimoda et al., *Genomics* 58: 219–232. All markers occupying the same positions on the map have equivalent genotypes in the mapping panel and are ordered arbitrarily. Accession numbers, primer sequences, and restriction enzymes (if applicable) are listed in Supplemental Table 1 (available online at www.genome.org).

Acknowledgments: Based on work supported by grants from the NHGRI/NIH under the Centers of Excellence in Genomic Science (CEGS) program, the NCRRI/NIH, the NICHD/NIH, and the Rita Allen Foundation.

Photos: Ian Woods and Will Talbot

Reconstruction of ancestral vertebrate proto-chromosomes by comparison of zebrafish and Tetraodon gene maps. The 25 zebrafish linkage groups are shown on top, and the 21 Tetraodon chromosomes are shown below. Genes are color-coded according to the positions of their human orthologs, and gene order within chromosomes of both species has been rearranged to highlight orthologous relationships with human genes. The letters at the bottom of the figure denote the ancestral chromosomes proposed by Jallion et al., *Nature* 431: 946–957. [For details, see Woods et al., *Genome Res.* 15: (9).]