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TWO ROUNDS OF WHOLE GENOME DUPLICATION IN THE
ANCESTRAL VERTEBRATE GENOME

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The hypothesis that the relatively large and complex vertebrate genome was created by two ancient, whole genome duplications has been hotly debated, but remains unresolved. We reconstructed the evolutionary relationships of all gene families from the complete gene sets of a tunicate, fish, mouse, and human, then determined when each gene duplicated relative to the evolutionary tree of the organisms. We confirmed the results of earlier studies that there remains little signal of these events in numbers of duplicated genes, gene tree topology, or the number of genes per multigene family. However, when we plotted the genomic map positions of only the subset of paralogous genes that were duplicated prior to the fish-tetrapod split, their global physical organization provides unmistakable evidence of two distinct genome duplication events early in vertebrate evolution indicated by clear patterns of 4-way paralogous regions covering a large part of the human genome. Our results highlight the potential for these large-scale genomic events to have driven the evolutionary success of the vertebrate lineage.

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