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genome can be recognized because they affect the sizes or numbers of restriction fragments. Point mutations are more difficult to detect. The ultimate map is to determine the sequence of the

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DNA. From the sequence, we can identify genes and the distances between them. By analyzing the protein-coding potential of a sequence of the DNA, we can

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Advances in
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annotation have eased the difficulty of identifying new gene sequences. Predicting the functions of these newly identified genes remains challenging. Genes descended from a common ancestral sequence are likely to have common functions. As a

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result, homology is widely used for gene function prediction.

Non-homology-based prediction of gene functions in maize ...

Genome synthesis potentially allows the researchers to gain a much greater degree of

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control of an organism, and it also leads to a completely new way to understand the biology of genomes. In 2008, the first mega-size bacteria genome was built from oligonucleotides . Next, the 4-Mb genome of E. coli was redesigned

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and engineered [2,
3].

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