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genome can be recognized because they affect the sizes or numbers of restriction fragments. Point mutations are more dif?cult to detect. The ultimate map is to determine the sequence of the DNA. From the sequence, we can identify genes and the distances between them. By analyzing the pro-tein-coding potential of a sequence of the DNA, we can

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Advances in genome sequencing and 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 result, homology is widely used for gene function prediction.

Non?homology?based prediction of gene functions in maize...
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To make the pan-genome represent the full range of genetic diversity of soybean, we sequenced a total of 2,898 soybean accessions (871 from our previous studies [Fang et al., 2017, Zhou et al., 2015] and 2,027 from this study) by Illumina technology with an average coverage depth of more than 13× for each accession (Figure 1A; Table S1).These accessions included 103 wild soybeans, 1,048 ...