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Protein domain analysis from genomic sequence data revealed the regulation of LRR related domains in plant transpiration in Ficus

Tiange Lang

Chinese Academy of Sciences, China

Abstract

We developed a pipeline which can predict protein domains directly from genomic sequence data without a reference genome. The pipeline avoided some complex problems of *de novo* assembly such as micro reads and small single repeats.

We used the pipeline on Ficus genomic data and found that the combination of LRRNT_2 and LRR_8 domains is related to hydrophobic process in Ficus. From the view of protein sequence, all those domains have leucine-rich repeats where leucine is a hydrophobic amino acid.