

## **Abstract**

The present disclosure provides a method for obtaining species-specific consensus sequences of microorganisms, which at least includes the following operations: S100, searching for a candidate consensus sequence: clustering specific sequences of target strains belonging to the same species based on a clustering algorithm to obtain a plurality of candidate species-specific consensus sequences; S200, verifying and obtaining a primary screened species-specific consensus sequence: judging whether the candidate species-specific consensus sequences meet the following conditions: 1) the strain coverage rate meets a preset value; 2) the effective copy number meets a preset value; if the candidate meet all the conditions, determining that the candidate species-specific consensus sequences are species-specific consensus sequences. The method is high in specificity and conservation; the obtained species-specific consensus sequences are accurate; the identified consensus sequences are conservative, and the maximum value of the strain coverage rate is achieved as much as possible with the least consensus sequences.

FIG. 1