

METHOD FOR PREPARING NESTED MULTIPLEX PCR HIGH-THROUGHPUT SEQUENCING LIBRARY AND KIT

FIELD

[0001] The present disclosure relates to the technical field of library preparation, and in particular, to a method for preparing high-throughput sequencing libraries based on nested multiplex PCR and a kit for preparing high-throughput sequencing libraries based on nested multiplex PCR.

BACKGROUND

[0002] The demand for re-sequencing of candidate genome segments is increasing with the development of sequencing technology. People pay more attention to sequences than a few SNPs, and the candidate segments may range from 5kb to 10M. The sequencing with the traditional Sanger's method or the targeted region hybridization capture sequencing is expensive, but this problem could be well solved by the use of targeted region capture sequencing. The targeted region capture technology can be roughly divided into two types, i.e., hybridization-based capture sequencing technology and multiplex PCR-based capture technology. By use of multiplex probes or primers, both of them could capture the genome region of interest at one time, and in combination with high-throughput sequencing technology, multiple samples can be sequenced at the same time to obtain the sequence information of the targeted region. Compared with whole-genome sequencing, the target capture sequencing technology greatly reduces costs while screening samples with a large size. The whole-genome sequencing requires cumbersome experimental procedures and high probe costs, which limit its clinical application. In contrast, the target capture sequencing technology has simple experimental operations and strong flexibility, and it is suitable for screening and diagnosis of Mendelian genetic diseases, GWAS candidate segment re-sequencing, QTL mapping segment