

Abstract

EFFICIENT BASE DETERMINATION IN SEQUENCING REACTIONS

The present invention is directed to compositions and methods for nucleic acid identification and detection. Compositions and methods of the present invention include extracting and fragmenting target nucleic acids from a sample, using the fragmented target nucleic acids to produce target nucleic acid templates and subjecting those target nucleic acid templates to amplification methods to form nucleic acid nanoballs. The invention also includes methods of detecting and identifying sequences using various sequencing applications, including sequencing by ligation methods.

Figure 1