

## **ABSTRACT**

Disclosed is a method for diagnosing cancer and predicting a cancer type using fragment end motif frequencies and sizes of cell-free nucleic acid, and more preferably, to a method for diagnosing cancer and predicting a cancer type by extracting nucleic acids from a biological sample to obtain sequence information, acquiring fragment end motif frequencies and sizes of nucleic acids based on the aligned reads, converting the fragment end motif frequencies and sizes of nucleic acids into vectorized data, inputting the vectorized data to a trained artificial intelligence model and analyzing a resulting calculated value. The method includes generating vectorized data and analyzing the same using an AI algorithm and thus is useful due to high sensitivity and accuracy thereof even in the case of low read coverage.