

The present invention relates to a method for constructing a free DNA methylation sequencing library and use of the method. According to the method, DNA methylation and fragmentomics can be detected at the same time. In the method of the present invention, when constructing a sequencing library, a phosphodiester bond gap on double-stranded DNA is first repaired, then a linker sequence is connected to the double-stranded DNA, and then the DNA methylation sequencing library is constructed by an enzymatic conversion method. The method of the present invention can preserve the integrity of the double-stranded DNA, prevent the breakage of DNA strands, and ensure that fragmentomics information in the sequencing library is not destroyed. At the same time, the method can prevent the erasure of DNA methylation modification downstream to the gap in the end repair process that leads to inaccurate DNA methylation information acquisition.

(Fig.1)