VAHTS® DNA Damage Repair Kit

N208

Version 21.2

Product Description

Metabolic processes in the body and environmental factors, including oxidation, hydrolysis, deamination, UV irradiation, radiation, and special chemical substances can cause DNA damage. The damage repair mechanism inherent in the body can repair most of the DNA damage, but the DNA damage caused by extraction during the research process will remain on the DNA. If it is not repaired, it will affect the subsequent experiment. VAHTS DNA Damage Repair Kit can be used to repair most DNA damage. The kit contains a variety of enzymes for DNA damage repairing and specially optimized buffer, suitable for a variety of DNA damages, such as apurine/apyrimidine sites, thymine dimers, de-aminocytosine, 8-oxoguanine, oxidized bases, nicks and gaps, deamination cytosine, 3' terminal half group blocking, etc. This kit can be used to repair formalin fixed paraffin embedding (FFPE) DNA damage and DNA damage caused by various environments or processing methods. But it cannot be used to repair all kinds of DNA damages, such as double-strand breaks and DNA-protein crosslink. This kit can effectively improve the quality of DNA. It has a wide range of compatibility, and the products can be directly used in PCR and second-generation sequencing library construction, third-generation sequencing library construction, etc.

Components

Components	N208-01 (24 rxns)	N208-02 (96 rxns)
DNA Damage Repair Buffer	120 μl	480 μl
DNA Damage Repair Enzyme	48 μl	192 μl

Storage

Store at -30 ~ -15℃ and transport at ≤0℃.

Applications

It is compatible with various type of templates: genomic DNA, cfDNA, ctDNA, FFPE DNA, ChIP DNA, Amplicons, etc. The input DNA amount is between 100 pg and 1 μg.

Notes

◇Starting material: 100 pg - 1 μg input DNA. High-quality input DNA (A260/A280 = 1.8 - 2.0) should be used. Table 1 lists the recommended input DNA amounts for conventional applications.

Table 1. Recommended input DNA amounts for conventional applications

Application	Sample type	Recommended input DNA amount
Whole genome sequencing	Complex genome	50 ng - 1 μg
Target capture sequencing	Complex genome	10 ng - 1 μg
Whole genome sequencing/Target capture sequencing	FFPE DNA	≥50 ng
Whole genome sequencing/Target capture sequencing	cfDNA/ctDNA	≥100 pg
Whole genome sequencing	Microbial genome	1 ng - 1 μg
Whole genome sequencing (PCR-free library)	Complex/simple genome	≥100 ng (No size selection) ≥200 ng (Perform size selection)
ChIP sequencing	ChIP DNA	≥100 pg

▲The above table shows the recommended amount of input DNA when using high-quality DNA. When the quality of the input DNA is poor, usage should be increased appropriately.

◇If size selection or purification is performed after Fragmentation, the concentration needs to be re-determined. The amount of DNA prior to Fragmentation cannot be directly used as the amount of input DNA. Otherwise, the library yield may be low due to insufficient amplification cycles.

◇If high concentration of metal ion chelating agents or other salts are brought into the DNA preparation process, it may affect the efficiency of DNA Damage Repair & End Preparation.

Experiment Process

1. Reaction system

Components	Volume
DNA Damage Repair Buffer	5 μl
DNA Damage Repair Enzyme	2 μl
DNA	100 pg - 1 μg
ddH_2O	To 50 μl

▲DNA Damage Repair Enzyme contains high concentration of glycerol. Centrifuge briefly before use. Collect the solution at the bottom of the tube and pipette gently. Mix well and pipette accurately.

2. PCR program

Place the PCR tubes in the PCR instrument. Set the hot lid temperature at above 60°C and run the following program:

Temperature	Volume
37°C	15 min
4°C	Hold

▲When the template input amount is large, the reaction time can be appropriately extended to improve the repair effect.