

Tinzyme Co., Limited

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NGS DNA Library Kit for Illumina (50 ng)

Product Number:PCK452

Shipping and Storage

Storage at -20°C and transport on dry ice.

Components

| Components | PCK452 | PCK452 |
|----------------------|---------|----------|
| | 24 rxns | 96rxns |
| TPS V50 | 144 μL | 576 μL |
| 5×FA Reaction Buffer | 144 µL | 576 µL |
| 2×HiFidelity PCR Mix | 600 µL | 2×1.2 mL |
| PPM | 48 μL | 192 µL |

Description

This kit is specially developed for the Illumina high-throughput sequencing platform. It provides the enzyme premix system and reaction buffer required for genomic DNA library construction, including all components except PCR primers. Compared with traditional library construction kits, this kit uses a novel transposase method for library construction, which can complete DNA fragmentation, end repair and adapter ligation in one simple enzymatic reaction, significantly reducing the amount of template used. reducing the experimental operation steps and shortening the library construction time; using high-fidelity DNA polymerase for library enrichment, unbiased PCR amplification, expanding the coverage area of the sequence, and efficiently preparing DNA for the Illumina next-generation sequencing platform library. This kit is suitable for starting template DNA input of 50 ng. All reagents in the kit have undergone strict quality control and functional verification to ensure the stability and reproducibility of library construction to the greatest extent.

Reagents to Be Supplied by User

- 1. Magnetic stand.
- 2. DNA purification and recovery kit
- 3. Library PCR primer kit and PCR thermal cycler
- 4. Absolute ethanol, deionized water (pH between 7.0-8.0).
- 5. Reaction tubes: It is recommended to use low adsorption PCR tubes and 1.5 ml centrifuge tubes.
- 6. Pipette tips: It is recommended to use high-quality filter tips to prevent contamination of kits and library samples.

Important Points Before Starting

- 1. Avoid repeated freezing and thawing of reagents.
- 2. The PCR products are easily contaminated due to improper operation, resulting in inaccurate experimental results. It is recommended to isolate the PCR reaction system preparation area from the PCR product purification area, and use a special pipette to regularly clean each experimental area.
- 3. Magnetic bead purification: The magnetic beads should be equilibrated to room temperature before use. All operations on the magnetic beads should be carried out at room temperature. 80% ethanol should be prepared and used immediately. After rinsing, the magnetic beads should be dried until the surface has no liquid reflection and is frosted. , Insufficient drying of magnetic beads will cause ethanol residue to affect subsequent experiments, and excessive drying of magnetic beads will affect DNA recovery efficiency.
- 4. This kit is suitable for the construction of human genomic DNA library. If the DNA sample is a PCR product, its length should be more than 500 bp. Since the transposase cannot act on the DNA end, it is recommended to extend the PCR product at both





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ends when preparing the PCR product. 50-100 bp to avoid low end sequencing coverage.

Sample preparation

- 1. DNA purity requirements: A260/A280 = 1.8-2.0.
- 2. Sample DNA: Dissolve in ultrapure water.
- 3. DNA quantification: Too much or too little DNA input will affect the quality of the library. It is recommended to use Nano to detect the purity of genomic DNA and then to use Qubit to detect the concentration of the genome. Each sample is measured 3 times and the average value is obtained (do not use Template quantification based on any absorbance measurement-based assay).

Protocol

DNA fragmentation, adapter ligation reaction

1. Add the following reagents to a 200µl PCR tube:

| Component | Volume |
|----------------------|----------|
| 50 ng DNA | XμL |
| TPS V50 | 6 µL |
| 5×FA Reaction Buffer | 6 µL |
| ddH ₂ O | Το 30 μL |

- 2. Mix by pipetting gently and centrifuge briefly to collect all components to the bottom of the tube.
- 3. Put the above PCR tube in the thermal cycler, open the hot cover, and the reaction procedure is as follows:

| Temperature | Time |
|-------------|-----------|
| 105°C | Hot cover |
| 55°C | 10 min |
| 10°C | Hold |

After the DNA fragmentation reaction is completed, the transposase is still in a high activity state and should be purified immediately to prevent the library fragment from becoming smaller due to excessive DNA fragmentation.

Fragmentation product purification

- 1. Magnetic Bead should be shaken and mixed before use, and then equilibrated at room temperature for 30 minutes.
- 2. Add 50 µl of magn etic beads equilibrated to room temperature to the fragmented product, vortex for 5 seconds, and then stand at room temperature for 5 minutes.
- 3. Centrifuge briefly, place the centrifuge tube on a magnetic stand, and separate the magnetic beads from the supernatant solution until the solution is clear (about 3-5 minutes), carefully aspirate the supernatant and discard, avoiding contact with the bound target during this time. DNA magnetic beads.

Note: Do not discard the magnetic beads.

4. Continue to keep the centrifuge tube fixed on the magnetic stand, add 200 μL of freshly prepared 80% ethanol to the centrifuge tube, leave at room temperature for 30 seconds, and carefully discard the supernatant.

Note: When adding ethanol, the liquid should not be pipetted directly onto the magnetic beads.

- 5. Repeat step 4.
- Keep the centrifuge tube fixed on the magnetic stand, let it dry at room temperature until the surface of the magnetic beads is slightly cracked, and add 23 μL ddH₂O to dissolve.

Note: Do not over-dry the magnetic beads to avoid affecting elution efficiency.

7. Remove the centrifuge tube from the magnetic stand, vortex to completely resuspend the magnetic beads, and let stand at room temperature for 5 minutes. Briefly centrifuge, place the tube on a magnetic rack until the solution is clear, transfer 21µL of the supernatant to a new 200µL PCR tube.

PCR amplification

1. Add the following reagents to a 200 μ L PCR tube:

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| Component | Volume |
|-----------------------|--------|
| Fragmentation product | 21 µL |
| PPM | 2 µL |
| Primer N5 | 1 µL |
| Primer N7 | 1 µL |
| 2×HiFidelity PCR Mix | 25 µL |

- 2. Mix by pipetting gently and centrifuge briefly to collect all components to the bottom of the tube.
- 3. Put the above PCR tube in the thermal cycler, open the hot cover, and the reaction procedure is as follows:

| Step | Temperature | Time | Cycles |
|-----------------|-------------|-------|---------------|
| Extend | 72°C | 3 min | |
| Predenaturation | 98°C | 30 s | |
| Transsexual | 98°C | 15 s | ٦ 5 10 |
| Annealing | 60°C | 30 s | J 5-10 |
| Extend | 72°C | 3 min | |
| Final Extension | 72°C | 5 min | |
| Save | 4°C | Hold | |

Selective recovery of library DNA fragments

Note: Amplification products can also be subjected to fragment length sorting and purification using a gel recovery kit. If there is no special requirement for the length distribution of the library, the amplified product may not be subjected to selective recovery of DNA fragments.

- 1. Magnetic Bead should be shaken and mixed before use, and then equilibrated at room temperature for 30 minutes.
- 2. Transfer the PCR product to a 1.5 ml centrifuge tube, add water to 100 µl, add a certain volume of magnetic beads equilibrated to room temperature, vortex for 5 seconds, and let stand at room temperature for 5 minutes.
- 3. Centrifuge briefly, place the centrifuge tube on a magnetic stand, and separate the magnetic beads from the supernatant until the solution is clear. Carefully transfer the supernatant to a new 1.5 ml centrifuge tube.

Note: Do not discard the supernatant.

- 4. Add several volumes of magnetic beads to the supernatant, vortex for 5 seconds, and let stand at room temperature for 5 minutes.
- 5. Briefly centrifuge, place the centrifuge tube on a magnetic stand, and separate the magnetic beads from the supernatant until the solution is clear. Carefully aspirate and discard the supernatant, avoiding contact with the magnetic beads bound to the target DNA.

Note: Do not discard the magnetic beads.

6. Continue to keep the centrifuge tube fixed on the magnetic stand, add 200 μl of freshly prepared 80% ethanol to the centrifuge tube, leave at room temperature for 30 seconds, and carefully discard the supernatant.

Note: When adding ethanol, the liquid should not be pipetted directly onto the magnetic beads.

- 7. Repeat step 6 once.
- 8. Keep the centrifuge tube fixed on the magnetic stand, let it dry at room temperature until the surface of the magnetic beads is slightly cracked, and add 22µl ddH₂O to dissolve.

Note: Do not over-dry the magnetic beads to avoid affecting elution efficiency.

9. Remove the centrifuge tube from the magnetic stand, vortex to completely resuspend the magnetic beads, and let stand at room temperature for 5 minutes. Centrifuge briefly, place the tube on the magnetic stand until the solution is clear, and transfer the supernatant solution to a new centrifuge tube.

Attached table: Recommended dosage of magnetic beads when selecting and recycling different fragments

| DNA library size | insert | 230 bp | 330 bp | 430 bp | |
|------------------|-------------------------|--------|--------|--------|--|
| DINA HOLATY SIZE | (insert+adaptor+primer) | 350 bp | 450 bp | 550 bp | |





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| Magnetic head degage | first choice | 65 µL | 55 µL | 45 μL |
|----------------------|--------------|-------|-------|-------|
| Magnetic bead dosage | first choice | 50 µL | 30 µL | 30 µL |

Library DNA Fragment Purification

- 1. Magnetic Bead should be shaken and mixed before use, and then equilibrated at room temperature for 30 minutes.
- 2. Add 50 µl of magnetic beads equilibrated to room temperature to the PCR product, vortex for 5 seconds, and then stand at room temperature for 5 minutes.
- 3. Centrifuge briefly, place the centrifuge tube on a magnetic stand, and separate the magnetic beads from the supernatant solution until the solution is clear (about 3-5 minutes). Carefully aspirate the supernatant and discard it, avoiding contact with the bound target DNA during this time. magnetic beads.

Note: Do not discard the magnetic beads.

4. Continue to keep the centrifuge tube fixed on the magnetic stand, add 200 µl of freshly prepared 80% ethanol to the centrifuge tube, leave at room temperature for 30 seconds, and carefully discard the supernatant.

Note: When adding ethanol, the liquid should not be pipetted directly onto the magnetic beads.

- 5. Repeat step 4.
- Keep the centrifuge tube fixed on the magnetic stand, let it dry at room temperature until the surface of the magnetic beads is slightly cracked, and add 22 μl ddH₂O to dissolve.

Note: Do not over-dry the magnetic beads to avoid affecting elution efficiency.

7. Remove the centrifuge tube from the magnetic stand, vortex to completely resuspend the magnetic beads, and let stand at room temperature for 5 minutes. Centrifuge briefly, place the tube on the magnetic stand until the solution is clear, and transfer the supernatant solution to a new centrifuge tube.

Library Quality Assurance

1. Library concentration determination

In order to obtain high-quality sequencing results, accurate quantification of the DNA library is required. First, it is recommended to use the Real-time PCR method for absolute quantification of the DNA library. In addition, fluorescent dye methods such as the Qubit method or the fluorescent dye picogreen method can also be used, and quantitative methods based on absorbance measurements should not be used here. The molarity of the DNA library can finally be converted using the following approximate formula.

| Average total library length | Approximate conversion formula |
|------------------------------|--------------------------------|
| 300 bp | 1 ng/µl=5.0 nM |
| 400 bp | 1 ng/µl=3.8 nM |
| 500 bp | 1 ng/µl=3.0 nM |

2. Library Fragment Distribution

The prepared DNA library can be detected by agarose gel electrophoresis or the automatic nucleic acid and protein analysis system Qsep100 to detect the fragment length distribution in the DNA library.

| | мs |
|---|-----|
| 10,000 bp 5,000 bp 3,000 bp 2,000 bp 1,500 bp | = |
| 1,000 bp — 750 bp — | = |
| 500 bp — | - 1 |
| 250 bp — | -8 |
| 100 bp — | - |
| | |

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3. Library structure

Index 2 (i5)

5'-AATGATACGGCGACCACCGAGATCTACACIIIIIIIITCGTCGGCAGCGTCAGAT GTGTATAAGAGACAG-NNNNN-CTGTCTCTTATACACATCTCCGAGCCCACGA GACIIIIIIIIATCTCGTATGCCGTCTTCTGCTTG-3'

Index 1 (i7)

IIIIIIII: Index 2 (i5), 8 bases; IIIIIIII: Index 1 (i7), 8 bases; NNNNNN: insertion sequence