



AFT™ Linked-Reads Whole-Genome Library Preparation Kit - 24 rxn

Protocol

PN: 6729001

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Introduction

AFT™ Linked-Reads Whole-Genome Library preparation technology utilizes multiple strand-displacement amplification by the strand-displacing enzymes to seamlessly integrate the Amplification, Fragmentation, and Tagging of the target DNA into one reaction, achieves ultimate efficiency in DNA sequencing Library preparation.

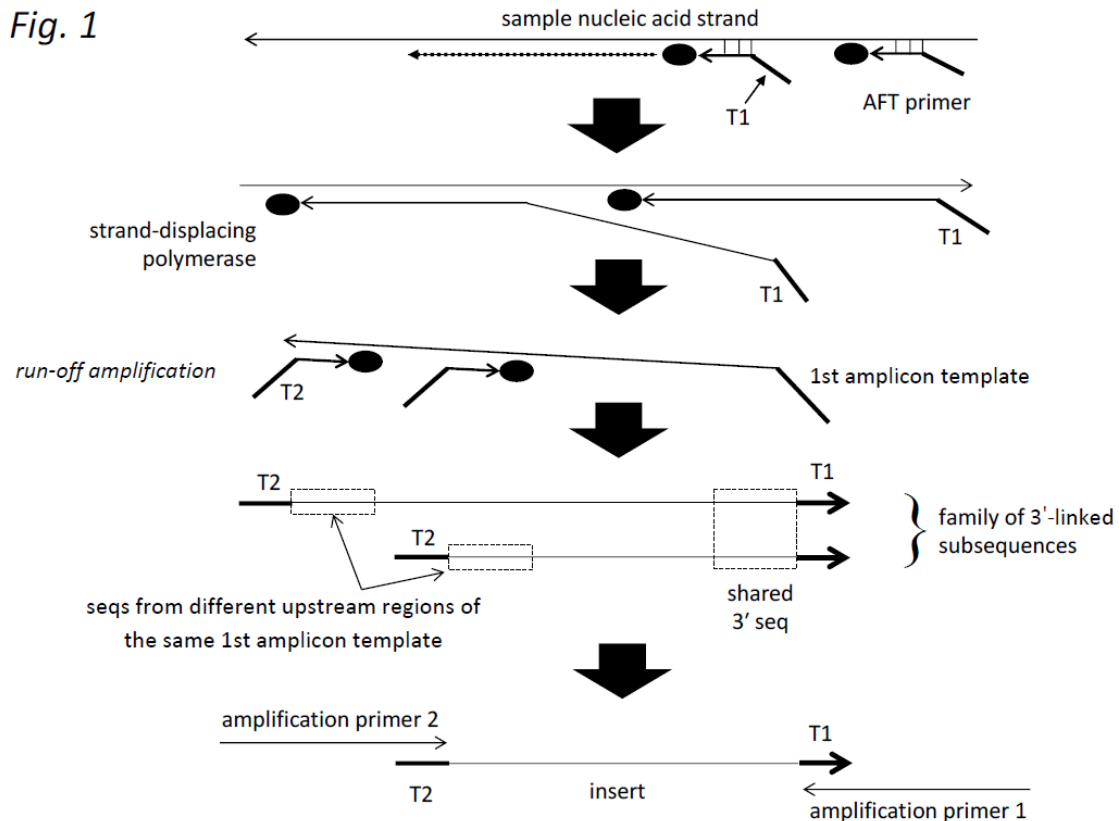
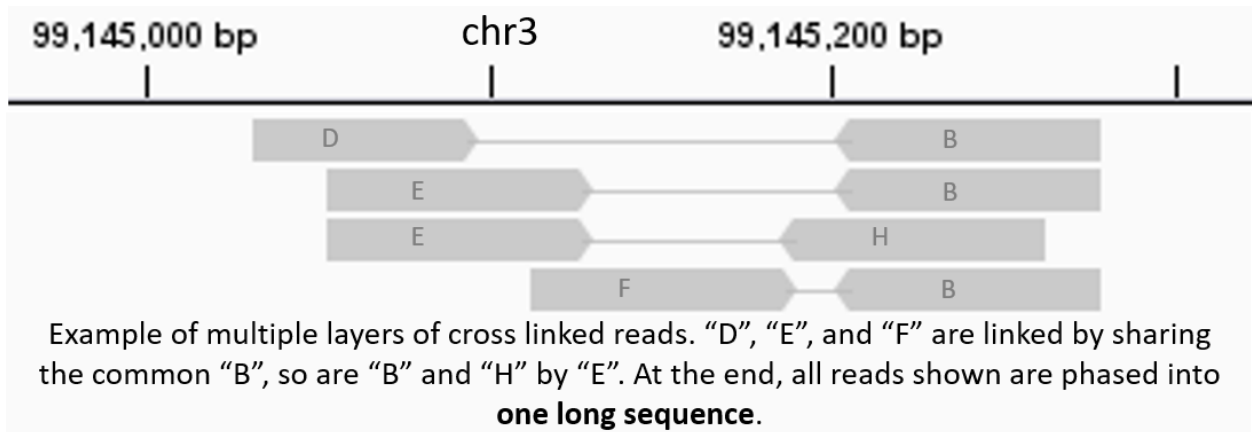


FIG. AFT™ primers are degenerate primers with 5' tag of a fixed sequence. AFT™ primers randomly bind to multiple sites of the target DNA. Strand-displacing DNA polymerase initiates the amplification from AFT™ primers; the front amplicons are displaced by the running-up amplicons and in turn become template for next iteration of AFT™ amplification. The new amplicons all run off at the 5' terminus of the template amplicon and share the same sequence at 3'. In the pair-end sequencing, the common read serves as a native barcode to link all these that amplify from the same template amplicon.

Introduction (Continued)

As a unique feature, groups of AFT™ reads are linked by one common pair-end read that arise from the running off at the same terminus of the same template. The linked reads facilitate the long scaffolding, de novo assembly, and chromosome phasing.



Currently, no bioinformatics software package is provided to utilize the linked-reads feature.

Kit contents and storage

The kit is shipped on gel ice for within US and dry ice for international delivery.

The kit should be stored at -20 °C on receipt.

Component	Volume (µL)
DNA Denaturant	12
2x AFT™ buffer	120
AFT™ enzymes	12
2x PCR Master Mix	600
i501 primer, 10 µM	60
i701 primer, 10 µM	60

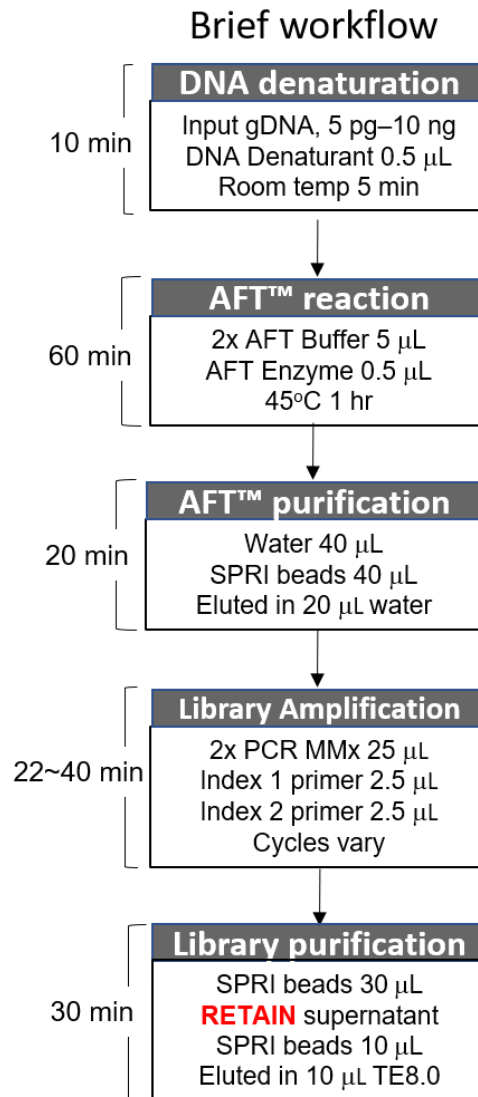
Materials and equipment required but not supplied

Item
SPRI beads
Ethanol
Multiplexing index primers, if multiplexing
Magnetic stand
1x TE Buffer, pH 8.0
Nuclease-free water
Thermal cycler
Microcentrifuge
Microcentrifuge tubes
Pipettors
Pipette tips, nuclease-free

Workflow_Overview

The AFT™ Linked-Reads Whole-Genome Library preparation kit workflow comprises of 2 functional steps: AFT™ reaction and Library PCR Amplification, there is also a SPRI beads-based purification step before and after Library PCR.

The total time is less than 3 hours, varies with the different DNA input levels, with limited hands-on time.



Workflow_AFT™ reaction

A. Amplification, Fragmentation, and Tagging (AFT™) of Genomic DNA

I. Preparation

- Thaw DNA Denaturant
- Bring the 2X AFT™ buffer to room temperature and vortex 3x 5 seconds.

II. Procedure

1. Add up to 4 µL of genomic DNA (5 pg to 10 ng) to a tube.
2. Add water to total 4 µL if necessary.
3. Add 0.5 µL of DNA Denaturant.
4. Briefly vortex and centrifugate to mix, sit at room temp for 5 min.
5. Add 5 µL of 2x AFT™ buffer.
 - 2x AFT™ buffer is viscous, allow at least 5 seconds for each aspiration and dispense.
 - Add 2x AFT™ buffer individually, do not make it into master mix
6. Vortex briefly to mix.
7. Add 0.5 µL of AFT™ enzyme.
8. Briefly vortex and centrifugate to mix
 - Do not pipette, pipetting produces bubbles.
9. Incubate at 45 °C for 1 hour.

Workflow_AFT™ Product Purification

B. AFT™ Product Purification

I. Preparation

- Bring SPRI beads to room temp.
- Vortex to resuspend SPRI beads.
- Prepare fresh 80% ethanol.

II. Procedure

1. Add 40 μ L of nuclease-free water.
2. Add 40 μ L of SPRI beads.
3. Briefly vortex and centrifuge to mix.
4. Sit for 5 min.
5. Pellet on a magnet stand for 5 min.
6. Discard the supernatant.
7. Keep the tube on the magnet stand.
8. Wash 2 times with 180 μ L 80% ethanol, completely remove ethanol.
9. Keep the tube on the magnet stand, dry the beads for 5 min.
10. Take the tube away from the magnet stand.
11. Resuspend beads in 23 μ L of nuclease-free water with pipetting.
12. Sit for 3 minutes for elution.
13. Place the tube on a magnet stand for 3 minutes.
14. Recover 20 μ L of supernatant for Library PCR.
 - We recommend to use ring magnetic stand, for the better and clear recovery of supernatant.

Workflow_Library PCR

C. Library PCR

I. Preparation

1. Thaw 2x PCR Master Mix and i501 and i701 primers.
2. (Optional) If multiplexing, pick and record the index primers from index primer kits (third-party vendor, NEB E7600S, etc.). Be careful in selecting third-party index primers; some index primers are based on Nextera transposase recognition sites, not the standard Illumina Read1 and Read2 primer sequences.

The correct index primer structures should be like below:

- P5(AATGATACGGCGACCACCGAGATCTACAC)-i5-Read1(ACACTCTTCCCTACACGACGCTCTTCCGATCT)
- P7(CAAGCAGAAGACGGCATACGAGAT)-i7-Read2(GTGAAGTGGAGTTCAGACGTGTGCTCTTCCGATCT)

3. Set up thermal cycler as following

98 ° C 30s

[98° C 10s, 55° C 30s, 72° C 30s]x n

72 ° C 3 min

4 ° C on hld

DNA Input	PCR cycles (n)
~ 10 ng	6
~ 1 ng	8
~ 100 pg	12
~ 10 pg	15
Single cell	16

Workflow_Library PCR (Continued)

II. Procedure

1. Add 20 μL of purified AFT™ product.
2. Add 25 μL of 2x PCR Master Mix.
3. Add 2.5 μL of 10 μM i5 index primer.
4. Add 2.5 μL of 10 μM i7 index primer.
5. Vortex and centrifuge briefly.
6. Place on thermal cycler and run the program.

Workflow Library Purification

D. Library Purification

I. Preparation

- Vortex to resuspend SPRI beads.

II. Procedure

1. Add 30 μ L of SPRI beads.
2. Vortex briefly to mix.
3. Sit for 5 min.
4. Pellet on a magnet stand for 5 min.
5. RETAIN and transfer 70 μ L of the supernatant to a new tube.
 - It's more than rare that the supernatant from this step is inadvertently discarded, we found it helps to dispense the 10 μ L of SPRI beads that's going to be used in the next step in a tube ahead of time, and transfer the retained supernatant into it.
6. Add 10 μ L of SPRI beads.
7. Briefly vortex and centrifugate to mix.
8. Sit for 5 min.
9. Pellet on a magnet stand for 5 min.
10. Keep the tube on the magnet stand.
11. Wash 2 times with 180 μ L 80% ethanol, completely remove ethanol.
12. Keep the tube on the magnet stand, dry the beads for 5 min.
13. Take the tube away from the magnet stand.
14. Resuspend beads in 13 μ L of TE pH8.0 with pipetting.
15. Sit for 3 minutes for elution.
16. Place the tube on a magnet stand for 3 minutes.
17. Recover 10 μ L of supernatant for quantification and sequencing.



Workflow_Library Quantification

E. Library Quantification

Quantify using Agilent BioAnalyzer or TapeStation, set region at 250 – 700 bp.

Troubleshooting

No library

1. The quantification of input DNA might be overestimated, try one or two more PCR cycles.
2. The DNA might be degraded and reduced to less than 1 kb; AFT™ technology prefers to work on DNA longer than 1 kb. Try to extract DNA at low temperature with mild conditions, store the extracted DNA at -20 °C or lower.
3. Excessive pipetting and vortexing during the workflow might reduce the target DNA to shorter than 1kb, avoid excessive pipetting or vortexing.
4. When recovering the elution from SPRI beads, leave at least 3 µL behind, don't try to recover all.
5. The third-party index primers are not compatible; some index primers are based on Nextera transposase recognition sites, not the standard Illumina Read1 and Read2 sequences. The correct index primer structures should be like below:
 - P5(AATGATACGGCGACCACCGAGATCTACAC)-i5-Read1(ACACTCTTCCCTACACGACGCTCTTCCGATCT)
 - P7(CAAGCAGAAGACGGCATACGAGAT)-i7-Read2(GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT)

PCR duplication rate is high

The PCR duplication rate from AFT™ kit is normally very low, less than 3%, the input DNA amount may be underestimated, try to use fewer PCR cycles, as long as the library has a molar concentration of greater than 1 nM for 250-700 bp range, it will be sufficient for a sequencing.