

## Notices

### Limitations of use

**For research use only. Not for use in diagnostic procedures.** Unless otherwise agreed to in writing, IDT does not intend these products to be used in clinical applications and does not warrant their fitness or suitability for any clinical diagnostic use. Purchaser is solely responsible for all decisions regarding the use of these products and any associated regulatory or legal obligations.

Safety data sheets pertaining to this product are available upon request.

### Safety Notices



**Reminder** symbols call attention to minor details that may be easily overlooked and compromise the procedure resulting in decreased assay performance.



**Caution** symbols denote critical steps in the procedure where risk of protocol failure or damage to the product itself could occur if not carefully observed.



**Stop** symbols indicate where this procedure may be safely suspended and resumed at a later time without risk of compromised assay performance. Make note of these steps and plan your workflow accordingly.

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## Revision history

Document Number	Date	Description of change
<i>PRO030.0</i>	April 2021	<ul style="list-style-type: none"> <li>Item number changed from LA377.A to PRO030.0.</li> <li>No document content changes were made.</li> </ul>
<i>PRO030.1</i>	November 2021	<ul style="list-style-type: none"> <li>Updates to email address.</li> <li>Updates to links.</li> <li>Removed Quantify, Normalize, and Sequence section.</li> </ul>
<i>PRO030.2</i>	July 2022	<ul style="list-style-type: none"> <li>Migrated protocol to new format.</li> <li>Removed liquid accessories.</li> <li>Updated figures.</li> </ul>
<i>PRO030.3</i>	November 2022	<ul style="list-style-type: none"> <li>Updated formatting.</li> <li>Aligned minor inconsistencies across protocols.</li> </ul>
<i>PRO030.4</i>	March 2023	<ul style="list-style-type: none"> <li>Updated formatting and branding.</li> </ul>
<i>RA-DOC-057/REV01</i>	June 2023	<ul style="list-style-type: none"> <li>Updated document number from PRO030 to RA-DOC-057.</li> <li>Updated branding and formatting.</li> </ul>
<i>RA-DOC-057/REV02</i>	November 2023	<ul style="list-style-type: none"> <li>Updated First and Second PCR cycling conditions to include separate anneal and extended steps.</li> <li>Clarified instructions under the “Working with lyophilized reagents” section.</li> <li>Updated formatting and branding.</li> <li>Updated links and email addresses.</li> </ul>

## Technical support

Contact us directly at [archer-tech@idtdna.com](mailto:archer-tech@idtdna.com).

## Overview

### Intended use

The Archer VARIANT*Plex* protocol is intended for research applications in conjunction with Archer reagent kits and corresponding target-enrichment panels to produce high-complexity libraries for use with Illumina next-generation sequencing (NGS) platforms.

VARIANT*Plex* sequencing data produced by this method should be processed using Archer™ Analysis software—a complete bioinformatics suite that leverages Anchored Multiplex PCR (AMP™) chemistry to identify unique sequence fragments, thus enabling error correction, read deduplication, and ultimately high-confidence alignment and mutation calling. Archer Analysis takes demultiplexed FASTQ files straight from the sequencer as input and produces both high-level and detailed mutation reporting, as well as raw text and BAM outputs for full transparency of the pipeline.

### Test principle

Anchored Multiplex PCR (AMP) is a rapid and scalable method to generate target-enriched libraries for NGS. AMP technology can be used for applications in targeted RNA sequencing, genomic DNA sequencing, and genotyping applications to generate a sequencing library in a matter of hours. Designed for low nucleic acid input, this process delivers robust performance across a variety of sample types.

AMP utilizes unidirectional gene-specific primers (GSPs) that enrich for both known and unknown mutations. Adapters that contain both molecular barcodes and sample indices permit quantitative multiplex data analysis, read deduplication, and accurate mutation calling.

The Archer Analysis software utilizes these molecular barcodes (MBCs) for duplicate read binning, error correction and read deduplication to support quantitative multiplex data analysis and confident mutation detection. Analysis reports both sequencing metrics and number of unique observations supporting called variants.

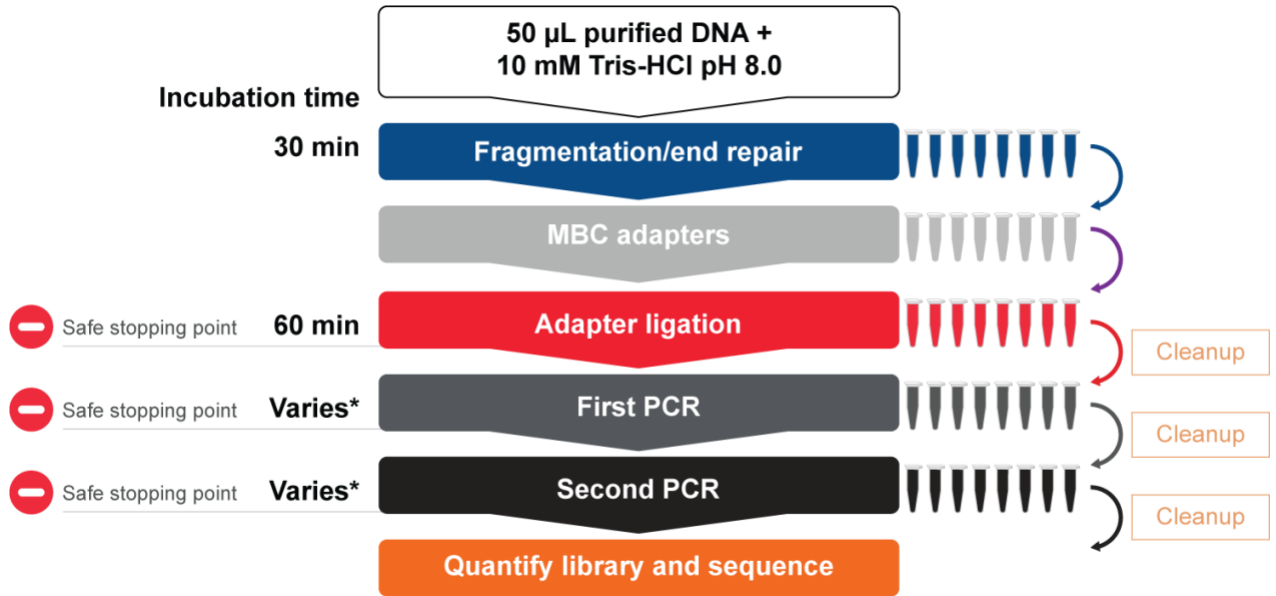
### Modular assay format Archer library preparation reagents include:

- Archer VARIANT*Plex* reagents in lyophilized format for each step of library preparation.
- GSPs that target panel-specific regions of interest during PCR amplification.
- Archer MBC adapters are proprietary adapters that tag each unique molecule with a barcode and common region prior to amplification.

### Modular assay format

Archer kits include library preparation reagents and assay-specific liquid primers, which are used in conjunction with Archer MBC adapters to construct sequencing-ready libraries from total nucleic acid (TNA) or DNA samples. See individual product inserts for panel targets and read depth requirements.

**Workflow**



\* First and Second PCR times vary based on the specific panel as well as individual lab cycling conditions. See Product Insert for more information.

### VARIANT<sup>™</sup>Plex Reagents for Illumina (SK0098)

Store at 2°C to 8°C - Allow pouches to reach room temperature before opening.

Description	Part Number (SK0098)	Quantity
DNA Fragmentation, End Repair, dA-Tailing	SA0039	1 pouch (8 reactions/one 8-tube strip)
Adapter Ligation	SA0005	
First PCR for Illumina-P	SA0109	
Second PCR Reactions 1 thru 8 for Illumina-P	SA0110	

### Additional components

Store at -30°C to -10°C

Materials Supplied		
Description	Part Number	Quantity
VARIANT <sup>™</sup> Plex Panel GSP1	Refer to product insert	Varies – Refer to Product Insert
VARIANT <sup>™</sup> Plex Panel GSP2	Refer to product insert	



Materials required, but not supplied have been optimized for proper application of the Archer Library preparation. Use of other materials have not been tested by IDT.

Materials Required, but not Supplied		
Description	Supplier	Part Number
Archer MBC adapters for Illumina	Archer	Varies
AMPure <sup>®</sup> XP beads	Beckman Coulter	A63880
1 M Tris-HCl, pH 8.0 (molecular biology grade)	Various	-
Ultrapure water (molecular biology grade)	Various	-

200 mM Tris-HCl, pH 7.0 (for sequencing)	Various	-
100% ethanol (ACS grade)	Various	-
Concentrated NaOH solution (ACS grade)	Various	-
RNase AWAY™	Thermo Fisher Scientific	7003
KAPA Universal Library Quantification Kit	KAPA Biosystems	KK4824
MiSeq® or NextSeq® Reagent Kit (300 cycle minimum)	Illumina	-
PhiX Control v3	Illumina	FC-110-3001
Standard PCR thermal cycler	Various	-
Real-Time PCR thermal cycler	Various	-
qPCR tubes	Various	-
0.2 mL PCR tubes	Various	-
DynaMag™ -96 Side Magnet	Thermo Fisher Scientific	12331D
Microcentrifuge	Various	-
Plate centrifuge	Various	-
Pipettes (P10, P20, P200 and P1000)	Pipetman or equivalent	-
Sterile, nuclease-free aerosol barrier pipette tips	Various	-
Vortex mixer	Various	-
PCR tube cooling block	Various	-
Gloves	Various	-
Qubit® Fluorometer (3.0 or higher)	Thermo Fisher Scientific	Q33216
Qubit dsDNA HS Assay Kit	Thermo Fisher Scientific	Q32851

## Before getting started

### Important precautions

- **Read through the entire protocol before starting your library preparation.**
- Take note of safe stopping points throughout the protocol where samples can be safely frozen (-30° C to -10° C) to plan your workflow.
- Use good laboratory practices to prevent contamination of samples by PCR products.
- Use nuclease-free PCR tubes, microcentrifuge tubes, and aerosol-barrier pipette tips.
- Wipe down workstation and pipettes with nuclease and nucleic acid cleaning products (e.g., RNase AWAY, Thermo Fisher Scientific).
- Verify that the thermal cycler used for library preparation is in good working order and currently calibrated according to manufacturer specifications. When using a thermal cycler with a 100% ramp rate >6°C/sec, set the ramp rate to go no higher than 6°C/sec for First PCR and Second PCR.
- Reaction cleanup with AMPure XP beads (Beckman Coulter) is performed at room temperature (20°C to 25°C) and is used repeatedly throughout the workflow. Ensure that AMPure XP beads are equilibrated to room temperature and fully resuspended by vortexing until homogenous in both color and appearance prior to drawing out material for **each** use.

### Working with lyophilized reagents

- Archer reagents are provided as individually lyophilized reaction pellets in 0.2 mL PCR tube strips.
- Allow pouches to reach room temperature (20°C to 25°C) by removing from 2°C to 8°C storage for at least 15 minutes before opening to reduce moisture condensation on tubes.
- Always centrifuge tubes briefly before opening to pull contents down.
- Detach the required number of reaction tubes and return any unused portion to the pouch with desiccant packet, reseal and store at 2°C to 8°C. **It is recommended to use the remaining reactions within 4 weeks after opening.**
  - For MBC adapters and Second PCR tubes remember to label prior to returning unused portions to storage.
- Dissolve, mix and spin down:
  - **Never touch the lysosphere with the pipette tip.**



- Add sample/reagents to pellets in tubes while on ice.
- Allow at least 5 seconds for pellets to dissolve.
- Pipette up and down 8 times to mix after the lysosphere has dissolved.
- Briefly centrifuge and return to ice before proceeding.

### Input nucleic acid

- Input nucleic acid (TNA or DNA) in EDTA-free buffer (pH 7-8) or ultrapure water is the optimal starting template for AMP library preparation. Do NOT use EDTA-containing buffers.
- Use the maximum allowable input mass (ng) whenever possible. Higher input quantities enable more sensitive variant detection:
  - 10 - 250 ng of DNA for VARIANT*Plex*
- Contact technical support ([archer-tech@idtdna.com](mailto:archer-tech@idtdna.com)) for commercially available extraction kit recommendations.

### Reagents to prepare before starting

- Make at least **10 mL** fresh 10 mM Tris-HCl, pH 8.0 from 1M Tris-HCl, pH 8.0 and ultrapure water.
  - Mix **100 µL** 1M Tris-HCl, pH 8.0 with **9,900 µL** ultrapure water.
  - 10 mM Tris-HCl, pH 8.0 can be used for up to one week after mixing.
- Make at least **50 mL** fresh 70% ethanol from 100% ethanol and ultrapure water.
  - Add **35 mL** 100% ethanol to **15 mL** ultrapure water.
  - Tightly close the cap to minimize evaporation when not in use.
  - 70% ethanol is appropriate for use for up to one week after mixing.

## Thermal cycler programs

- Preprogram your thermal cycler with these specific programs.
- Use the appropriate programs for the specific Archer assay.
- Verify programming before initiating runs.

	Step	Temperature (°C)	Time (min)
<b>DNA Fragmentation, End Repair, dA-Tailing</b>	1	4	1
	2	37	12
	3	72	20
	4	4	Hold

	Step	Temperature (°C)	Time (min)
<b>Adapter Ligation (Heated lid off)</b>	1	16	30
	2	22	30
	3	4	Hold

	Step	Temperature (°C)	Time	Cycles
<b>First PCR</b>	1	95	3 min	1
	2	95	30 sec	<i>Varies—See panel specific product insert)</i>
	3	<i>Varies—See panel specific product insert</i>	10 sec	
	4		<i>Varies—See panel specific product insert) 100% ramp rate*</i>	
	5	72	3 min	1
	6	4	Hold	1

\*See ramp rate guidelines in the “Before getting started” section.

	Step	Temperature (°C)	Time	Cycles
<b>Second PCR</b>	1	95	3 min	1
	2	95	30 sec	<i>Varies—See panel specific product insert)</i>
	3	<i>Varies—See panel specific product insert)</i>	10 sec	
	4		<i>Varies—See panel specific product insert) 100% ramp rate*</i>	
	5	72	3 min	1
	6	4	Hold	1

\*See ramp rate guidelines in the “Before getting started” section.

## Molecular barcoding, sample indexing, and multiplexed sequencing

Molecule-level barcoding (or unique molecule identifier tagging) and sample-level barcoding (also known as index tagging) are both incorporated during Archer MBC ligation. Molecular barcodes are an integral component of the Archer Analysis software suite. Sample barcodes (i.e., index tags) allow pooled libraries to be sequenced simultaneously thereby enabling maximum sequencing throughput and data demultiplexing during downstream bioinformatics analysis.

### Sample multiplexing

- To efficiently utilize the throughput of the MiSeq (or other Illumina sequencing platform) as well as prevent low index diversity within your sequencing run, multiple samples should be sequenced simultaneously. Samples can be identified through a combination of two unique nucleotide sequences (see below for more details), which are subsequently read during the sequencing process. The unique nucleotide sequence is often termed an “index”.
- The Archer Library Preparation Reagents for Illumina use a combination of two indices to distinguish between samples. Index 2 is added during Adapter Ligation and is embedded in the Archer MBC adapters for Illumina (p5/i5 index). Index 1 is added during the Second PCR and is embedded in Illumina Index 1 Primers (p7/i7) within the Second PCR reaction pellets.
- To maintain appropriate coverage depth, it is recommended that users determine the maximum number of samples that can be run on a flow cell. In general, larger panels with more targets will require higher sequencing coverage depth and should be run with fewer samples. Refer to product insert for panel specific read depth recommendations.
- Contact [archer-tech@idtdna.com](mailto:archer-tech@idtdna.com) to receive tools that can help define the appropriate number of samples per sequencer and flow cell type.

## Barcode diversity

- Illumina sequencers work best when index diversity within a run is high. For example, if eight samples are included in a run, and the user chooses to use only one MBC adapter paired with eight different Index 1 Primers, the run may fail due to low barcode diversity. In this example it is recommended to use eight different Archer MBC adapters paired with eight different Index 1 Primers.
- To facilitate a high index diversity, each tube in the 8-strip of MBC adapters for Illumina as well as Second PCR contains a unique index. When preparing one batch of 8 or less samples, this results in 8 samples with unique dual indices and barcode diversity is not a concern. Only when combining very few samples of different batches, it becomes necessary to pay attention to the index diversity, as the i7 indices (added with Second PCR) are the same in each kit.
- If using more than 48 MBCs, contact [archer-tech@idtdna.com](mailto:archer-tech@idtdna.com) for adapter compatibility.

## Protocol

Before beginning, review precautions in “Working with Lyophilized Reagents” section for additional information regarding best practices using lyophilized reagents.

### Step 1: DNA Fragmentation, End Repair, dA-Tailing

- Place an appropriate number of **DNA Fragmentation, End Repair, dA-Tailing** (SA0039) reaction tubes on ice.
- Adjust purified DNA (10 - 250 ng) samples to a final volume of **50 µL** with 10 mM Tris-HCl, pH 8.0 or ultrapure water and transfer to new PCR tubes. Keep input samples on ice.

Component	Reaction Mix
10 mM Tris-HCl, pH 8.0 or Ultrapure water	50 - Xµl
Purified nucleic acid	Xµl
<i>Total volume</i>	<i>50µl</i>

- Transfer **50 µL** reaction mix to the DNA Fragmentation, End Repair, dA-Tailing reaction tubes.
  - Dissolve, mix and spin down.
  - Return tubes to ice.
- Start the following thermal cycler program, and only transfer reactions to the block once temperature reaches 4°C. Pause the program if necessary.
  - Use a heated lid (≥100°C).

#### **DNA Fragmentation, End Repair, dA-Tailing Incubation Conditions**

Step	Temperature (°C)	Time (minutes)
<b>1</b>	4	1
<b>2</b>	37	12
<b>3</b>	72	20
<b>4</b>	4	Hold

- After the program has reached 4°C, briefly spin down reactions and place on ice.

## Step 2: MBC Adapter Incorporation

1. Label MBC adapter tubes with the sample index tag letter (A, B, or C) and number (1-48) from the MBC adapters pouch label.
  - a. Use a permanent laboratory marker and orient lid hinges to the back as illustrated:



**Important:** As this step incorporates the P5 index tag for sample-level tracking, be sure to record which MBC adapter is being used for each sample. Unused tubes must be labeled before returning to the pouch.

2. Place an appropriate number of MBC adapter reaction tubes on ice.
3. Add **50 µL** of the DNA Fragmentation, End Repair, dA-Tailing product to a unique MBC adapter reaction tube.
  - a. Dissolve, mix and spin down.
4. Immediately proceed to Step 3: Ligation Step 2.

## Step 3: Adapter Ligation

1. Place an appropriate number of **Adapter Ligation** (SA0005) reaction tubes on ice.
2. Transfer the **entire volume** of each DNA sample from Step 2: MBC Adapter Incorporation to Adapter Ligation tubes.
  - a. Dissolve, mix and spin down.
  - b. Return tubes to ice.
3. Transfer reactions to a thermal cycler and initiate an incubation using the following program and guidelines:
  - a. Heated lid off.

**Adapter Ligation Incubation Conditions**

Step	Temperature (°C)	Time (minutes)
1	16	30
2	22	30
3	4	Hold

- b. After the program has reached 4°C, briefly spin down reactions and place on ice.

## Reaction Cleanup after Adapter Ligation

Refer to Important Precautions section for guidance on working with AMPure XP beads.

1. Completely resuspend AMPure XP beads by vortexing.
2. Remove tubes from ice and add **0.8X** volume (**40 µL**) of AMPure XP beads to each Complete End Repair reaction.
3. Vortex well or pipette 10 times to mix and visually inspect the color of the sample to ensure a homogenous mixture.
4. Incubate for **5 minutes** at room temperature (20°C to 25°C).
5. Briefly spin down tubes.
6. Place tubes on the magnet for **4 minutes or until beads are fully pelleted** against the tube wall.
7. Without disturbing the bead pellet, use a pipette to remove and discard the supernatant. If the pellet becomes dislodged from the magnet and a portion is drawn into the pipette tip, return contents to the tube and repeat magnet incubation step.
8. Wash beads **two times** with 70% ethanol while still on the magnet. For each wash:
  - a. Add **200 µL** 70% ethanol.
  - b. Incubate for **30 seconds** at room temperature (20°C to 25°C).
  - c. Carefully remove ethanol and discard.
9. After the final wash, use a pipette (≤20 µL capacity) to completely remove visible supernatant residue and allow tubes to dry for **3-5 minutes** at room temperature with open lids. **Take care not to over-dry beads** as this will significantly decrease overall recovery (yield) of nucleic acid.
10. Elute DNA by resuspending beads in the volume of 10mM Tris-HCl, pH 8.0 specified in the panel specific **Product Insert (A)**.
11. Place tubes back on the magnet for **2 minutes**.
12. Transfer the volume of purified eluate specified in the panel specific **Product Insert (C)** to a new 0.2mL PCR tube and store reactions as indicated below or proceed directly to Step 4: First PCR.



**Safe stopping point:** It is okay to stop and store the reactions at -30°C to -10°C.

## Step 4: First PCR

1. Place an appropriate number of **First PCR for Illumina-P** (SA0109) reaction tubes on ice.
  - a. Label tubes by sample number.
2. Pipette the volume of **GSP1 (red cap)** specified in the panel specific **Product Insert (B)** into each First PCR tube.
  - a. Spin down and return tubes to ice.
3. Pipette the entire volume of eluate from Reaction Cleanup after Adapter Ligation, step 12 (**Product Insert (C)**) into appropriately labeled First PCR tubes.
  - a. Dissolve, mix and spin down.
  - b. Return tubes to ice.
4. Transfer reactions to a preheated thermal cycler and immediately initiate the program specified in the panel specific **Product Insert (First PCR Reaction)**.
  - a. Use a heated lid ( $\geq 100^{\circ}\text{C}$ ).
  - b. After the program has reached  $4^{\circ}\text{C}$ , briefly spin down reactions and place on ice. It is also acceptable to leave tubes in the thermal cycler at  $4^{\circ}\text{C}$  overnight.



### Reaction Cleanup after First PCR

Refer to **Important Precautions** section for guidance on working with AMPure XP beads.

1. Completely resuspend AMPure XP beads by vortexing.
2. Add **0.8X** volume (**16  $\mu\text{L}$** ) of AMPure XP beads to each reaction.
3. Vortex well or pipette 10 times to mix and visually inspect the color of the sample to ensure a homogenous mixture.
4. Incubate for **5 minutes** at room temperature ( $20^{\circ}\text{C}$  to  $25^{\circ}\text{C}$ ).
5. Briefly spin down tubes.
6. Place tubes on the magnet for **4 minutes or until beads are fully pelleted** against the tube wall.
7. Without disturbing the bead pellet, use a pipette to remove and discard the supernatant. If the pellet becomes dislodged from the magnet and a portion is drawn into the pipette tip, return contents to the tube and repeat magnet incubation step.
8. Wash beads **two times** with 70% ethanol while still on the magnet. For each wash:



- a. Add **200 µL** 70% ethanol
  - b. Incubate for **30 seconds** at room temperature (20°C to 25°C)
  - c. Carefully remove ethanol and discard
9. After the final wash, use a pipette (≤20 µL capacity) to completely remove visible supernatant residue and allow tubes to dry for **3-5 minutes** at room temperature with open lids. **Take care not to over-dry beads** as this will significantly decrease overall recovery (yield) of nucleic acid.
  10. Elute DNA by resuspending beads in the volume of 10 mM Tris-HCl, pH 8.0 specified in the panel specific **Product Insert (D)**.
  11. Place tubes back on the magnet for **2 minutes**.
  12. Transfer the volume of purified eluate specified in the panel specific **Product Insert (E)** to a new 0.2mL PCR tube and store reactions as indicated below or proceed directly to Step 5: Second PCR.



**Safe stopping point:** It is okay to stop and store the reactions at -30°C to -10°C (or leave in thermal cycler on 4°C hold for no more than 24 hours).

## Step 5: Second PCR

1. Place an appropriate number of **Second PCR 1-8 for Illumina-P (SA0110)** reaction tubes on ice.



**Important: The Index 1 (P7) index tag is incorporated during this step.**

- a. Use a permanent marker to label the tubes 1 to 8 from left to right as shown below.  
 (Review the Molecular Barcoding, Sample Indexing & Multiplexed Sequencing section above).



- b. Unused tubes must be labeled before returning to the pouch.
2. Pipette the volume of purified First PCR eluate specified in the panel specific **Product Insert (E)** into each Second PCR tube.
    - a. Record which P7 index sequence is used with which sample.
  3. Pipette the volume of **GSP2 (black cap)** specified in the panel specific **Product Insert (F)** into each Second PCR tube.

- a. Dissolve, mix and spin down.
- b. Return tubes to ice.
4. Transfer reactions to a preheated thermal cycler and immediately initiate the program specified in the panel specific **Product Insert (Second PCR Reaction)**.
  - a. Use a heated lid ( $\geq 100^{\circ}\text{C}$ ).
  - b. After the program has reached  $4^{\circ}\text{C}$ , briefly spin down reactions and place on ice. It is also acceptable to leave tubes in the thermal cycler at  $4^{\circ}\text{C}$  overnight.



## Reaction Cleanup after Second PCR

Refer to Important Precautions section for guidance on working with AMPure XP beads.

1. Completely resuspend AMPure XP beads by vortexing.
2. Add **0.8X** volume (**16  $\mu\text{L}$** ) of AMPure XP beads to each Second PCR reaction.
3. Vortex well or pipette 10 times to mix and visually inspect the color of the sample to ensure a homogenous mixture.
4. Incubate for **5 minutes** at room temperature ( $20^{\circ}\text{C}$  to  $25^{\circ}\text{C}$ ).
5. Briefly spin down tubes.
6. Place tubes on the magnet for **4 minutes or until beads are fully pelleted** against the tube wall.
7. Without disturbing the bead pellet, use a pipette to remove and discard the supernatant. If the pellet becomes dislodged from the magnet and a portion is drawn into the pipette tip, return contents to the tube and repeat magnet incubation step.
8. Wash beads **two times** with 70% ethanol while still on the magnet. For each wash:
  - a. Add **200  $\mu\text{L}$**  70% ethanol.
  - b. Incubate for **30 seconds** at room temperature ( $20^{\circ}\text{C}$  to  $25^{\circ}\text{C}$ ).
  - c. Carefully remove ethanol and discard.
9. After the final wash, use a pipette ( $\leq 20 \mu\text{L}$  capacity) to completely remove visible supernatant residue and allow tubes to dry for **3-5 minutes** at room temperature with open lids. **Take care not to over-dry beads** as this will significantly decrease overall recovery (yield) of nucleic acid.
10. Elute DNA by resuspending beads in **20  $\mu\text{L}$**  10 mM Tris-HCl, pH 8.0.
11. Place tubes back on the magnet for **2 minutes**.

12. Transfer **18 µL** of the purified solution to a new 0.2mL PCR tube. Be sure to avoid transferring beads to the fresh tube.
13. Stop or proceed directly to Quantify, Normalize and Sequence.



**Safe stopping point:** It is okay to stop and store the reactions at -30°C to -10°C.

## Quantify, Normalize, and Sequence

Refer to the Quantify, Normalize, and sequence Protocol for Illumina (RA-DOC-054) for information on quantifying, normalizing and sequencing Archer AMP libraries.

## Data analysis

Archer AMP libraries should be demultiplexed to FASTQs prior to analysis. Analyze data with Archer Analysis using either a local software installation or Archer Unlimited. Visit our website or contact [archer-tech@idtdna.com](mailto:archer-tech@idtdna.com) for more information.

VARIANT*Plex* assays may also require a one-time upload of a GTF file (a text file, in GTF format, which directs the software on how to analyze data from the panel). Additionally, if the DNA SNP/indel pipeline is chosen, there is also an option to select a target mutation file (a text file, in VCF format, which lists specific variants of interest). This file also requires a one-time upload. Both files can be obtained by contacting [archer-tech@idtdna.com](mailto:archer-tech@idtdna.com).

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