



my Baits®

Hybridization Capture for Targeted NGS

User Manual

Version 5.01 March 2021

For myBaits Custom DNA-Seq
myBaits Custom RNA-Seq
myBaits Expert (excluding Wheat Exome and Human Affinities)

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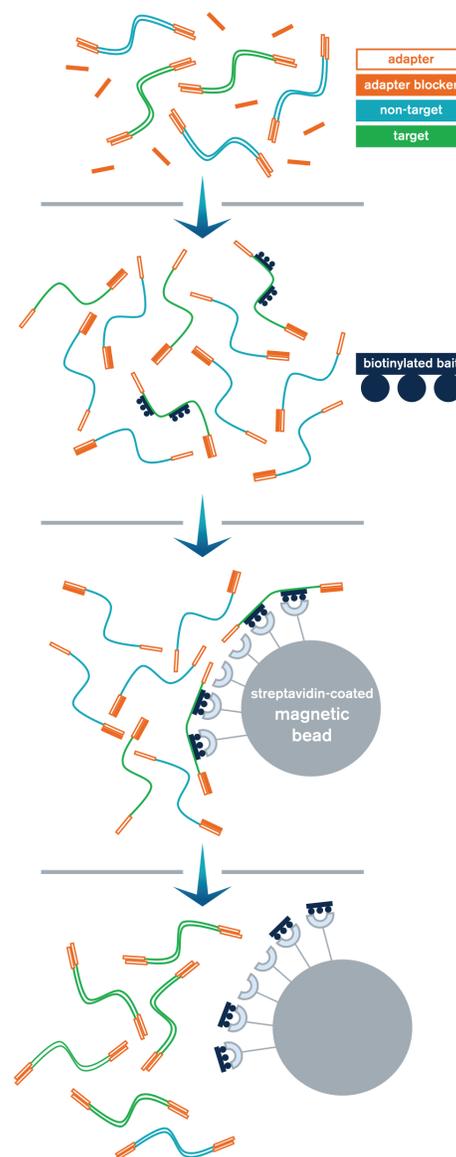
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INTRODUCTION

myBaits® is an in-solution NGS library target enrichment system, compatible with Illumina®, Ion Torrent®, and essentially any amplifiable sequencing library. We use a versatile nucleic acid synthesis technology to produce biotinylated RNA “baits” that are complementary to your sequence targets. Baits and other reagents for NGS target enrichment are supplied with your myBaits kit. After enrichment with myBaits, libraries may then be sequenced on the aforementioned platforms, or further prepared for PacBio® or Oxford Nanopore Technologies® sequencing.

Procedure Overview

1. Amplified sequencing library, adapter blockers, and other hybridization reagents are combined.
2. Libraries are denatured, allowing blockers to hybridize to adapters. Baits are then introduced and hybridized to targets for several hours.
3. Bait-target hybrids are bound to streptavidin-coated magnetic beads and pulled out of suspension with a magnet.
4. Most non-target DNA is washed away. The remaining library is then amplified and either taken directly to sequencing or further treated.



Arbor Biosciences products compatible with this manual

This manual is compatible with current generation myBaits Custom DNA-Seq, Custom RNA-Seq, and Expert kits, but not Custom Methyl-Seq, Expert Wheat Exome, or Expert Human Affinities kits. Visit arborbiosci.com/mybaits-manual to download other manuals, or email techsupport@arbor.daicel.com for assistance. See Page 4 to select the correct protocol within this manual to follow for your application.

Changes since myBaits manual version 4.01

- Three distinct myBaits protocols are included for different applications (See Page 4)

 *These protocols are compatible with v4 reagents and baits*

- **Block X** replaces Block A and typically provides improved specificity
- **Buffer E** is now supplied for post-cleanup bead resuspension
- New application-specific recommendations for experiment design are included

Note for returning myBaits users: This updated reagent chemistry typically provides significantly higher target specificity (= percentage of on-target reads) compared to previous versions. If this is undesired for your application, please contact us for recommendations.

Kit components and stability

	Reagent	Cap color	Volume (8 rxn)	Volume (16 rxn)	Volume (48+ rxn)
Box 1 <i>Store at 4°C</i>	Hyb N	Red	175 µL	175 µL	500 µL
	Hyb S	Teal	750 µL	750 µL	750 µL
	Beads	Clear	550 µL	550 µL	1600 µL
	Binding Buffer	-	12 mL	12 mL	36 mL
	Wash Buffer	-	20 mL	20 mL	60 mL
Box 2 <i>Store at -20°C</i>	Hyb D	Yellow	70 µL	70 µL	190 µL
	Hyb R	Purple	25 µL	25 µL	70 µL
	Block C	Dark Green	50 µL	50 µL	130 µL
	Block O	Blue	90 µL	90 µL	270 µL
	Block X	Orange	5 µL	9 µL	27 µL
	Buffer E	Light Green	550 µL	550 µL	1600 µL
Box 3 <i>Store at -80°C</i>	Baits	White	50 µL per 8 rxns	50 µL per 8 rxns	50 µL per 8 rxns

At the recommended storage temperatures, myBaits kit components have a shelf life of one year.

It is strongly recommended that sub-aliquots of Baits are made in reaction sizes appropriate for your experiment plans to minimize freeze-thaw cycles.

IMPORTANT READ BEFORE PROCEEDING

CHOOSE A PROTOCOL

This manual includes three separate myBaits protocols. Please select from the list below depending on the nature of your sequencing libraries. If you are unsure which protocol to follow, email techsupport@arbor.daicel.com for consultation with one of our NGS scientists.

Note that these are suggested starting points. Identification of optimal parameters for enrichment with a specific bait set and library will require testing and evaluation. These protocols have worked well across many bait set and library combinations.

Standard **Begins Page 5** For most targeted sequencing applications

Recommended when enriching NGS libraries that:

- derive from high-quality genomic DNA of target fragments 80-1,000 bp in length,
- contain a mean insert sequence GC content of >25%,
- are free of substantial (>50%) contamination from non-target organisms, and
- do not have extensive base substitutions (from e.g. deamination or bisulfite conversion)

High Sensitivity **Begins Page 17** For high background contamination, ancient DNA, high bait-target divergence, and/or short insert fragments

Recommended when enriching NGS libraries that have ANY of the following characteristics:

- derive from DNA samples heavily contaminated with exogenous DNA (e.g. pathogen targets in host DNA background, ancient DNA, environmental DNA),
- contain mostly target sequences shorter than 80 bp in length,
- contain a mean target sequence GC content of less than 25%, or
- contain targets that are on average 25% or more divergent from the bait sequences

Long Insert **Begins Page 29** For target enrichment of NGS libraries containing inserts 1-10 kilobase pairs in length

Recommended when enriching NGS libraries that:

- are dominated by inserts >1,000 bp in length, and
- can be amplified with universal adapter primers prior to platform-specific library prep (e.g. PacBio or Nanopore library prep)



Standard Protocol

For most targeted sequencing applications

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REQUIREMENTS AND RECOMMENDATIONS

Input library

TYPE Use myBaits with PCR-amplified and amplifiable NGS libraries, including Illumina TruSeq®-style, Illumina Nextera® Flex-style, Ion Torrent, or other libraries with universal adapter priming sites. **It is NOT recommended to use myBaits with PCR-free libraries; additionally, myBaits are incompatible with libraries made using original Nextera or Nextera XT library preparation kits, or any library type containing biotin.** Dual-indexed libraries are strongly recommended to reduce the hazard of mis-indexing induced by PCR jumping events.

VOLUME Each myBaits target enrichment reaction has space for 7 µL total NGS library volume. Many pools will require concentration to 7 µL with vacuum centrifugation or other means. Complete this in advance of your myBaits experiments. Libraries should be suspended in nuclease-free buffer or water.

MASS A wide range of total library mass can be successfully enriched with myBaits (nanograms to micrograms). However, best results are seen when 100 ng or more total mass is used per enrichment reaction. It is strongly recommended that library qPCR is used to measure library mass, rather than e.g. dye assay or electrophoresis. See note below on default recommendations for mass input for library pools.

POOLING Optimal pooling parameters (both in terms of number of libraries and total mass per library) will vary between library types and bait sets, and will require trials to identify. However, many configurations should work well. To minimize variation in capture performance among pooled samples, only pool libraries based on comparable anticipated bait-genome sequence identity (i.e. taxon), DNA quality, starting DNA amount, library insert length, and relative target constituent vs. background. Pool equal amounts of each library. We recommend that when libraries derive from organisms with genome sizes smaller than 5 Gbp, pool eight libraries, 250 ng each, for a total of 2 µg per enrichment reaction. For genomes 5 Gbp or larger, pool eight libraries, 1 µg each for a total of 8 µg.

Blocking oligos

When ordering your myBaits kit, please indicate the sequencing library configuration you intend to enrich. The standard adapter blocking reagent provided with the kit (**Block X**) is compatible with Illumina TruSeq-style or Nextera-style libraries with single 6-12 bp or dual 6-12 bp indexing. For different adapter configurations, we recommend ordering Custom IDT® xGen® Blocking Oligos customized for your NGS library adapter sequences. At a concentration of 1 µg/µL, any custom adapter-blocking oligos can be used in lieu of myBaits Block X.

Equipment required

Item	Notes
50 mL tubes	1 per 44 reactions
Microcentrifuge tubes (1.5, 1.7, or 1.8 mL)	2 per 8 reactions
0.2 mL PCR strips with attached lids	2 per 8 reactions (e.g., VWR Cat# 93001-118)
Pipettors and tips for 0.5 - 500 μ L	Multichannel for 20 and 500 μL recommended
[†] Thermal cycler with heated lid compatible with 0.2 mL strips	1 or 2
Magnetic particle collector for microcentrifuge tubes	1 (e.g., ThermoFisher Cat# 12321D)
Magnetic particle collector for 0.2 mL strips	1 (e.g., Permagen Cat# S500)
Vortex mixer and mini-centrifuge for tubes and strips	
Water bath or incubation oven at 65°C	
Heat block for microcentrifuge tubes at 60°C	

[†] Ensure that the thermal cycler and strips allow no more than 4 μ L of 30 μ L volume evaporation overnight at 65°C

Reagents required

Reagent	Notes
Nuclease-free ("NF") water	900 μ L per reaction
PCR primers to amplify sequencing libraries after capture, e.g.:	
Illumina P5: AATGATACGGCGACCACCGA	2.5 μ L @ 10 μ M per reaction
Illumina P7: CAAGCAGAAGACGGCATACGA	2.5 μ L @ 10 μ M per reaction
PCR reagents for post-capture amplification	1 per reaction (e.g. Roche Cat# 07958927001)
PCR purification system, e.g., silica columns or SPRI beads	1 cleanup per reaction

PROCEDURE

PART 1: Hybridization setup

Sequencing libraries are mixed with various blocking nucleic acids, denatured, and then combined with other hybridization reagents (including baits). These hybridization reactions incubate for several hours to allow baits to encounter and hybridize with target library molecules.

S1.1 Choose a hybridization temperature (T_H)

65°C

When bait-target sequence divergence is expected to be less than 10%

62°C

When bait-target sequence divergence is expected to be 10 to 15%

60°C

When bait-target sequence divergence is expected to be 15 to 25%

S1.2 Prepare materials

Reagents	Equipment
Hyb N and Hyb S from Box 1	Nuclease-free microcentrifuge tubes (x2)
Hyb D and Hyb R from Box 2	0.2 mL strips with attached lids (x1 per 8 reactions)
Block C, Block O, and Block X from Box 2	Pipettors and tips; multichannel for 20 μ L recommended
Baits from Box 3 KEEP ON ICE	Vortex mixer and mini-centrifuge for above tube types
Libraries or library pools in 7 μ L per reaction	Heat block set to 60°C
	Thermal cyclers; 2 blocks recommended for 24 or more reactions

Program the thermal cycler:



Set lid temperature 5 to 10°C above each step temperature to minimize evaporation

Step	Temperature	Time
1	95°C	5m
2	T_H	5m
3	T_H	∞

S1.3 Hybridization Mix setup

- Once the Hyb reagents have thawed, vortex to homogenize and then briefly centrifuge.



Heat Hyb N and Hyb S to 60°C and vortex to dissolve any precipitate present after thawing

- Assemble the Hybridization Mix in a microcentrifuge (MC) tube, briefly vortex and briefly centrifuge the contents to collect. **The following volumes are already adjusted for pipetting error:**

Component	μL / Reaction
Hyb N	9.25
Hyb D	3.5
Hyb S*	0.5
Hyb R	1.25
Baits	5.5
TOTAL	20

**Cloudiness caused by Hyb S addition will clear after step 3*

- Incubate the Hybridization Mix at 60°C for 10 minutes in the heat block. Vortex occasionally to collect the condensate. Remove from the heat block and let sit 5 minutes at room temperature.
- For each capture reaction, aliquot 18.5 μL of Hybridization Mix to a 0.2 mL well/tube.

These reaction aliquots of Hybridization Mix are now referred to as "HYBs"

S1.4 Blockers Mix setup

- Assemble the Blockers Mix **specific for your target taxon/taxa** in an appropriately-sized tube and mix by pipetting. **The following volumes are already adjusted for pipetting error:**

MOST TAXA		PLANTS		SALMONIDS	
Component	μL / Reaction	Component	μL / Reaction	Component	μL / Reaction
Block O	2.5	Block O	5.0	Block O	-
Block C	2.5	Block C	-	Block C	2.5
Block X	0.5	Block X	0.5	Block X	0.5
NF Water	-	NF Water	-	NF Water	2.5
TOTAL	5.5	TOTAL	5.5	TOTAL	5.5

- For each capture reaction, aliquot 5 μL of Blockers Mix to a 0.2 mL well/tube.
- Add 7 μL of individual or pooled libraries to each Blockers Mix aliquot and mix by pipetting.

These libraries mixed with Blockers Mix aliquots are now referred to as "LIBs"

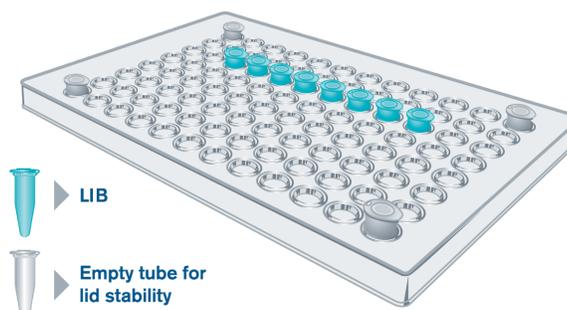
S1.5 Reaction assembly

Double-check the thermal program:

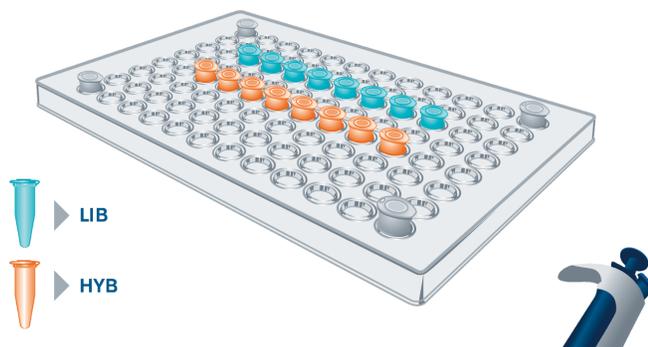
 *Set lid temperature 5 to 10°C above each step temperature to minimize evaporation*

Step	Temperature	Time
1	95°C	5m
2	T _H	5m
3	T _H	∞

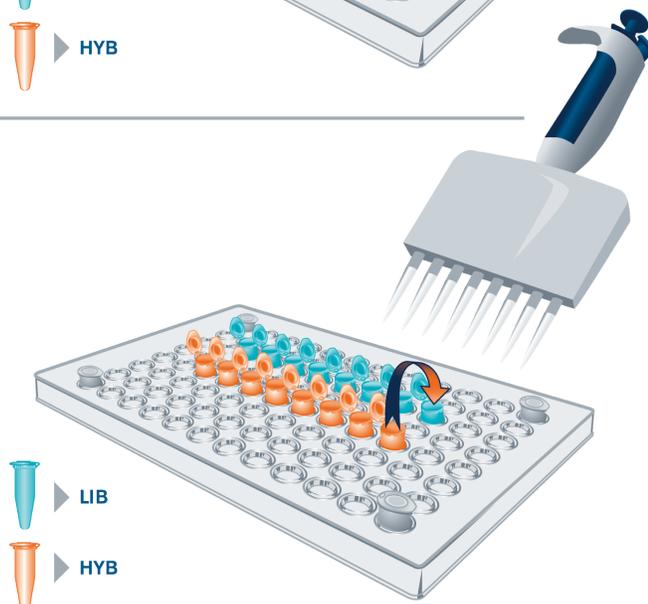
- Put the **LIBs** in the thermal cycler, close the lid, and start the thermal program.



- Once the cycler reaches the hybridization temperature during step 2, pause the program, put the **HYBs** in the thermal cycler, close the lid, and resume the program.



- After step 2 of the program is complete, leaving all tubes in the thermal cycler, pipette **18 µL of each HYB to each LIB**. Use a multichannel pipettor for easier execution. Gently homogenize by pipetting up and down 5 times.



- Dispose of the HYB tubes. Briefly spin down the LIBs, return to the thermal cycler, close the lid, and allow the reactions to incubate overnight (16 to 24 hours).

PART 2: Bind and Wash (“Cleanup”)

Bait-target hybrids are bound to streptavidin-coated magnetic beads, and then most non-target DNA is removed with several rounds of washing with a warm buffer. This is usually performed the day following completion of Part 1.

S2.1 Choose a wash temperature (T_w - typically identical to T_H)

65°C

When bait-target sequence divergence is expected to be 10% or less

62°C

When bait-target sequence divergence is expected to be 10 to 15%

60°C

When bait-target sequence divergence is expected to be 15 to 25%

S2.2 Prepare materials

 *Start at least 90 minutes before intended hybridization stop time*

Reagents

Hyb S (Box 1) *

Binding Buffer (Box 1) *

Wash Buffer (Box 1) *

Beads (Box 1)

Nuclease-free (NF) Water (up to 900 μ L per reaction)

** Allow these reagents to come to room temperature before use; warm to 60°C and vortex to dissolve precipitate if necessary*

Equipment

Water bath or incubation oven set to the T_w (e.g., 65°C)

Receptacles for 50 mL tubes, 0.2 mL strips and microcentrifuge tubes compatible with above incubation device

Vortex mixer and mini-centrifuge for 0.2 mL strips and MC tubes

Magnetic particle collector(s) (MPC) for above strips and/or tubes

When using only a microcentrifuge (MC) tube-compatible MPC

Nuclease-free 50 mL tube, 1 per 44 cleanups

Nuclease-free MC tubes, 1 per reaction

Heat block set to the T_w

Pipettors and tips for 20 – 500 μ L

When using a 0.2 mL tube-compatible MPC

Nuclease-free 50 mL tube, 1 per 68 cleanups

Nuclease-free 0.2 mL PCR strips with individually-attached lids, 1 vessel per reaction

Thermal cycler set to T_w

Pipettors and tips for 20 – 200 μ L;

multichannel pipettor strongly recommended

S2.3 Wash Buffer X preparation

This step generates enough Wash Buffer X for 44 reactions in microcentrifuge (“MC”) tube cleanup format, and 68 reactions in 0.2 mL cleanup format; scale up or down if needed.

1. Thaw and thoroughly homogenize Wash Buffer and Hyb S prior to aliquoting in order to dissolve any visible precipitate; warm slightly if necessary.
2. Combine 400 μ L Hyb S, 39.6 mL NF water and 10 mL Wash Buffer in a 50 mL tube. Vortex thoroughly, label “Wash Buffer X.” *Wash Buffer X can be stored at 4°C for 1 month*
3. Heat the Wash Buffer X to the T_w in the water bath or oven for at least 30 minutes before use.

S2.4 Bead preparation *Prepare beads immediately prior to use*

1. For each capture reaction, aliquot 30 μ L beads to a microcentrifuge tube.
2. Pellet the beads in the MPC until the suspension is clear (1-2 minutes).
Leaving the tubes on the magnet, remove and discard the supernatant.
3. Add 200 μ L Binding Buffer to each bead aliquot. Vortex to resuspend the beads and centrifuge briefly. Place tube in the MPC and pellet beads; remove and discard the supernatant.
4. Repeat Step 3 above twice for a total of three washes.
5. Resuspend each washed bead aliquot in 70 μ L Binding Buffer. If proceeding to washing in 0.2 mL format, transfer the aliquots to PCR strips.

TIP: Beads can be prepared in 8 (or fewer) reaction batches (240 μ L) in a microcentrifuge tube. Multiply all volumes by the number of reactions in the batch; i.e., for 8 reactions-worth, wash with 1.6 mL and resuspend in 560 μ L Binding Buffer, then aliquot 70 μ L suspension to individual tubes.

S2.5 Binding beads and hybrids

1. Heat the bead aliquots to the T_w (e.g., 65°C) for at least 2 minutes.
2. Transfer each capture reaction to the heated bead aliquots. Mix by pipetting.
3. Incubate the libraries + beads on the heat block or thermal cycler for 5 minutes. Agitate at the 2.5 minute mark by flicking or inverting the tubes to keep the beads suspended, followed by briefly centrifuging.

S2.6 Bead washing

1. Pellet the beads with the MPC until the solution is clear. Remove and discard the supernatant.
2. Add 375 μ L (MC tube format) or 180 μ L (0.2 mL format) warmed Wash Buffer X to the beads, remove from the MPC, place on heat block for 15 seconds, and briefly vortex or mix by pipetting. Briefly centrifuge the mixture.
3. Incubate for 5 minutes at the T_w in the heat block or thermal cycler. Agitate at the 2.5 minute mark via gentle vortexing and then briefly centrifuge.
4. Repeat steps 1 through 3 two times for MC tube format (three washes total), or three times for 0.2 mL format (four washes total). **After the last wash and pelleting, remove as much liquid as possible without touching the bead pellet.**

PART 3: Library Resuspension and Amplification

Bead-bound enriched library is resuspended in Buffer E and amplified.

S3.1 Prepare materials

Reagents	Equipment
Buffer E (Box 2)	Tubes appropriate for PCR master mix assembly
PCR primers for amplifying libraries (e.g., P5 and P7)	Tubes or strips for 50 µL PCR amplification
PCR reagents for post-capture amplification	Pipettors and tips capable of 5 – 100 µL volumes
PCR purification system, e.g., silica columns or SPRI beads	Vortex mixer and mini-centrifuge for above tube types
Nuclease-free (NF) Water	Thermal cycler

S3.2 Enriched library recovery

- Add 30 µL Buffer E to the washed beads and thoroughly resuspend by pipetting. Then, depending on your library amplification system, choose workflow A or B:

WORKFLOW A: When using KAPA HiFi HotStart or NEB Ultra II Q5 polymerase systems for amplification

- Proceed directly to section S3.3 using this bead resuspension as the template in amplification

WORKFLOW B: When not using the polymerase systems for amplification in workflow A

- Incubate the suspension at 95°C for 5 minutes
- Immediately pellet the beads in the MPC and collect the supernatant containing the enriched libraries

S3.3 Library amplification

This is an example post-capture amplification using KAPA HiFi HotStart ReadyMix and Illumina libraries:

- Assemble the following PCR master mix:

Component	Final Concentration	µL / Reaction	Sequence
NF Water	-	5	-
2X KAPA HiFi HotStart Ready Mix	1 X	25	-
P5 library primer (at 10 µM)	500 nM	2.5	AATGATACGGCGACCACCGA
P7 library primer (at 10 µM)	500 nM	2.5	CAAGCAGAAGACGGCATACGA
Enriched Library (on- or off-bead)	-	15 *	-
TOTAL		50	-

*Remaining bead-bound library can be stored at -20°C for several months.

S3.3 Library amplification (continued)

2. Cycle the reactions with the following thermal program:

Step	Temperature	Time
1	98°C	2 minutes
2	98°C	20 seconds
3	60°C	30 seconds
4	72°C	45 seconds
5	72°C	5 minutes
6	8°C	∞

×8 to 14
cycles*

**Minimize cycles where possible. Cycles required to meet molarity requirements of sequencing platform may exceed 14.*

3. After amplification:
- **If beads were included in the amplification reaction and you intend to use silica columns for purification**, pellet the beads first and purify only the supernatant.
 - Otherwise, purify the reaction using your preferred PCR cleanup (e.g., silica columns or SPRI beads).

The enriched libraries are now ready for quantification, quality-assessment, and sequencing.

APPENDIX

SA1: Troubleshooting

During hybridization, my thermal cycler dropped below the hybridization temperature.

You can expect a lower on-target read proportion and target read complexity for these libraries than if the temperature remained where intended, but not outright enrichment failure. Shallow preliminary sequencing will determine whether targets are likely to be retrieved at sufficient coverage within budget.

My enriched and amplified library is not visible on electrophoresis gel or similar.

Successful captures frequently yield a total mass of just a few nanograms even after re-amplification, which can be difficult to visualize with electrophoresis. This is most common when capturing especially small targets (<100 bp), or targets that are present at low frequency in the starting library (like those in degraded/ancient/environmental DNA), or if there is under-re-amplification of the library post-capture. Often a few more cycles of library amplification will render the captured product sufficiently high in concentration to view with electrophoresis. Alternatively, determine with library qPCR whether the library is of sufficient mass for sequencing. If cycling is halted before reaching PCR plateau, the qPCR product can be visualized with electrophoresis to determine length distribution. Consult with your sequencing provider for library concentration and volume requirements.

My enriched and amplified library appears significantly longer than my original library, or has two peaks.

This may happen if the libraries are over-amplified and have formed 'daisy-chains' or 'bubbles' by experiencing cycles of denature-renature without template extension. These can be reverted to their original appearance in electrophoresis by applying three PCR cycles using regular library amplification.

I observe a high ratio of PCR duplicates in my enriched library sequence data.

Percent duplicates in sequencing data (i.e. "clonality" or "duplication rate") increases as you sequence deeper, and therefore it can only be fairly compared between experiments when the sequencing depth is normalized before analysis. Evaluate whether you have simply over-sequenced the libraries by plotting raw sequencing reads obtained on the X axis, and unique reads observed on the Y axis. If this **complexity curve** has plateaued, but you achieved sufficient unique reads, you sequenced more deeply than necessary. If it has not flattened, or you need to increase the total potential unique read yield of the library, **use more DNA per library preparation and/or more library per capture reaction. Avoid diluting baits before capture.** When working with heavily contaminated or damaged DNA target molecules, consider reducing temperatures used in all steps to improve capture sensitivity. Reducing PCR cycles when possible may also improve target coverage uniformity and complexity for a given sequencing depth, in some cases having an indirect effect on duplication rate. For more information about library complexity for any NGS application, we recommend Daley & Smith 2013 (doi: 10.1038/nmeth.2375).

SA2: myBaits Procedure Quick Guide - Standard Protocol

- For each reaction, build the following Mixes; pipetting error is built in:

Hybridization Mix		Blockers Mix	
Component	µL / Reaction	Component	µL / Reaction
Hyb N	9.25	Block X	0.5
Hyb D	3.5	Block C	2.5
Hyb S	0.5	Block O	2.5*
Hyb R	1.25	NF Water	0 [†]
Baits	5.5		
TOTAL	20	TOTAL	5.5

*Plants: 5.0; Salmonids: 0
[†]Plants: 0; Salmonids: 2.5

- After pre-warming the Hybridization mix for 10 minutes @ 60°C, for each reaction, aliquot **18.5 µL** of Hybridization Mix to their own tubes – now “**HYBs**”.
- For each reaction, aliquot **5 µL** of Blockers Mix and then add **7 µL** of each library – now “**LIBs**”.
- Incubate the LIBs in the thermal cycler for 5 minutes @ 95°C and then drop to the hybridization temperature (e.g., 65°C). **Be sure to use a heated lid.**
- Put the HYBs in the thermal cycler and warm to the hybridization temperature for 5 minutes.
- Transfer **18 µL** of each HYB to each LIB, mix by pipetting, and incubate for 16-24 hours.
- 1.5 hours before step 9**, prepare Wash Buffer X by combining 400 µL Hyb S, 39.6 mL nuclease-free molecular biology-grade water and 10 mL Wash Buffer in a 50 mL tube. Vortex thoroughly and warm to the hybridization temperature for at least 45 minutes.
- Prepare 30 µL of beads per reaction by washing three times in 200 µL Binding Buffer. Resuspend the washed bead aliquots in 70 µL Binding Buffer and warm the suspensions to the hybridization temperature for at least 2 minutes.
- Combine the warmed beads with the hybridization reactions and incubate for 5 minutes at the hybridization temperature, agitating at 2.5 minutes to keep beads suspended.
- Pellet the beads and remove the supernatant. If using microcentrifuge tubes for cleanup, wash the beads three times with 375 µL warmed Wash Buffer X, incubating 5 minutes at the hybridization temperature. Wash four times with 180 µL washes if using a 96-well magnetic particle concentrator and 0.2 mL strips/tubes.
- Resuspend the beads in 30 µL Buffer E and then use 15 µL of this in a 50 µL amplification reaction with KAPA[®] HiFi or NEB Ultra II Q5 polymerase systems. If not using these polymerase systems, instead elute the library from the beads by incubating the suspension for 5 minutes at 95°C, immediately pellet the beads, and then use 15 µL of the supernatant in a 50 µL amplification reaction.
- Purify the amplification reactions using silica columns or SPRI beads. **If using silica columns and beads were included in the amplification reaction, pellet the beads first and purify only the supernatant.**



High Sensitivity Protocol

For high background contamination, ancient DNA, high bait-target divergence, and/or short insert fragments

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REQUIREMENTS AND RECOMMENDATIONS

Input library

TYPE Use myBaits with PCR-amplified and amplifiable NGS libraries, including Illumina TruSeq®-style, Illumina Nextera® Flex-style, Ion Torrent, or other libraries with universal adapter priming sites. **It is NOT recommended to use myBaits with PCR-free libraries; additionally, myBaits are incompatible with libraries made using original Nextera or Nextera XT library preparation kits, or any library type containing biotin.** Dual-indexed libraries are strongly recommended to reduce the hazard of mis-indexing induced by PCR jumping events.

VOLUME Each myBaits target enrichment reaction has space for 7 µL total NGS library volume. Many pools will require concentration to 7 µL with vacuum centrifugation or other means. Perform this in advance of your myBaits experiments. Libraries should be suspended in nuclease-free buffer or water.

MASS & POOLING A wide range of total library mass can be successfully enriched with myBaits (nanograms to micrograms). Optimal pooling parameters (both in terms of number of libraries and total mass per library) will vary between library types and bait sets and may require trials to identify. However, many configurations should work well.

Non-degraded, non-contaminated DNA libraries (e.g. libraries with bait-target divergence expected mean >25%): To minimize variation in capture performance among pooled samples, only pool libraries of comparable anticipated bait-genome sequence identity (i.e. taxon), DNA quality, starting DNA amount, library insert length, and relative target constituent vs. background. Pool equal amounts of each library. When libraries derived from organisms with genome sizes smaller than 5 Gbp, pool eight libraries, 250 ng each, for a total of 2 µg per enrichment reaction. For genomes 5 Gbp or larger, pool eight libraries, 1 µg each for a total of 8 µg.

Degraded and contaminated DNA libraries: Pool as few libraries as possible, and input as much as possible to capture, up to a total of 12 µg. If pooling is required, make certain that libraries are balanced by endogenous content to ensure each sample contributes the same amount of target content. For example, if two libraries are to be pooled, and library A has 20% endogenous template and library B has 10% endogenous template, include twice the mass of library B as library A in the enrichment pool.

Blocking oligos

When ordering your myBaits kit, please indicate the sequencing library configuration you intend to enrich. The standard adapter blocking reagent provided with the kit (**Block X**) is compatible with Illumina TruSeq-style or Nextera-style libraries with single 6-12 bp or dual 6-12 bp indexing. For different adapter configurations, we recommend ordering Custom IDT® xGen® Blocking Oligos customized for your NGS

library adapter sequences. At a concentration of 1 µg/µL, any custom adapter-blocking oligos can be used in lieu of myBaits Block X.

Special note on two-round enrichment protocols:

The High Sensitivity protocol includes two rounds of enrichment. This may require that you purchase additional myBaits Reagents (without Baits). For example, if you plan to use all 16 reactions of a myBaits kit in the High Sensitivity protocol, you will need to have both the 16 reaction kit as well as at least 16 additional reactions-worth of myBaits Reagents. These can be purchased in 16 or 48 reaction kits, catalog numbers 300016 and 300048, respectively.

Equipment required

Item	Notes
50 mL tubes	1 per 44 reactions
Microcentrifuge tubes (1.5, 1.7, or 1.8 mL)	2 per 8 reactions
0.2 mL PCR strips with attached lids	2 per 8 reactions (e.g., VWR Cat# 93001-118)
Pipettors and tips for 0.5 - 500 µL	Multichannel for 20 and 500 µL recommended
[†] Thermal cycler with heated lid compatible with 0.2 mL strips	1 or 2
Magnetic particle collector for microcentrifuge tubes	1 (e.g., ThermoFisher Cat# 12321D)
Magnetic particle collector for 0.2 mL strips	1 (e.g., Permagen Cat# S500)
Vortex mixer and mini-centrifuge for tubes and strips	
Water bath or incubation oven at 65°C	
Heat block for microcentrifuge tubes at 60°C	

[†] Ensure that the thermal cycler and strips allow no more than 4 µL of 30 µL volume evaporation overnight at 65°C

Reagents required

Reagent	Notes
Nuclease-free ("NF") water	900 µL per reaction
PCR primers to amplify sequencing libraries after capture, e.g.:	
Illumina P5: AATGATACGGCGACCACCGA	2.5 uL @ 10 µM per reaction
Illumina P7: CAAGCAGAAGACGGCATACGA	2.5 uL @ 10 µM per reaction
PCR reagents for post-capture amplification	1 per reaction (e.g. Roche Cat# 07958927001)
PCR purification system, e.g., silica columns or SPRI beads	1 cleanup per reaction

PROCEDURE

PART 1: Hybridization setup

Sequencing libraries are mixed with various blocking nucleic acids, denatured, and then combined with other hybridization reagents (including baits). These hybridization reactions incubate for several hours to allow baits to encounter and hybridize with target library molecules.

H1.1 Choose a hybridization temperature (T_H)

63°C

For DNA libraries with low GC content or with expected bait-target divergence of less than 15%

60°C

For libraries with expected bait-target sequence divergence of 15 to 25%

55°C

For libraries with insert length distributions mostly shorter than the myBaits probe length, or expected bait-target sequence divergence higher than 25%

H1.2 Prepare materials

Reagents	Equipment
Nuclease-free Water ("H ₂ O")	Nuclease-free microcentrifuge tubes (x2)
Hyb N and Hyb S from Box 1	0.2 mL strips with attached lids (x1 per 8 reactions)
Hyb D and Hyb R from Box 2	Pipettors and tips; multichannel for 20 μ L recommended
Block C, Block O, and Block X from Box 2	Vortex mixer and mini-centrifuge for above tube types
Baits from Box 3 KEEP ON ICE	Heat block set to 60°C
Libraries or library pools in 7 μ L per reaction	Thermal cyclers; 2 blocks recommended for 24 or more reactions

Program the thermal cycler:

 Set lid temperature 5 to 10°C above each step temperature to minimize evaporation

Step	Temperature	Time
1	95°C	5m
2	T_H	5m
3	T_H	∞

H1.3 Hybridization Mix setup

- Once the Hyb reagents have thawed, vortex them to homogenize and then briefly centrifuge.

 Heat Hyb N and Hyb S to 60°C and vortex to dissolve any precipitate present after thawing

- Assemble the Hybridization Mix in a microcentrifuge (MC) tube, briefly vortex and briefly centrifuge to collect the sample. **The following volumes are already adjusted for pipetting error:**

Component	μL / Reaction	
Hyb N	9.25	
Hyb D	3.5	
Hyb S*	0.5	<i>*Cloudiness caused by Hyb S addition will clear after step 3</i>
Hyb R	1.25	
H2O (round 1 / round 2)	1.1 / 4.4	<i>First enrichment round: 1.1 μL Second round: 4.4 μL</i>
Baits (round 1 / round 2)	4.4 / 1.1	<i>First enrichment round: 4.4 μL Second round: 1.1 μL</i>
TOTAL	20	

- Incubate the Hybridization Mix at 60°C for 10 minutes in the heat block. Vortex occasionally to collect condensate. Remove from the heat block and let sit 5 minutes before proceeding.
- For each capture reaction, aliquot 18.5 μL of Hybridization Mix to a 0.2 mL well/tube.

These reaction aliquots of Hybridization Mix are now referred to as "HYBs"

H1.4 Blockers Mix setup

- Assemble the Blockers Mix **specific for your target taxon/taxa** in an appropriately-sized tube and mix by pipetting. **The following volumes are already adjusted for pipetting error:**

MOST TAXA		PLANTS		SALMONIDS	
Component	μL / Reaction	Component	μL / Reaction	Component	μL / Reaction
Block O	2.5	Block O	5.0	Block O	-
Block C	2.5	Block C	-	Block C	2.5
Block X	0.5	Block X	0.5	Block X	0.5
NF Water	-	NF Water	-	NF Water	2.5
TOTAL	5.5	TOTAL	5.5	TOTAL	5.5

- For each capture reaction, aliquot 5 μL of Blockers Mix to a 0.2 mL well/tube.
- Add 7 μL of individual or pooled libraries to each Blockers Mix aliquot and mix by pipetting.

These libraries mixed with Blockers Mix aliquots are now referred to as "LIBs"

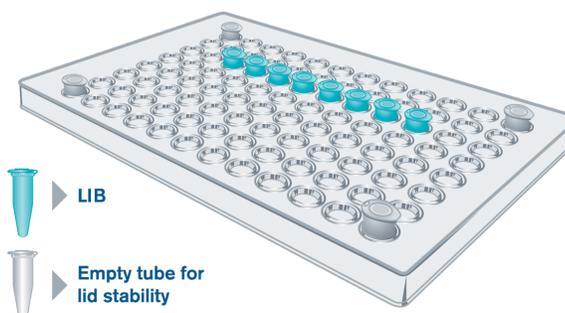
H1.5 Reaction assembly

Double-check the thermal program:

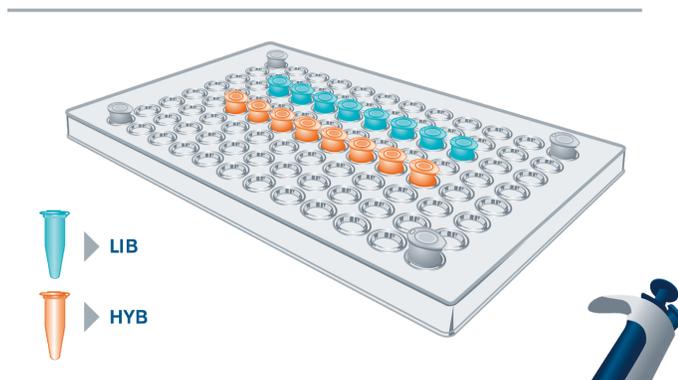
 *Set lid temperature 5 to 10°C above each step temperature to minimize evaporation*

Step	Temperature	Time
1	95°C	5m
2	T _H	5m
3	T _H	∞

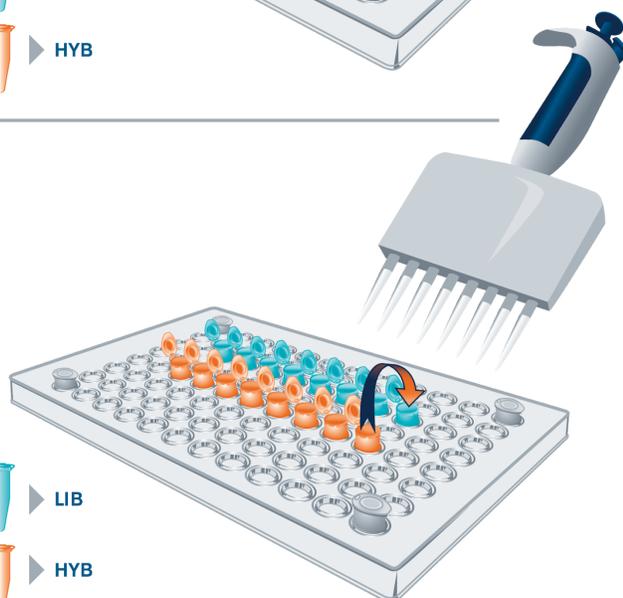
- Put the **LIBs** in the thermal cycler, close the lid, and start the thermal program.



- Once the cycler reaches the hybridization temperature during step 2, pause the program, put the **HYBs** in the thermal cycler, close the lid, and resume the program.



- After step 2 of the program is complete, leaving all tubes in the thermal cycler, **pipette 18 µL of each HYB to each LIB**. Use a multichannel pipettor for easier execution. Gently homogenize by pipetting up and down 5 times.



- Dispose of the HYB tubes. Briefly spin down the LIBs, return to the thermal cycler, close the lid, and allow the reactions to incubate overnight (16 to 24 hours).

PART 2: Bind and Wash (“Cleanup”)

Bait-target hybrids are bound to streptavidin-coated magnetic beads, and then most non-target DNA is removed with several rounds of washing with a warm buffer. This is usually performed the day following completion of Part 1.

H2.1 Choose a wash temperature (T_w - typically identical to T_H)

63°C

When bait-target sequence divergence is expected to be 15% or less

60°C

When bait-target sequence divergence is expected to be 15 to 25%

55°C

When bait-target sequence divergence is expected to be higher than 25%

H2.2 Prepare materials



Start at least 90 minutes before intended hybridization stop time

Reagents

Hyb S (Box 1) *

Binding Buffer (Box 1) *

Wash Buffer (Box 1) *

Beads (Box 1)

Nuclease-free (NF) Water (up to 900 μ L per reaction)

** Allow these reagents to come to room temperature before use; warm to 60°C and vortex to dissolve precipitate if necessary*

Equipment

Water bath or incubation oven set to the T_w (e.g., 65°C)

Receptacles for 50 mL tubes, 0.2 mL strips and microcentrifuge tubes compatible with above incubation device

Vortex mixer and mini-centrifuge for 0.2 mL strips and MC tubes

Magnetic particle collector(s) (MPC) for above strips and/or tubes

When using only a microcentrifuge (MC) tube-compatible MPC

Nuclease-free 50 mL tube, 1 per 44 cleanups

Nuclease-free MC tubes, 1 per reaction

Heat block set to the T_w

Pipettors and tips for 20 – 500 μ L

When using a 0.2 mL tube-compatible MPC

Nuclease-free 50 mL tube, 1 per 68 cleanups

Nuclease-free 0.2 mL PCR strips with individually-attached lids, 1 vessel per reaction

Thermal cycler set to T_w

Pipettors and tips for 20 – 200 μ L;

multichannel pipettor strongly recommended

H2.3 Wash Buffer X preparation

This step generates enough Wash Buffer X for 44 reactions in microcentrifuge (“MC”) tube cleanup format, and 68 reactions in 0.2 mL cleanup format; scale up or down if needed.

1. Thaw and thoroughly homogenize Wash Buffer and Hyb S prior to aliquoting in order to dissolve any visible precipitate; warm slightly if necessary.
2. Combine 400 μL Hyb S, 39.6 mL NF water and 10 mL Wash Buffer in a 50 mL tube. Vortex thoroughly, label “Wash Buffer X.” *Wash Buffer X can be stored at 4°C for 1 month*
3. Heat the Wash Buffer X to the T_w in the water bath or oven for at least 30 minutes before use.

H2.4 Bead preparation Prepare beads immediately prior to use

1. For each capture reaction, aliquot 30 μL beads to a microcentrifuge tube.
2. Pellet the beads in the MPC until the suspension is clear (1-2 minutes).
Leaving the tubes on the magnet, remove and discard the supernatant.
3. Add 200 μL Binding Buffer to each bead aliquot. Vortex to resuspend the beads and centrifuge briefly. Pellet in the MPC, remove and discard the supernatant.
4. Repeat Step 3 above twice for a total of three washes.
5. Resuspend each washed bead aliquot in 70 μL Binding Buffer. If proceeding to washing in 0.2 mL format, transfer the aliquots to PCR strips.

TIP: Beads can be prepared in 8 (or fewer) reaction batches (240 μL) in a microcentrifuge tube. Multiply all volumes by the number of reactions in the batch; i.e., for 8 reactions-worth, wash with 1.6 mL and resuspend in 560 μL Binding Buffer, then aliquot 70 μL suspension to individual tubes.

H2.5 Binding beads and hybrids

1. Heat the bead aliquots to the T_w (e.g., 63°C) for at least 2 minutes.
2. Transfer each capture reaction to the heated bead aliquots. Mix by pipetting.
3. Incubate the libraries + beads on the heat block or thermal cycler for 5 minutes. Agitate at the 2.5 minute mark by flicking or inverting the tubes to keep the beads suspended, followed by briefly centrifuging to collect.

H2.6 Bead washing

1. Pellet the beads with the MPC until the solution is clear. Remove and discard the supernatant.
2. Add 375 μL (MC tube format) or 180 μL (0.2 mL format) warmed Wash Buffer X to the beads, remove from the MPC, place on heat block for 15 seconds, and briefly vortex or mix by pipetting. Briefly centrifuge to collect.
3. Incubate for 5 minutes at the T_w in the heat block or thermal cycler. Agitate at the 2.5 minute mark via gentle vortexing and briefly centrifuge.
4. Repeat steps 1 through 3 two times for MC tube format (three washes total), or three times for 0.2 mL format (four washes total). **After the last wash and pelleting, remove as much fluid as possible without touching the bead pellet.**

PART 3: Library Resuspension and Amplification

Bead-bound enriched library is resuspended in Buffer E and amplified.

H3.1 Prepare materials

Reagents	Equipment
Buffer E (Box 2)	Tubes appropriate for PCR master mix assembly
PCR primers for amplifying libraries (e.g., P5 and P7)	Tubes or strips for 50 μ L PCR amplification
PCR reagents for post-capture amplification	Pipettors and tips capable of 5 – 100 μ L volumes
PCR purification system, e.g., silica columns or SPRI beads	Vortex mixer and mini-centrifuge for above tube types
Nuclease-free (NF) Water	Thermal cycler

H3.2 Enriched library recovery

- Add 30 μ L Buffer E to the washed beads and thoroughly resuspend by pipetting. Then, depending on your library amplification system, choose workflow A or B:

WORKFLOW A: When using KAPA HiFi HotStart or NEB Ultra II Q5 polymerase systems for amplification

- Proceed directly to section H3.3 using this bead resuspension as template in amplification

WORKFLOW B: When not using the polymerase systems for amplification in workflow A

- Incubate the suspension at 95°C for 5 minutes
- Immediately pellet the beads in the MPC and collect the supernatant containing the enriched libraries

H3.3 Library amplification

This is an example post-capture amplification using KAPA HiFi HotStart ReadyMix and Illumina libraries.



If this is the first time performing step H3.3, generate two of the following reactions per enrichment reaction (each with 15 μ L enriched library as template). Otherwise, generate only one:

- Assemble the following PCR master mix:

Component	Final Concentration	μ L / Reaction	Sequence
NF Water	-	5	-
2X KAPA HiFi HotStart Ready Mix	1 X	25	-
P5 library primer (at 10 μ M)	500 nM	2.5	AATGATACGGCGACCACCGA
P7 library primer (at 10 μ M)	500 nM	2.5	CAAGCAGAAGACGGCATACGA
Enriched Library (on- or off-bead)	-	15 *	-
TOTAL		50	-

*Remaining bead-bound library can be stored at -20°C for several months.

H3.3 Library amplification (continued)

- Cycle the reactions with the following thermal program:

Step	Temperature	Time	
1	98°C	2 minutes	
2	98°C	20 seconds	×14 or 8 cycles*
3	60°C	30 seconds	
4	72°C	45 seconds	
5	72°C	5 minutes	
6	8°C	∞	

*First round of enrichment: 14
Second round of enrichment: 8

- After amplification:
 - **If beads were included in the amplification reaction and you intend to use silica columns for purification**, pellet the beads first and purify only the supernatant.
 - Otherwise, purify the reaction using your preferred PCR cleanup (e.g., silica columns or SPRI beads).

H3.4 Perform a second round of enrichment

If this is the end of the first time through step H3.3 (one of two):

- Combine both purified amplification reactions generated above and concentrate to 7 µL.
- Repeat steps H1.1 through H3.3 using this once-enriched template as input.

If this is the end of your second time through step H3.3 (two of two), the enriched libraries are now ready for quantification, quality-assessment, and sequencing.

APPENDIX

HA1: Troubleshooting

During hybridization, my thermal cycler dropped below the hybridization temperature

You can expect a lower on-target read proportion and target read complexity for these libraries than if the temperature had remained where intended, but not outright enrichment failure. Shallow preliminary sequencing will determine whether targets are likely to be retrieved at sufficient coverage within budget.

My enriched and amplified library is not visible on electrophoresis gel or similar

Successful captures frequently yield a total mass of just a few nanograms even after re-amplification, which can be difficult to visualize with electrophoresis. This is most common when capturing especially small targets (<100 bp), or targets that are present at low frequency in the starting library (like those in degraded/ancient/environmental DNA), or if there is under-re-amplification of the library post-capture. Often a few more cycles of library amplification will render the captured product sufficiently high in concentration to view with electrophoresis. Alternatively, determine with library qPCR whether the library is of sufficient mass for sequencing. If cycling is halted before reaching PCR plateau, the qPCR product can be visualized with electrophoresis to determine length distribution. Consult with your sequencing provider for library concentration and volume requirements.

My enriched and amplified library appears significantly longer than my original library, or has two peaks.

This may happen if the libraries are over-amplified and have formed 'daisy-chains' or 'bubbles' by experiencing cycles of denature-renature without template extension. These can be reverted to their original appearance in electrophoresis by applying three PCR cycles using regular library amplification.

I observe a high ratio of PCR duplicates in my enriched library sequence data.

Percent duplicates in sequencing data (i.e. "clonality" or "duplication rate") increases as you sequence deeper, and therefore it can only be fairly compared between experiments when the sequencing depth is normalized before analysis. Evaluate whether you have simply over-sequenced the libraries by plotting raw sequencing reads obtained on the X axis, and unique reads observed on the Y axis. If this **complexity curve** has plateaued, but you achieved sufficient unique reads, you sequenced more deeply than necessary. If it has not flattened, or you need to increase the total potential unique read yield of the library, **use more DNA per library preparation and/or more library per capture reaction. Avoid diluting baits before capture.** When working with heavily contaminated or damaged DNA target molecules, consider reducing temperatures used in all steps to improve capture sensitivity. Reducing PCR cycles when possible may also improve target coverage uniformity and complexity for a given sequencing depth, in some cases having an indirect effect on duplication rate. For more information about library complexity for any NGS application, we recommend Daley & Smith 2013 (doi: 10.1038/nmeth.2375).

HA2: myBaits Procedure Quick Guide - High Sensitivity Protocol

- For each reaction, build the following Mixes; pipetting error is built in:

Hybridization Mix	
Component	μL / Reaction
Hyb N	9.25
Hyb D	3.5
Hyb S	0.5
Hyb R	1.25
Baits (round 1 / 2)	4.4 / 1.1
H2O (round 1 / 2)	1.1 / 4.4
TOTAL	20

Blockers Mix	
Component	μL / Reaction
Block X	0.5
Block C	2.5
Block O	2.5*
NF Water	0 [†]
TOTAL	5.5

*Plants: 5.0; Salmonids: 0
[†]Plants: 0; Salmonids: 2.5

- After pre-warming the Hybridization mix for 10 minutes @ 60°C, for each reaction, aliquot **18.5 μL** of Hybridization Mix to their own tubes – now “**HYBs**”.
- For each reaction, aliquot **5 μL** of Blockers Mix and then add **7 μL** of each library – now “**LIBs**”.
- Incubate the LIBs in the thermal cycler for 5 minutes @ 95°C and then drop to the hybridization temperature (e.g., 63°C). **Be sure to use a heated lid.**
- Put the HYBs in the thermal cycler and warm to the hybridization temperature for 5 minutes.
- Transfer **18 μL** of each HYB to each LIB, mix by pipetting, and incubate for 16-24 hours.
- 1.5 hours before step 9**, prepare Wash Buffer X by combining 400 μL Hyb S, 39.6 mL nuclease-free molecular biology-grade water and 10 mL Wash Buffer in a 50 mL tube. Vortex thoroughly and warm to the hybridization temperature for at least 45 minutes.
- Prepare 30 μL of beads per reaction by washing three times in 200 μL Binding Buffer. Resuspend washed bead aliquots in 70 μL Binding Buffer and warm the suspensions to the hybridization temperature for at least 2 minutes.
- Combine the warmed beads with the hybridization reactions and incubate for 5 minutes at the hybridization temperature, agitating at 2.5 minutes to keep beads suspended.
- Pellet the beads and remove the supernatant. If using microcentrifuge tubes for cleanup, wash the beads three times with 375 μL warmed Wash Buffer X, incubating 5 minutes at the hybridization temperature. Wash four times with 180 μL washes if using a 96-well magnetic particle concentrator and 0.2 mL strips/tubes.
- Resuspend the beads in 30 μL Buffer E and then use 15 μL of this in a 50 μL amplification reaction with KAPA[®] HiFi or NEB Ultra II Q5 polymerase systems. If not using these polymerase systems, instead elute the library from the beads by incubating the suspension for 5 minutes at 95°C, immediately pellet the beads, and then use 15 μL of the supernatant in a 50 μL amplification reaction. Do two amplifications if this is the first round of enrichment; do one if this is the second and last round of enrichment.
- Purify the amplification reactions using silica columns or SPRI beads. **If using silica columns and beads were included in the amplification reaction, pellet the beads first and purify only the supernatant.**
- If this is the end of your first round of enrichment: combine both post-capture amplifications and concentrate to 7 μL, then repeat steps 1-12. Otherwise, the enriched libraries are ready for QC and sequencing.



Long Insert Protocol

For target enrichment of NGS libraries containing inserts 1-10 kilobase pairs in length

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REQUIREMENTS AND RECOMMENDATIONS

Input library

TYPE Use myBaits with PCR-amplified and amplifiable NGS libraries with universal adapter priming sites. For long insert library preparation, we recommend the procedure described in Witek et al. 2016 (doi: 10.1038/protex.2016.027). **It is NOT recommended to use myBaits with PCR-free libraries; additionally, myBaits are incompatible with libraries made using original Nextera or Nextera XT library preparation kits, or any library type containing biotin.** Dual-indexed libraries are strongly recommended to reduce the hazard of mis-indexing induced by PCR jumping events.

VOLUME Each myBaits target enrichment reaction has space for 7 μ L total NGS library volume. Many pools will require concentration to 7 μ L with vacuum centrifugation or other means. Complete this in advance of your myBaits experiments. Libraries should be suspended in nuclease-free buffer or water.

MASS For long insert capture, we recommend using 250 ng total library per enrichment reaction, as quantified with intercalating dye assay (e.g. Qubit).

POOLING Optimal pooling parameters (both in terms of number of libraries and total mass per library) will vary between library types and bait sets, and will require trials to identify. However, many configurations should work well. To minimize variation in capture performance among pooled samples, only pool libraries of comparable anticipated bait-genome sequence identity (i.e. taxon), starting DNA amount, library insert length, and relative target constituent vs. background. Pool equal amounts of each library. For long insert capture, by default we recommend pooling three libraries, 83 ng each, for a total of ~250 ng per enrichment reaction.

Blocking oligos

When ordering your myBaits kit, please indicate the sequencing library configuration you intend to enrich. The standard adapter blocking reagent provided with the kit (**Block X**) is compatible with Illumina TruSeq-style or Nextera-style libraries with single 6-12 bp or dual 6-12 bp indexing. For different adapter configurations, we recommend ordering Custom IDT® xGen® Blocking Oligos customized for your NGS library adapter sequences. At a concentration of 1 μ g/ μ L, any custom adapter-blocking oligos can be used in lieu of myBaits Block X.

Special note for handling long-insert libraries

Use gentle repeated pipetting rather than vortexing to homogenize solutions that contain both beads (MyOne C1 or SPRI) and long insert library. This helps reduce potential mechanical shearing.

Equipment required

Item	Notes
50 mL tubes	1 per 44 reactions
Microcentrifuge tubes (1.5, 1.7, or 1.8 mL)	2 per 8 reactions
0.2 mL PCR strips with attached lids	2 per 8 reactions (e.g., VWR Cat# 93001-118)
Pipettors and tips for 0.5 - 500 μ L	Multichannel for 20 and 500 μL recommended
[†] Thermal cycler with heated lid compatible with 0.2 mL strips	1 or 2
Magnetic particle collector for microcentrifuge tubes	1 (e.g., ThermoFisher Cat# 12321D)
Magnetic particle collector for 0.2 mL strips	1 (e.g., Permagen Cat# S500)
Vortex mixer and mini-centrifuge for tubes and strips	
Water bath or incubation oven at 65°C	
Heat block for microcentrifuge tubes at 60°C	

[†] Ensure that the thermal cycler and strips allow no more than 4 μ L of 30 μ L volume evaporation overnight at 65°C

Reagents required

Reagent	Notes
Nuclease-free ("NF") water	900 μ L per reaction
PCR primers to amplify sequencing libraries after capture, e.g.:	
Illumina P5: AATGATACGGCGACCACCGA	2.5 μ L @ 10 μ M per reaction
Illumina P7: CAAGCAGAAGACGGCATACGA	2.5 μ L @ 10 μ M per reaction
PCR reagents for post-capture amplification	1 per reaction (e.g. Roche Cat# 07958927001)
PCR purification system, e.g., silica columns or SPRI beads	1 cleanup per reaction

PROCEDURE

PART 1: Hybridization setup

Sequencing libraries are mixed with various blocking nucleic acids, denatured, and then combined with other hybridization reagents (including baits). These hybridization reactions incubate for several hours to allow baits to encounter and hybridize with target library molecules.

L1.1 Choose a hybridization temperature (T_H)

65°C

When bait-target sequence divergence is expected to be less than 10%

62°C

When bait-target sequence divergence is expected to be 10 to 15%

60°C

When bait-target sequence divergence is expected to be 15 to 25%

L1.2 Prepare materials

Reagents	Equipment
Hyb N and Hyb S from Box 1	Nuclease-free microcentrifuge tubes (x2)
Hyb D and Hyb R from Box 2	0.2 mL strips with attached lids (x1 per 8 reactions)
Block C, Block O, and Block X from Box 2	Pipettors and tips; multichannel for 20 μ L recommended
Baits from Box 3 KEEP ON ICE	Vortex mixer and mini-centrifuge for above tube types
Libraries or library pools in 7 μ L per reaction	Heat block set to 60°C
	Thermal cyclers; 2 blocks recommended for 24 or more reactions

Program the thermal cycler:



Set lid temperature 5 to 10°C above each step temperature to minimize evaporation

Step	Parameters
1	60°C, 10 minutes
2	95°C, 10 minutes
3	Reduce 0.1°C per second to T_H
4	Hold at T_H

L1.3 Hybridization Reaction Setup

- Once all reagents have thawed, vortex them to homogenize and then briefly centrifuge.



Heat Hyb N and Hyb S to 60°C and vortex to dissolve any precipitate present after thawing

- Assemble the Capture Mix in a microcentrifuge (MC) tube combining the reagents in the order indicated. **The following volumes are already adjusted for pipetting error:**

MOST TAXA		PLANTS		SALMONIDS	
Component	µL / Reaction	Component	µL / Reaction	Component	µL / Reaction
Hyb N	9.25	Hyb N	9.25	Hyb N	9.25
Hyb D	3.5	Hyb D	3.5	Hyb D	3.5
Hyb S*	0.5	Hyb S*	0.5	Hyb S*	0.5
Hyb R	1.25	Hyb R	1.25	Hyb R	1.25
Block O	2.5	Block O	5.0	Block O	-
Block C	2.5	Block C	-	Block C	2.5
Block X	0.5	Block X	0.5	Block X	0.5
NF Water	-	NF Water	-	NF Water	2.5
Baits	5.5	Baits	5.5	Baits	5.5
TOTAL	25.5	TOTAL	25.5	TOTAL	25.5

**Cloudiness caused by Hyb S addition will clear after step 3*

Briefly vortex and centrifuge to collect.

- For each capture reaction, aliquot **23 µL** of Capture Mix to a 0.2 mL well/tube.
- Add 7 µL of individual or pooled libraries to each Capture Mix aliquot and mix by gently pipetting.
- Place the reactions in the thermal cycler and run the thermal program, incubating overnight.



Set lid temperature 5 to 10°C above each step temperature to minimize evaporation

Step	Parameters
1	60°C, 10 minutes
2	95°C, 10 minutes
3	Reduce 0.1°C per second to T _H
4	Hold at T _H

PART 2: Bind and Wash (“Cleanup”)

Bait-target hybrids are bound to streptavidin-coated magnetic beads, and then most non-target DNA is removed with several rounds of washing with a warm buffer. This is usually performed the day following completion of Part 1.



For long insert libraries, mix reactions using gentle pipetting or inversion rather than vortexing in order to minimize shearing effects

L2.1 Choose a wash temperature (T_w - typically identical to T_H)

65°C

When bait-target sequence divergence is expected to be 10% or less

62°C

When bait-target sequence divergence is expected to be 10 to 15%

60°C

When bait-target sequence divergence is expected to be 15 to 25%

L2.2 Prepare materials



Start at least 90 minutes before intended hybridization stop time

Reagents

Hyb S (Box 1) *

Binding Buffer (Box 1) *

Wash Buffer (Box 1) *

Beads (Box 1)

Nuclease-free (NF) Water (up to 900 μ L per reaction)

** Allow these reagents to come to room temperature before use; warm to 60°C and vortex to dissolve precipitate if necessary*

Equipment

Water bath or incubation oven set to the T_w (e.g., 65°C)

Receptacles for 50 mL tubes, 0.2 mL strips and microcentrifuge tubes compatible with above incubation device

Vortex mixer and mini-centrifuge for 0.2 mL strips and MC tubes

Magnetic particle collector(s) (MPC) for above strips and/or tubes

When using only a microcentrifuge (MC) tube-compatible MPC	When using a 0.2 mL tube-compatible MPC
Nuclease-free 50 mL tube, 1 per 44 cleanups	Nuclease-free 50 mL tube, 1 per 68 cleanups
Nuclease-free MC tubes, 1 per reaction	Nuclease-free 0.2 mL PCR strips with individually-attached lids, 1 vessel per reaction
Heat block set to the T_w	Thermal cycler set to T_w
Pipettors and tips for 20 – 500 μ L	Pipettors and tips for 20 – 200 μ L; multichannel pipettor strongly recommended

L2.3 Wash Buffer X preparation

This step generates enough Wash Buffer X for 44 reactions in microcentrifuge (“MC”) tube cleanup format, and 68 reactions in 0.2 mL cleanup format; scale up or down if needed.

1. Thaw and thoroughly homogenize Wash Buffer and Hyb S prior to aliquoting in order to dissolve any visible precipitate; warm slightly if necessary.
2. Combine 400 μ L Hyb S, 39.6 mL NF water and 10 mL Wash Buffer in a 50 mL tube. Vortex thoroughly, label “Wash Buffer X.” **Wash Buffer X can be stored at 4°C for 1 month.**
3. Heat the Wash Buffer X to the T_w in the water bath or oven for at least 30 minutes before use.

L2.4 Bead preparation Prepare beads immediately prior to use

1. For each capture reaction, aliquot 30 μ L beads to a microcentrifuge tube.
2. Pellet the beads in the MPC until the suspension is clear (1-2 minutes).
Leaving the tubes on the magnet, remove and discard the supernatant.
3. Add 200 μ L Binding Buffer to each bead aliquot. Vortex to resuspend the beads and centrifuge briefly. Pellet in the MPC, remove and discard the supernatant.
4. Repeat Step 3 above twice for a total of three washes.
5. Resuspend each washed bead aliquot in 70 μ L Binding Buffer. If proceeding to washing in 0.2 mL format, transfer the aliquots to PCR strips.

TIP: Beads can be prepared in 8 (or fewer) reaction batches (240 μ L) in a microcentrifuge tube. Multiply all volumes by the number of reactions in the batch; i.e., for 8 reactions-worth, wash with 1.6 mL and resuspend in 560 μ L Binding Buffer, then aliquot 70 μ L suspension to individual tubes.

L2.5 Binding beads and hybrids

1. Heat the bead aliquots to the T_w (e.g., 65°C) for at least 2 minutes.
2. Transfer each capture reaction to the heated bead aliquots. Mix by pipetting.
3. Incubate the libraries + beads on the heat block or thermal cycler for 5 minutes. Agitate at the 2.5 minute mark by flicking or inverting the tubes to keep the beads suspended, followed by briefly centrifuging to collect.

L2.6 Bead washing

1. Pellet the beads with the MPC until the solution is clear. Remove and discard the supernatant.
2. Add 375 μ L (MC tube format) or 180 μ L (0.2 mL format) warmed Wash Buffer X to the beads, remove from the MPC, place on heat block for 15 seconds, and mix by pipetting. Briefly centrifuge to collect.
3. Incubate for 5 minutes at the T_w in the heat block or thermal cycler. Agitate at the 2.5 minute mark by gentle pipetting. Briefly centrifuge to collect the mixture.
4. Repeat steps 1 through 3 two times for MC tube format (three washes total), or three times for 0.2 mL format (four washes total). **After the last wash and pelleting, remove as much liquid as possible without touching the bead pellet.**

PART 3: Library Resuspension and Amplification

Bead-bound enriched library is resuspended in Buffer E and amplified.

L3.1 Prepare materials

Reagents	Equipment
Buffer E (Box 2)	Tubes appropriate for PCR master mix assembly
PCR primers for amplifying libraries (e.g., P5 and P7)	Tubes or strips for 50 μ L PCR amplification
PCR reagents for post-capture amplification	Pipettors and tips capable of 5 – 100 μ L volumes
PCR purification system, e.g., silica columns or SPRI beads	Vortex mixer and mini-centrifuge for above tube types
	Thermal cycler

S3.2 Enriched library recovery

- Add 30 μ L Buffer E to the washed beads and thoroughly resuspend by pipetting. Then, depending on your library amplification system, choose workflow A or B:

WORKFLOW A: When using KAPA HiFi HotStart or NEB Ultra II Q5 polymerase systems for amplification

- Proceed directly to section L3.3 using this bead resuspension as template in amplification

WORKFLOW B: When not using the polymerase systems for amplification in workflow A

- Incubate the suspension at 95°C for 5 minutes
- Immediately pellet the beads in the MPC and collect the supernatant containing the enriched libraries

L3.3 Library amplification

This is an example post-capture amplification using KAPA HiFi HotStart ReadyMix and Illumina libraries:

- Assemble the following PCR master mix:

Component	Final Concentration	μ L / Reaction	Sequence
NF Water	-	5	-
2X KAPA HiFi HotStart Ready Mix	1 X	25	-
P5 library primer (at 10 μ M)	500 nM	2.5	AATGATACGGCGACCACCGA
P7 library primer (at 10 μ M)	500 nM	2.5	CAAGCAGAAGACGGGCATACGA
Enriched Library (on- or off-bead)	-	10 *	-
TOTAL		50	-

*Remaining bead-bound library can be stored at -20°C for several months.

L3.3 Library amplification (continued)

2. Cycle the reactions with the following thermal program:

Step	Temperature	Time	
1	98°C	3 minutes	
2	95°C	30 seconds	×25 cycles*
3	62°C	20 seconds	
4	68°C	10 minutes	
6	8°C	∞	

**Minimize cycles where possible. Cycles required to meet molarity requirements of sequencing platform may exceed 25.*

3. After amplification:
- **If beads were included in the amplification reaction and you intend to use silica columns for purification**, pellet the beads first and purify only the supernatant.
 - Otherwise, purify the reaction using your preferred PCR cleanup (e.g., silica columns or SPRI beads).

The enriched libraries are now ready for quantification, quality-assessment, additional size-selection (if required), and then platform-specific library preparation and sequencing.

If insufficient total mass was acquired from a single amplification reaction for e.g. PacBio or Oxford Nanopore library preparation, perform additional amplifications using the remaining non-amplified enriched library.

APPENDIX

LA1: Troubleshooting

During hybridization, my thermal cycler dropped below the hybridization temperature.

You can expect a lower on-target read proportion and target read complexity for these libraries than if the temperature had remained where intended, but not outright enrichment failure. Shallow preliminary sequencing will determine whether targets are likely to be retrieved at sufficient coverage within budget.

My enriched and amplified library is not visible on electrophoresis gel or similar.

Successful captures frequently yield a total mass of just a few nanograms even after re-amplification, which can be difficult to visualize with electrophoresis. This is most common when capturing especially small targets (<100 bp), or targets that are present at low frequency in the starting library (like those in degraded/ancient/environmental DNA), or if there is under-re-amplification of the library post-capture. Often a few more cycles of library amplification will render the captured product sufficiently high in concentration to view with electrophoresis. Alternatively, determine with library qPCR whether the library is of sufficient mass for sequencing. If cycling is halted before reaching PCR plateau, the qPCR product can be visualized with electrophoresis to determine length distribution. Consult with your sequencing provider for library concentration and volume requirements.

My enriched and amplified library appears significantly longer than my original library, or has two peaks.

This may happen if the libraries are over-amplified and have formed 'daisy-chains' or 'bubbles' by experiencing cycles of denature-renature without template extension. These can be reverted to their original appearance in electrophoresis by applying three PCR cycles using regular library amplification.

I observe a high ratio of PCR duplicates in my enriched library sequence data.

Percent duplicates in sequencing data (i.e. "clonality" or "duplication rate") increases as you sequence deeper, and therefore it can only be fairly compared between experiments when the sequencing depth is normalized before analysis. Evaluate whether you have simply over-sequenced the libraries by plotting raw sequencing reads obtained on the X axis, and unique reads observed on the Y axis. If this **complexity curve** has plateaued, but you achieved sufficient unique reads, you sequenced more deeply than necessary. If it has not flattened, or you need to increase the total potential unique read yield of the library, **use more DNA per library preparation and/or more library per capture reaction. Avoid diluting baits before capture.** When working with heavily contaminated or damaged DNA target molecules, consider reducing temperatures used in all steps to improve capture sensitivity. Reducing PCR cycles when possible may also improve target coverage uniformity and complexity for a given sequencing depth, in some cases having an indirect effect on duplication rate. For more information about library complexity for any NGS application, we recommend Daley & Smith 2013 (doi: 10.1038/nmeth.2375).

LA2: myBaits Procedure Quick Guide - Long Insert Protocol

- For each reaction, build in the following Capture Mix appropriate to your target taxon; pipetting error is built in:

MOST TAXA		PLANTS		SALMONIDS	
Component	μL / Reaction	Component	μL / Reaction	Component	μL / Reaction
Hyb N	9.25	Hyb N	9.25	Hyb N	9.25
Hyb D	3.5	Hyb D	3.5	Hyb D	3.5
Hyb S	0.5	Hyb S	0.5	Hyb S	0.5
Hyb R	1.25	Hyb R	1.25	Hyb R	1.25
Block O	2.5	Block O	5.0	Block O	-
Block C	2.5	Block C	-	Block C	2.5
Block X	0.5	Block X	0.5	Block X	0.5
NF Water	-	NF Water	-	NF Water	2.5
Baits	5.5	Baits	5.5	Baits	5.5
TOTAL	25.5	TOTAL	25.5	TOTAL	25.5

- For each enrichment reaction, aliquot **23 μL** of Capture Mix to their own tubes.
- To each Capture Mix aliquot, add **7 μL** of each library or library pool.
- Incubate the reactions in the thermal cycler for 10 minutes @ 60°C, then 10 minutes @ 95°C, and then drop to the hybridization temperature (e.g., 65°C) at a rate of 0.1°C per second. **Be sure to use a heated lid.** Incubate at the hybridization temperature for 16-24 hours.
- 1.5 hours before step 9**, prepare Wash Buffer X by combining 400 μL Hyb S, 39.6 mL nuclease-free molecular biology-grade water and 10 mL Wash Buffer in a 50 mL tube. Vortex thoroughly and warm to the hybridization temperature for at least 45 minutes.
- Prepare 30 μL of beads per reaction by washing three times in 200 μL Binding Buffer. Resuspend the washed bead aliquots in 70 μL Binding Buffer and warm the suspensions to the hybridization temperature for at least 2 minutes.
- Combine the warmed beads with the hybridization reactions and incubate for 5 minutes at the hybridization temperature, agitating at 2.5 minutes to keep beads suspended.
- Pellet the beads and remove the supernatant. If using microcentrifuge tubes for cleanup, wash the beads three times with 375 μL warmed Wash Buffer X, incubating 5 minutes at the hybridization temperature. Wash four times with 180 μL washes if using a 96-well magnetic particle concentrator and 0.2 mL strips/tubes.
- Resuspend the beads in 30 μL Buffer E and then use 10 μL of this in a 50 μL library amplification reaction with KAPA® HiFi or NEB Ultra II Q5 polymerase systems. If not using these polymerase systems, instead elute the library from the beads by incubating the suspension for 5 minutes at 95°C, immediately pellet the beads, and then use 10 μL of the supernatant in a 50 μL amplification reaction.
- Purify the amplification reactions using silica columns or SPRI beads. **If using silica columns and beads were included in the amplification reaction, pellet the beads first and purify only the supernatant.** The enriched libraries are now ready for quantification, quality-assessment, and sequencing.