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GENOMICS

MERCURIUS™

**BRB-seq
Library Preparation kit
for 96 samples
(MGI)**

PN 10913

User Guide

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Related Products

Kit name	Kit PN	Module name	Module PN
BRB-seq Library Preparation 96 kit (MGI)	10913	Barcoded Oligo-dT Adapters Module 96 samples (MGI)	10533
		BRB-seq Library Preparation Module 96 samples (MGI)	10621
		Indexing Adapters Module (MGI, 1 kit)	10612

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Kit Components

Reagents supplied

Barcoded Oligo-dT Set 96 MGI V1A10 Module (PN 10533)

Component Name	Label	Amount	Storage
Plate with 96 barcoded oligo-dT primers, Set A (PN 10433)	96 MGI V1A10 OdT	1 plate	-20°C
Aluminium Seal	-	2 pcs	-20°C/RT

BRB-seq Library Preparation Module (PN 10621)

Component Name	Label	Cap colour	Volume (µL)	Storage
First Strand Enzyme	FSE	magenta	45	-20°C
First Strand Buffer	FSB	magenta	550	-20°C
Exonuclease I Enzyme	EXO	purple	10	-20°C
Exonuclease Buffer	EXB	purple	20	-20°C
Second Strand Enzyme	SSE	orange	20	-20°C
Second Strand Buffer	SSB	orange	45	-20°C
Fragmentation Enzyme	FE	red	22	-20°C
Fragmentation Buffer	FB	red	11	-20°C
End Repair Enzyme	EE	brown	11	-20°C
End Repair Buffer	EB	brown	15	-20°C
Ligation Enzyme	LE	black	22	-20°C
Ligation Buffer	LB	black	70	-20°C
Library Amplification Mix	LAM	green	200	-20°C
Library PCR Primer Mix	LPM	transparent	25	-20°C

Index Adapters Module (PN 10612)

Component Name	Label	Cap colour	Volume (µL)	Storage
Index Adapter 1	MGI.AD.01	transparent	10	-20°C
Index Adapter 2	MGI.AD.02	transparent	10	-20°C
Index Adapter 3	MGI.AD.03	transparent	10	-20°C
Index Adapter 4	MGI.AD.04	transparent	10	-20°C
Index Adapter 5	MGI.AD.05	transparent	10	-20°C
Index Adapter 6	MGI.AD.06	transparent	10	-20°C
Index Adapter 7	MGI.AD.07	transparent	10	-20°C
Index Adapter 8	MGI.AD.08	transparent	10	-20°C

Additional required reagents and equipment (supplied by the user)

Plasticware	Manufacturer	Product number
15 mL conical tubes	Greiner	188271
0.2ml 8-Strip Non-Flex PCR Tubes	Starlab	I1402-3700
25 mL reservoir for spin columns	Zymo	C1039-25
Disposable Pipetting Reservoir 25mL polystyrene	Integra	4382
Solution reservoir 150 mL polystyrene (optional)	Integra	6318

Reagents	Manufacturer	Product number
DNA Clean and Concentrator-5 kit	Zymo	D4014
MGIEasy DNA Clean Beads	MGI	1000005278
Qubit™ dsDNA HS Assay Kit	Invitrogen	Q32851
Qubit™ ssDNA Assay Kit	Invitrogen	Q10212
MGIEasy Circularization Kit	MGI	1000005259
High Sensitivity NGS Fragment Analysis Kit	Agilent	DNF-474
SYBR Green	Thermofisher	S7563
Ethanol, 200 proof	-	-
Nuclease-free water	Thermofisher	A57775

Equipment	Manufacturer	Product number
Benchtop centrifuge for plates	-	-
Benchtop centrifuge for 1.5 mL tubes	-	-
Single and Multichannel pipettes	-	-
Fragment Analyser / Bioanalyzer / TapeStation	Agilent	M5310AA
Qubit™	Invitrogen	Q33238
Magnetic stand for 0.2 mL tubes	Permagen	MSR812
Magnetic stand for 1.5 mL tubes	Permagen	MSR06
12-channel pipette, 0.5-12.5 µL VIAFLO or similar	Integra	4631
12-channel pipette, 5-125 µL VIAFLO or similar	Integra	4632
8-channel adjustable tip spacing pipette, VOYAGER, 2 – 50 µL	Integra	4726
Pipetboy	Integra	155 000
Vacuum manifold Qiagen Qiavac 24 Plus or similar	Qiagen	19413
Vacuum pump	-	-
Real-Time PCR Instrument (optional)	-	-
VIAFLO instrument (optional)	Integra	6001
VIAFLO 96 channel pipetting head, 0.5-12.5 µL (optional)	Integra	6101

Protocol Overview and Timing

The MERCURIUS™ BRB-seq kit allows the preparation of 3' RNA sequencing libraries for 96 RNA samples for MGI instruments in a time and cost-efficient manner.

The kit contains barcoded MERCURIUS™ Oligo-dT primers designed to tag RNA samples with individual barcodes during the first strand synthesis reaction, allowing the pooling of the resulting cDNA samples from each experimental group into a single tube for streamlined sequencing library preparation.

The BRB-seq technology can be used to generate high-quality sequencing data starting with 10 - 1000 ng of total purified RNA per sample. Notably, the kit can be used for the preparation of up to 4 libraries from up to 96 samples with two considerations:

- The total RNA amount per pool should be at least 1000 ng.
- Pooling less than eight samples may result in low-complexity reads during sequencing, decreasing the overall sequencing quality.

The libraries are indexed following the ligation procedure and provided adapters. The kit contains four adapters. Every adapter can be used to prepare an individual BRB-seq library. Libraries with different adapters can be pooled and sequenced in a single flow cell.

Figure 1 provides an estimation of the time required to accomplish each step of the protocol, assuming that RNA samples have been previously quality-checked and diluted.

Protocol Workflow

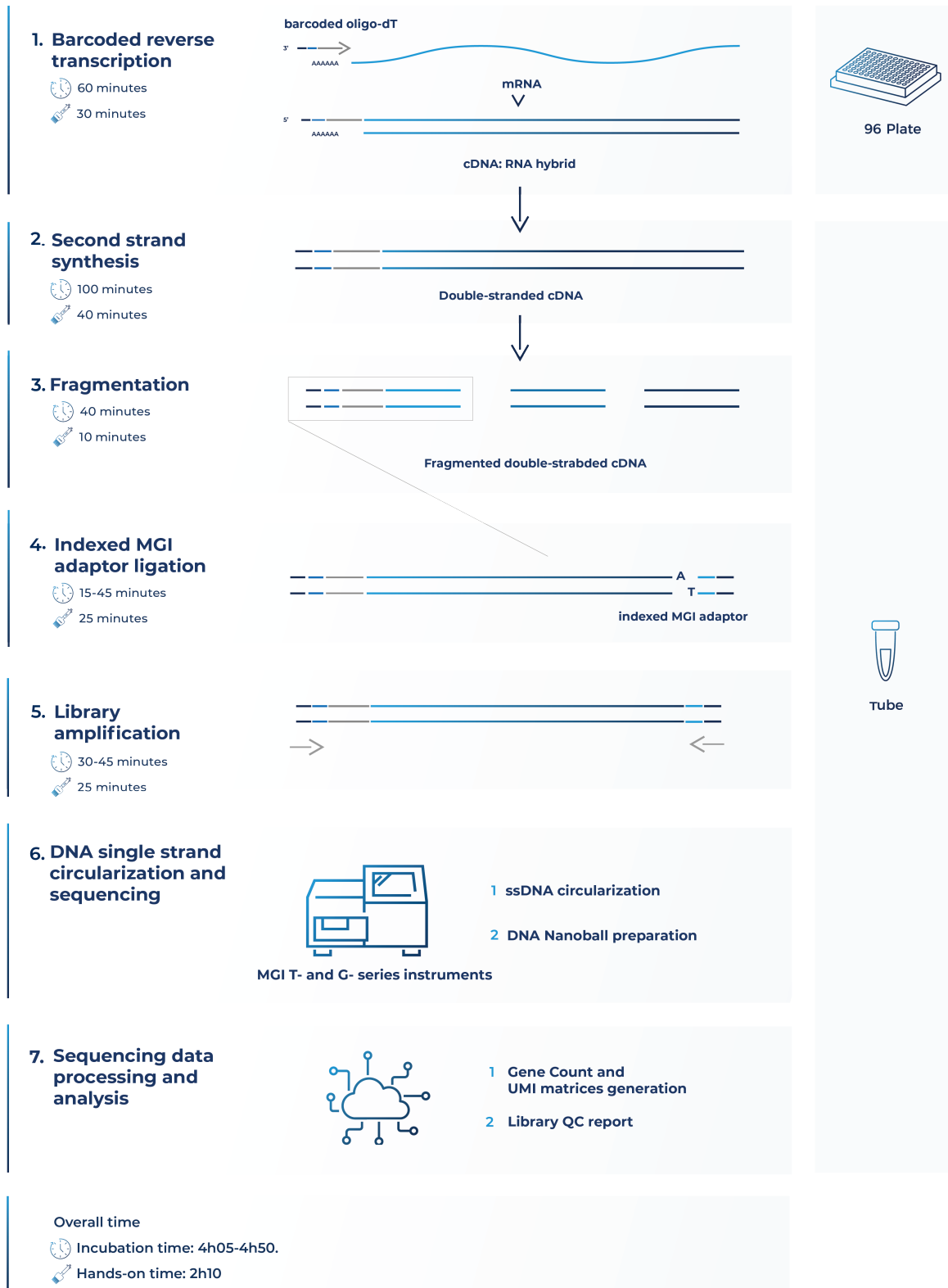


Figure 1 Schematic illustration of the protocol workflow

Part 1. PREPARATION OF RNA SAMPLES

Guidelines for RNA samples

The BRB-seq protocol is based on early sample multiplexing; therefore, it is critical to ensure the quantity, purity, and quality of RNA is uniform for all samples before starting the library preparation. Individual sample quality checks and adjustments will not be possible after pooling.

Quantity

The tested range of total RNA amount per well is 10 – 1000 ng. The recommended starting amount is 120 ng per well for the library prepared with at least 8 wells pooled after RT. Usually, when more RNA is used in the RT, the higher library complexity is observed after sequencing.

Purity

RNA samples extracted using TRIzol™, phenol, or chloroform compounds are prone to residual contamination with organic solvents that may inhibit reverse transcription reaction. This usually results in low cDNA library yields; loss of sequencing reads for a fraction of pooled samples, and uneven read distributions. To ensure the high purity of RNA, assess the 260/230 ratio of at least a few samples from the same RNA isolation batch using a spectrophotometer (i.e., Nanodrop). The 260/230 ratio values should be >1.5.

Uniformity

To ensure an even distribution of reads after sequencing, the RNA amount, integrity (RIN number), and 260/230 values of the starting RNA samples must be as uniform as possible, i.e., 50 ng ($\pm 10\%$) of starting material with RIN = 6 for every sample. To obtain such uniform amounts, we, therefore recommend to:

- Measure the RNA concentration of all samples with a dye-based method (e.g., Qubit Quant-iT or RiboGreen for a large number of samples).
- Dilute samples to obtain the same RNA concentration in all wells ($\pm 10\%$).
- Re-measure the RNA concentration of all samples to confirm uniform concentrations across the samples.
- Ensure that the 260/230 ratios are >1.5 and similar across the samples.
- Ensure that the RIN values are similar across the samples, preferably > 6.

Contact info@alitheagenomics.com for technical support.

Part 2. LIBRARY PREPARATION PROTOCOL

NOTE: Before starting every step, briefly spin down tubes and plates before opening them to ensure that all liquid or particles are collected at the bottom of the tube/plate.

2.1. Reverse transcription

At this step, each individual RNA sample is reverse-transcribed using barcoded oligo-dT primers provided in a 96-well plate. Subsequently, all barcoded samples can be pooled in one tube.

NOTE: Barcoded oligo-dT primers are provided lyophilized with the addition of dye. The dye has no impact on the enzymatic reactions and is used solely for better visualization of reaction preparation and pooling.

Despite variations in appearance caused by a drying process, wells may exhibit traces of dried dye ranging from dispersed to solid dots on the bottom. The following addition of RT reagents will enable the visualization of red color, confirming the presence of oligos in all wells.

Preparation

- Thaw the RNA samples on ice.
- Thaw the **FSB** reagent at room temperature and mix well before use.
- Briefly spin down the 96-well plate(s) containing dried oligo-dT primers. This plate will be referred to as the RT plate(s).
- Prepare Program 1_RT on the thermocycler (set the lid at 90°C):

Step	Temperature, °C	Time
Incubation	42	50 min
Inactivation	65	10 min
Keep	4	pause

NOTE: All the manipulations with RNA samples and RT enzyme should be performed in an RNase-free environment, with the use of RNase-free consumables and filter tips, on ice, and using gloves.

Procedure

- 2.1.1. Keep the RT plate on ice. Using a multichannel pipette, transfer 10 µL of RNA sample directly to the corresponding wells and pipette 3-5 times to ensure proper reconstitution of dried oligo-dT.
- 2.1.2. Carefully re-seal the RT plate(s) and briefly spin it in the centrifuge.
- 2.1.3. Leave the RT plate(s) on ice for 5 min.
- 2.1.4. Prepare the Master Mix for the RT reaction (+10%) as follows:

Reagent	Per well, µL	96 wells +10%, µL
FSB	5.0	528.0
FSE	0.4	42.2
Water	4.6	485.8
TOTAL	10.0	1056.0

- 2.1.5. Keep the RT plate(s) on ice and, using a multichannel pipette, transfer 10 µL of Master Mix to each well containing the RNA sample.
- 2.1.6. Carefully re-seal the RT plate(s) and briefly spin it in the centrifuge.
- 2.1.7. Transfer the plate to the thermocycler and start Program 1_RT.

Safe stop: After this step, the RT plate(s) can be kept at 4°C overnight.

2.2. Sample pooling and column purification

After pooling, the barcoded RT samples can be purified with either column-based Zymo Clean & Concentration Kit (Zymo, D4014) or magnetic beads (MGIEasy DNA Clean Beads, MGI, 1000005278). Both approaches produce comparable outcomes and can be used interchangeably. Depending on the availability of 3rd party reagents and instruments, the corresponding method should be applied.

NOTE: Library normalization

The volume used for pooling from each well can be adjusted to re-equilibrate the proportion of samples in the pool, helping to improve the distribution of sequencing reads in the library, especially if some samples risk obtaining too many reads.

Shallow sequencing allows for assessing the coverage per sample unequivocally. For this approach, we recommend pooling only a fraction of the RT volume from each well (i.e., 5 μ L out of 20 μ L) for the library preparation. After the library QC by sequencing (see section 2.7), the volume used for pooling can be re-adjusted to reduce the variation at the sequencing stage.

The procedure of cDNA pre-cleaning and purification using the column-based method

After the cDNA from each well is pooled in a reservoir, mix it with a 7x volume of DNA binding buffer (Zymo, D4004-1-L). We strongly recommend using a vacuum manifold for the cDNA purification to avoid column membrane damage due to multiple centrifugation rounds.

Pooling volumes	Per well, μ L	For 96 wells (mL)
First-strand cDNA	20	1.92
DNA Binding Buffer	140	13.44
TOTAL	160	15.36

Table 1 Reagent volumes to be used depending on the number of pooled samples

Preparation

- Add Ethanol to Zymo DNA Wash buffer.

Procedure

- 2.2.1. Using a multichannel pipette, or pipetting robot, transfer the entire RT volume of each sample into a reservoir (Integra, 4382 or 6318).
- 2.2.2. Mix the pool well and transfer it to a falcon tube with a pipette.
- 2.2.3. Using a pipette, measure the volume of the pool, transfer it to a 50 mL falcon tube, and add a 7x DNA Binding buffer accordingly (see Table 1). The color of the mix should turn yellow.
- 2.2.4. Connect the 25 mL funnel (Zymo, C1039-25) to a Zymo column and place it on a vacuum manifold.
- 2.2.5. Gently mix the cDNA in the binding buffer mixture and transfer it to a 25 mL funnel using a pipetboy.
- 2.2.6. Turn on the vacuum pump and let the liquid pass through the column.
- 2.2.7. Transfer any remaining volume to the funnel. Do not let the membrane overdry.
- 2.2.8. After the entire pool mix has passed through the column, add 200 μ L of DNA Wash buffer (with Ethanol added) directly to the membrane of the column.
- 2.2.9. Repeat step 2.2.8 once the wash buffer passes through the filter.
- 2.2.10. Remove the column from the vacuum manifold, put it in a 1.5 mL tube, and centrifuge for 1 min to remove leftovers from the washing buffer.
- 2.2.11. Add 37 μ L of water to the column matrix and incubate for 1 min.
- 2.2.12. Transfer the column into a new labeled 1.5 mL tube and centrifuge for 30 sec.
- 2.2.13. The expected volume of the eluate is 35 μ L.
- 2.2.14. Immediately proceed to step 2.3.

The procedure of cDNA purification using the MGIEasy DNA Clean bead-based method

Perform cDNA purification with SPRI magnetic beads at a 1:1 (DNA:beads slurry) ratio. The purification of large volumes (i.e., 2 mL of the pool from a 96-well plate) requires three 1.5 mL tubes and a corresponding magnetic stand (Permagen, MSR06).

If the volume of the pool is higher than 750 μ L, split it equally into the required number of 1.5 mL tubes and add the identical volume of beads (i.e., a pool of 1 mL divided into 2 tubes with 500 μ l per tube and add 500 μ L of beads per tube).

Preparation

Pre-warm SPRI magnetic beads at room temperature for 30 minutes and vortex them vigorously before pipetting.

Procedure

- 2.2.15. Pool the RT samples as described in step 2.2.1.
- 2.2.16. Transfer the collected pool to a 2 mL or 15 mL tube, depending on the pooled volume. Consider that the final volume will be twice higher due to the addition of the beads.
- 2.2.17. Add pre-warmed beads in a 1:1 ratio (i.e., for 960 μ L of pooled RT volume, add 960 μ L of beads slurry), and mix by pipetting up and down ten times.
- 2.2.18. Incubate for 5 min at room temperature.
- 2.2.19. Place the tube on the magnetic stand, wait 5 min or until a solution becomes completely clear, then carefully remove and discard the supernatant.
- 2.2.20. To wash the beads, pipette 1 mL of freshly prepared 80% ethanol into the tube.
- 2.2.21. Incubate for 30 sec.
- 2.2.22. Carefully remove the ethanol without touching the bead pellet.
- 2.2.23. Repeat step 2.2.20 for a total of two washes.
- 2.2.24. Remove the tube from the magnetic stand and let the beads dry for 1-2 min.
- 2.2.25. Resuspend the beads in 37 μ L of water.
- 2.2.26. Incubate for 1 min.
- 2.2.27. Place tubes on the magnetic stand and wait for 5 min.
- 2.2.28. Gently aspirate 35 μ L of supernatant and transfer it into a new tube. Avoid beads carry-over.
- 2.2.29. Immediately proceed to step 2.3.

If the RT pool was split into several tubes for SPRI magnetic beads purification, at step 2.2.25, use one of the following options:

- **[Two tubes only]**, resuspend the beads in **both tubes** in 20 μ L/tube, and combine both elutions in one tube;
- **[Two or more tubes]**, resuspend the beads in the **first tube** in 40 μ L of water. Keep other tubes closed to avoid over-drying of the beads. Transfer obtained elution to the next tube and resuspend beads. Repeat this step for every tube;
- **[Two or more tubes]**, resuspend **every** tube in 37 μ L. Combine all elutions in one tube and perform one additional purification of the pool adding beads slurry accordingly to the pool volume (steps 2.2.17 - 2.2.28). Elute in 37 μ L of water and collect 35 μ L in a new tube.

2.3. Free primer digestion

It is recommended to perform non-incorporated primer digestion immediately after pooling.

Preparation

- Label 0.2 mL PCR tubes corresponding to the number of pools prepared.
- Thaw **EXB** at room temperature.
- Keep **EXO** on ice.
- Prepare the **Program 2_FPD** on the thermocycler (set the lid at 90°C):

Step	Temperature, °C	Time
Incubation	37	30 min
Incubation	80	20 min
Keep	4	pause

Procedure

2.3.1. Depending on the cDNA volume obtained from step 2.2, transfer 35 µL of the eluate from each tube into a new labeled 0.2 mL PCR tube.

2.3.2. Prepare the EXO reaction mix as follows (with 10% excess):

Reagent	Per reaction, µL
EXB	4.0
EXO	1.0
TOTAL	5.0

2.3.3. According to the table, transfer 5 µL of **EXO** reaction mix into each PCR tube with purified cDNA.

2.3.4. Mix by pipetting up and down 5 times.

2.3.5. Briefly spin down in the bench-top centrifuge.

2.3.6. Incubate in thermocycler **Program 2_FPD**.

2.3.7. Proceed immediately to step 2.4. or keep the tube at 4°C overnight.

Safe stop: After this step, the tube(s) can be kept at 4°C overnight.

2.4. Second strand synthesis

At this step, double-stranded full-length cDNA is generated and purified using SPRI magnetic beads.

Preparation

- Pre-warm SPRI magnetic beads at room temperature for ~30 min.
- Prepare 5 mL of 80% ethanol.
- Thaw the **SSB** reagent at room temperature and mix well before use.
- Keep **SSE** reagent constantly on ice.
- Prepare the **Program 3_SSS** on the thermocycler (set the lid at 70°C):

Step	Temperature, °C	Time
Incubation	37	20 min
Incubation	65	30 min
Keep	4	pause

Second strand synthesis reaction setup

2.4.1. Prepare the SSS reaction mix for the second strand synthesis as follows (with 10% excess):

Reagent	Per reaction, µL
SSB	7.0
SSE	3.0
TOTAL	10.0

2.4.2. Transfer 10 µL of SSS reaction mix to the tube from step 2.3.7 and mix well by pipetting up and down 5 times.

2.4.3. Incubate in thermocycler **Program 3_SSS**.

2.4.4. Proceed immediately to step 2.4.5.

cDNA clean-up with SPRI magnetic beads

Perform the double-stranded cDNA purification with SPRI magnetic beads using a 0.6x ratio (i.e., 30 µL of bead slurry plus 50 µL of cDNA).

NOTE: Use pre-warmed SPRI magnetic beads and vortex them vigorously before pipetting.

2.4.5. Complement the final volume to 50 µL with water.

2.4.6. Add 30 µL of beads and mix by pipetting up and down 10 times.

2.4.7. Incubate for 5 min at room temperature.

2.4.8. Place the tube on the magnetic stand, wait 5 min, and carefully remove and discard the supernatant.

2.4.9. To wash the beads, pipette 200 µL of freshly prepared 80% ethanol into the tube.

2.4.10. Incubate for 30 sec.

2.4.11. Carefully remove the ethanol without touching the bead pellet.

2.4.12. Repeat step 2.4.9 for a total of two washes.

2.4.13. Remove the tube from the magnetic stand and let the beads dry for 1-2 min.

2.4.14. Resuspend the beads in 21 µL of water.

2.4.15. Incubate for 1 min.

2.4.16. Place tubes on the magnetic stand, wait 5 min, and carefully remove 20 µL of supernatant into a new tube to avoid bead carry-over.

2.4.17. Use 2 µL to measure the concentration with Qubit.

2.4.18. [Optional] Assess the cDNA profile via TapeStation or Fragment Analyzer.

Safe stop: At this step, the cDNA can be safely kept at -20°C for a few weeks.

2.5. Fragmentation and Index Adapter Ligation

At this step, the full-length cDNA is fragmented, and MGI library indexing adapters are ligated. The adapter index sequences are indicated in [Appendix 1](#).

Depending on the amount of cDNA used in fragmentation indexing primers should be added to the PCR amplification mix at different stock concentrations. It is recommended to use 20 ng of cDNA for fragmentation to obtain a higher library complexity with less PCR amplification.

To ensure proper balancing of bases in the sequencing run, the indexes of all eight provided Adapters should be used to index the libraries subjected to sequencing on the same flow cell lane. If only one library will be sequenced per flow cell, use a pooled Index Adapter prepared by mixing an equal volume of each of the 8 Adapters provided. See [Table 2](#) for different pooling scenarios depending on the number of sequencing libraries to be sequenced on the same lane.

1 library	2 libraries	3 libraries	4 libraries	5 libraries	6 libraries	7 libraries	8 libraries
MGI.AD.01	MGI.AD.01	MGI.AD.01	MGI.AD.01	MGI.AD.01	MGI.AD.01	MGI.AD.01	MGI.AD.01
MGI.AD.02	MGI.AD.02	MGI.AD.02	MGI.AD.02	MGI.AD.02	MGI.AD.02	MGI.AD.02	MGI.AD.02
MGI.AD.03	MGI.AD.03	MGI.AD.03	MGI.AD.03	MGI.AD.03	MGI.AD.03	MGI.AD.03	MGI.AD.03
MGI.AD.04	MGI.AD.04	MGI.AD.04	MGI.AD.04	MGI.AD.04	MGI.AD.04	MGI.AD.04	MGI.AD.04
MGI.AD.05	MGI.AD.05	MGI.AD.05	MGI.AD.05	MGI.AD.05	MGI.AD.05	MGI.AD.05	MGI.AD.05
MGI.AD.06	MGI.AD.06	MGI.AD.06	MGI.AD.06	MGI.AD.06	MGI.AD.06	MGI.AD.06	MGI.AD.06
MGI.AD.07	MGI.AD.07	MGI.AD.07	MGI.AD.07	MGI.AD.07	MGI.AD.07	MGI.AD.07	MGI.AD.07
MGI.AD.08	MGI.AD.08	MGI.AD.08	MGI.AD.08	MGI.AD.08	MGI.AD.08	MGI.AD.08	MGI.AD.08

Table 2 Index Adapter mix preparation to ensure the best balancing

Preparation

- Pre-warm SPRI magnetic beads at room temperature for ~30 min.
- If needed, prepare fresh 5 mL of 80% ethanol.
- Thaw the **FB**, **EB**, and **LB** reagents at room temperature and mix well before use.
- Keep the **FE**, **EE**, and **LE** reagents constantly on ice.
- Thaw the required number of **Index Adapters (MGI.AD.01 - MGI.AD.08)** at room temperature and briefly spin them before use.
- Depending on the amount of cDNA used for fragmentation, pre-dilute **Index Adapters** (15 µM stock) to the indicated concentration (0.6 µM or 3 µM).

Procedure

- 2.5.1. Prepare the **Fragmentation Mix** on ice in a PCR tube. If several cDNA samples are fragmented, prepare the Master mix as follows (with 10% excess):

Reagent	Per reaction, µL
FB	2.5
FE	5.0
cDNA	X
Water	17.5 – X
TOTAL	25

- 2.5.2. Keep the mix on ice and pipette up and down 10 times. Vortex gently to ensure thorough mixing. Spin down briefly.
- 2.5.3. Incubate for 10 min at 37°C in the PCR machine (pre-cool it to 4°C before starting the incubation). Keep the tube on ice or at 4°C.
- 2.5.4. Prepare the **End Repair Mix** on ice in a PCR tube. If several cDNA samples are fragmented, prepare the Master mix as follows (with 10% excess):

Reagent	Per reaction, µL
EB	3.5
EE	1.5
TOTAL	5.0

- 2.5.5. Add 5 μL of the **End Repair Mix** to the reaction mix from step 2.5.3.
- 2.5.6. Pipette and vortex gently to ensure thorough mixing, and spin down briefly.
- 2.5.7. Incubate for 30 min at 65°C in the PCR machine. Keep the tube on ice or at 4°C.
- 2.5.8. Prepare the **Ligation Mix** as follows. If several libraries are to be prepared and sequenced in one run, use different adapters. Depending on the amount of cDNA used at step 2.5.1, dilute the Adapter to the indicated concentration and use 2.5 μL of prepared dilution.

Reagent	Per reaction (μL), for cDNA inputs	
	<1 ng	1-20 ng
LB	15.0	15.0
LE	5.0	5.0
Index Adapter or Adapter Mix	2.5 (of 0.6 μM stock)	2.5 (of 3 μM stock)
Water	2.5	2.5
TOTAL	50.0	50.0

- 2.5.9. Add 25 μL of the **Ligation Mix** to the reaction mix from step 2.5.7
- 2.5.10. Pipette and vortex gently to ensure thorough mixing, and spin down briefly.
- 2.5.11. Incubate for 15 min at 20°C in the PCR machine. Keep the tube on ice or at 4°C.

Fragmented cDNA clean-up with SPRI magnetic beads

Purify the fragmented cDNA with SPRI magnetic beads using a 0.8x ratio.

NOTE: Use pre-warmed SPRI magnetic beads and vortex them vigorously before pipetting.

- 2.5.12. Add 44 μL of beads to 55 μL of fragmented cDNA and mix by pipetting up and down 10 times.
- 2.5.13. Incubate for 5 min at room temperature.
- 2.5.14. Place the tubes on the magnetic stand, wait 5 min, and carefully remove and discard the supernatant.
- 2.5.15. To wash the beads, pipette 200 μL of freshly prepared 80% ethanol into the tube.
- 2.5.16. Incubate for 30 sec.
- 2.5.17. Carefully remove the ethanol without touching the bead pellet.
- 2.5.18. Repeat steps 2.5.15 - 2.5.17 for a total of two washes.
- 2.5.19. Remove tubes from the magnetic stand and let the beads dry for 1-2 minutes.
- 2.5.20. Resuspend the beads in 21 μL of water.
- 2.5.21. Incubate for 1 min.
- 2.5.22. Place tubes on the magnetic stand, wait 5 min and carefully transfer 20 μL of the supernatant into a new tube to avoid bead carry-over.

Safe stop: At this step, the cDNA libraries can be safely kept at -20°C for a few weeks.

2.6. Library amplification

At this step, 5' terminal fragments are amplified using the **Library PCR Primer mix**.

The number of amplification cycles required for library preparation is usually in the range of 12-17. We recommend performing 15 cycles for the 10-20 ng of input cDNA. The optimal number depends on the RNA samples and the input cDNA amount used for fragmentation. To determine the optimal number of cycles, follow the Library Quantification Protocol in [Appendix 2](#).

Preparation

- Pre-warm the SPRI magnetic beads at room temperature for ~30 mins.
- Prepare 10 mL of 80% ethanol.
- Thaw the **LAM** reagent on ice and mix well before use.
- Thaw the required number of **LPM** at room temperature and briefly spin before use.
- Prepare the **Program 4 AMP** (set the lid at 100°C) on the thermocycler (* The exact number of PCR cycles should be determined following [Appendix 2](#)):

Step	Temperature, °C	Time	Cycles
Initial denaturation	98	30 sec	
Denaturation	98	10 sec	
Annealing	63	30 sec	15 or TBD*
Extension	72	1 min	
Final extension	72	5 min	
Keep	4	pause	

Library amplification reaction setup

2.6.1. Prepare the PCR amplification reaction as follows:

Reagent	Per reaction, µL
LAM	25.0
LPM	5.0
Fragmented cDNA	20.0
TOTAL	50.0

2.6.2. Pipette up and down 5 times.

2.6.3. Put the tube in the PCR machine and start **Program 4 AMP** with the cycles shown in [Appendix 2](#) to determine the optimal number of amplification cycles.

Indexed cDNA library clean-up and double-side size selection with SPRI magnetic beads

For optimal results, the library should be double-side size selected with SPRI magnetic beads to preserve the fragments in a range of 200-800 bp.

NOTE: Use pre-warmed SPRI magnetic beads and vortex them vigorously before pipetting.

2.6.4. Adjust the library volume to 50 µL with water.

2.6.5. Add 25 µL of beads and mix by pipetting up and down 10 times.

2.6.6. Incubate for 5 min at room temperature.

2.6.7. Place the tubes on the magnetic stand, wait 5 min, and carefully transfer 75 µL of the supernatant to the new labeled tube.

2.6.8. Discard tubes with beads.

2.6.9. Add 15 µL of beads slurry to the tube containing the supernatant obtained from step [2.6.7](#). to obtain the final ratio of 0.8x.

2.6.10. Incubate for 5 min at room temperature.

2.6.11. Place the tubes on the magnetic stand, wait 5 min, and carefully remove the supernatant.

- 2.6.12. To wash the beads, pipette 200 μ L of freshly prepared 80% ethanol into each tube.
- 2.6.13. Incubate for 30 sec.
- 2.6.14. Carefully remove the ethanol without touching the bead pellet.
- 2.6.15. Repeat step 2.6.12 for a total of two washes.
- 2.6.16. Remove tubes from the magnetic stand and let the beads dry for 1-2 min.
- 2.6.17. Resuspend the beads in 21 μ L of water.
- 2.6.18. Incubate for 1 min.
- 2.6.19. Place tubes on the magnetic stand, wait 5 minutes, and carefully remove 20 μ L of supernatant into a new tube to avoid bead carry-over.

Safe stop: At this step, the cDNA libraries can be safely kept at -20°C for a few weeks.

2.7. dsDNA library quality control

Pooled library quality control

Before sequencing, the libraries should be subjected to fragment analysis (with Fragment Analyzer, Bioanalyzer, or TapeStation) and quantification (with Qubit). This information is required to assess the molarity of the libraries and prepare the appropriate library dilution for sequencing.

NOTE: The final library yield should be >1 pmol (in 48 μ L) to allow successful downstream circularization. In case of lower yield, a few extra PCR cycles can be performed. Follow steps 2.6.1 – 2.6.19.

A successful library contains fragments in the range of 200 – 800 bp with a peak at 400-700 bp; see Figure 2 for an example of a standard BRB-seq library profile.

Underfragmented libraries have a broader fragment range distribution with a peak at 1200-2000 bp (Figure 3). Only a fraction of such libraries contains fragments that can be efficiently sequenced; therefore, for the best results, it is recommended to re-fragment the cDNA.

Importantly, fragments >1000 bp will impact the downstream library circularization and DNB preparation procedure (Figure 4). Therefore, it is strongly recommended to perform a double-side size selection (see step 2.6.4).

Pre-sequencing library QC:

- Use 2 μ L of the library to measure the concentration with Qubit.
- Use 2 μ L of the library to assess the profile with the Fragment Analyzer instrument or similar.

Figure 2 A successful library profile with fragments between 200-1000 bp

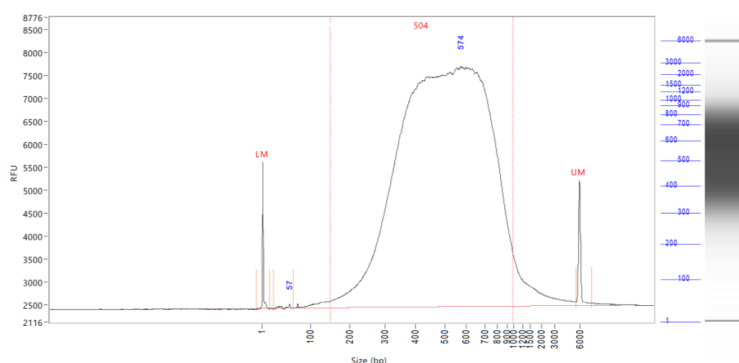


Figure 3 An example of an under-fragmented library profile with an extra peak >1000 bp

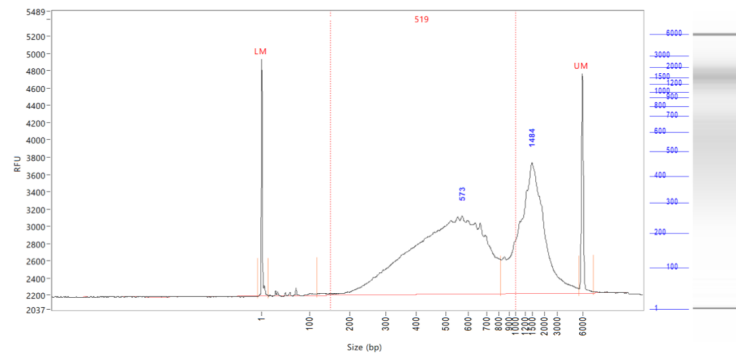
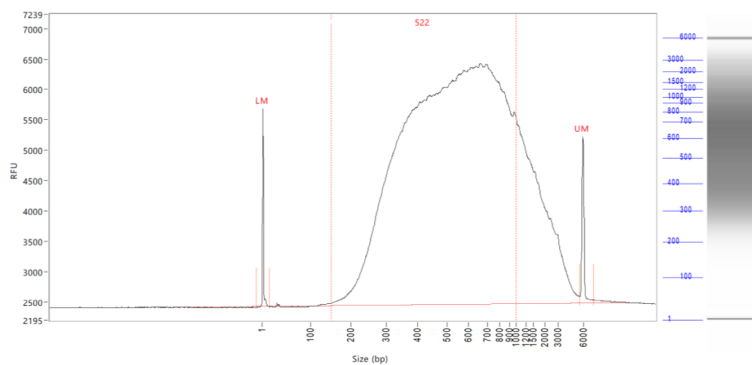


Figure 4 An example of library profile after a single purification (0.8x) with a >1000bp smear



Assessing uniformity of read distribution across the samples

For projects involving highly heterogeneous RNA samples, it is recommended to validate the uniformity of read coverage across the samples by shallow library sequencing (see step 2.2). This approach ensures that every sample will obtain enough reads required for the analysis. BRB-seq libraries can be added as spike-ins to the compatible sequencing run (see Part 3). For this validation, 0.5-1M sequencing reads per library is sufficient to assess the fraction of reads attributed to every sample.

2.8. Library circularisation and DNB preparation

Follow the manual of the MGIEasy Circularization kit (MGI, 1000005259) to prepare DNB using a double-stranded fragmented cDNA library from step 2.6 as the input.

Part 3. LIBRARY SEQUENCING

Each DNB library prepared with MERCURIUS™ BRB-seq kit for MGI is indexed with a single Index Adapter or a mix of Adapters to ensure proper MGI Barcode (Index) balancing (see Appendix 1).

The DNB libraries prepared with different MGI Barcode indexing pools can be sequenced on the same lane of the flow cell. The sequencing structure is provided in Table 3.

Read	Cycles number	Comment
Read1	23	<ul style="list-style-type: none"> • Sample barcode: cycles 1-14 (12 + 2 “dark mode” cycles) • UMI: cycles 15-23 (9 cycles) NOTE: Cycles 13 and 14 should be done in a “dark mode”.
MGI Barcode Read	10	MGI Library Barcode (index) read
Read2	80-150	Gene fragment

Table 3 Sequencing structure of BRB-seq libraries

NOTE: Sequencing depth

- The recommended sequencing depth is 1-5 Mio reads per sample. Deeper sequencing can also be performed to enable the detection of very low expressed genes.
- If only one library is sequenced on a lane of a flow cell, the MGI Barcode Read can be skipped.
- The loading molarity for the library depends on the sequencing instrument and should be discussed with the sequencing facility or an experienced person.

Part 4. SEQUENCING DATA PROCESSING

Following MGI sequencing and standard library index demultiplexing, the user obtains raw read1 and read2 *fastq* sequencing files (e.g., *mylibrary_R1.fastq.gz* and *mylibrary_R2.fastq.gz*).

This section explains how to generate ready-for-analysis genes and UMI read count matrices from raw *fastq* files.

4.1. OPTION 1: Cloud-based platform for data processing

The users of BRB-seq kits are offered free access to the devoted cloud-based BRB-seq data processing pipeline. This easy-to-use workflow enables data processing to generate gene and UMI count matrices for downstream RNA-seq analysis from raw *fastq* files. The pipeline also produces a QC report and can be operated by a user without bioinformatics or coding skills.

The pipeline, still in the developer beta testing mode, is accessible via the following [link \(https://gcw-portal.ali.genomsys.com/\)](https://gcw-portal.ali.genomsys.com/). Please request credentials to access the pipeline by email at info@alitheagenomics.com

Currently, only the human, mouse, and fly genomes are supported.

4.2. OPTION 2: Manual data processing

To obtain the data ready for analysis, the user needs to align the sequencing reads to the genome and perform the gene/UMI read count generation that can be done in parallel with the sample demultiplexing.

The user requires a terminal and a server or powerful computer with an installed set of standard bioinformatic tools for manual data processing.

4.2.1. Required software

- [fastQC](#) (version v0.11.7 or greater). Software for QC of *fastq* or *bam* files. This software is used to assess the quality of the sequencing reads, such as the number of duplicates, adapter contamination, repetitive sequence contamination, and GC content. The software is freely available from <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>. The website also contains informative examples of [good](#) and [poor](#) quality data.
- [STAR](#) (version 2.7.10a). Software for read alignment on reference genome (Dobin et al., 2013). It can be downloaded from [Github](https://github.com/alexdobin/STAR) (<https://github.com/alexdobin/STAR>). STAR can only be run on UNIX systems and requires:
 - x86-64 compatible processors
 - 64-bit Linux or Mac OS X.
 - ~30-40Gb of RAM
- [FeatureCounts](#) (v.1.6.0 or greater). Software for counting genome-aligned reads for genomic features, such as genes and exons.
- [Picard](#) (v.2.17.8 or greater) and [Samtools](#) (v.1.9 or greater). Collections of command-line utilities to manipulate with BAM files. Note: Picard requires [Java version 8 or higher](#) to be installed.
- R Software (version 3 or greater).
- (Optional) [BRBseqTools](#) (version 1.6). The software suite for processing BRB-seq libraries is available from: <https://github.com/DeplanckeLab/BRB-seqTools>.

4.2.2. Merging *fastq* files from individual lanes and/or libraries

After sequencing each library will result in generating 8 individual Read1 and Read2 (R1/R2) *fastq* files corresponding to library barcodes. For the optimal downstream processing those *fastq* files should be merged in a single R1.*fastq* and R2.*fastq* files.

4.2.2.1 Below is an example of four R1/R2 *fastq* files

```
> mylibrary_L001_R1.fastq.gz, mylibrary_L002_R1.fastq.gz,  
mylibrary_L003_R1.fastq.gz, mylibrary_L004_R1.fastq.gz  
> mylibrary_L001_R2.fastq.gz, mylibrary_L002_R2.fastq.gz,  
mylibrary_L003_R2.fastq.gz, mylibrary_L004_R2.fastq.gz
```

4.2.2.2 Use the `cat` command in a terminal to merge the files. Following example will generate two files: `mylibrary_R1.fastq.gz` and `mylibrary_R2.fastq.gz`, containing the information of the entire library.

```
> cat mylibrary_L001_R1.fastq.gz mylibrary_L002_R1.fastq.gz
mylibrary_L003_R1.fastq.gz mylibrary_L004_R1.fastq.gz > mylibrary_R1.fastq.gz
> cat mylibrary_L001_R2.fastq.gz mylibrary_L002_R2.fastq.gz
mylibrary_L003_R2.fastq.gz mylibrary_L004_R2.fastq.gz > mylibrary_R2.fastq.gz
```

4.2.2.3 Move these 2 `fastq` files in a new folder, which will be referenced in this manual as `$fastqfolder`.

NOTE: This step can also be done if you sequenced your library in multiple sequencing runs or lanes of the same flow cell.

Warning: The order of merging files should be kept the same (for e.g., L001, L002, L003, L004, not L002, L001 ...) to avoid issues when demultiplexing the samples.

4.2.3. Sequencing data quality check

4.2.3.1 Run fastQC on both R1 and R2 fastq files. Use `--outdir` option to indicate the path to the output directory. This directory will contain HTML reports produced by the software.

```
> fastqc --outdir $QCdir/ mylibrary_R1.fastq.gz
> fastqc --outdir $QCdir/ mylibrary_R2.fastq.gz
```

4.2.3.2 Check fastQC reports to assess the quality of the samples (see Software and materials).

NOTES:

- The report for the R1 `fastq` file may contain some "red flags" because it contains barcodes/UMIs. Still, it can provide useful information on the sequencing quality of the barcodes/UMIs.
- The main point of this step is to check the R2 `fastq` report. Of note, *per base sequence content* and *kmer content* are rarely green. If there is some *adapter contamination* or *overrepresented sequence* detected in the data, it may not be an issue (if the effect is limited to <10~20%). These are lost reads but most of them will be filtered out during the next step.

4.2.4. Preparing the reference genome

The `fastq` files must be aligned (or "mapped") on a reference genome. The [STAR](#) (Dobin et al., 2013¹) aligner is one of the most efficient tools for RNA-seq reads mapping. It contains a "soft-clipping" tool that automatically cuts the beginning or the end of reads to improve the mapping efficiency, thus allowing the user to skip the step of trimming the reads for adapter contamination. Moreover, STAR has a mode called STARsolo, designed to align multiplexed data (such as BRB-seq) and directly generate count matrices.

The STAR aligner requires a genome assembly together with a genome index file. The index file generation is a time-consuming process that is only performed once on a given genome assembly so that it can be complete in advance and the index files can be stored on the server for subsequent analyses.

4.2.4.1 Download the correct genome assembly fasta file (e.g. `Homo_sapiens.GRCh38.dna.primary_assembly.fa`) and gene annotation file in gtf format (e.g. `Homo_sapiens.GRCh38.102.gtf`) from Ensembl or UCSC repository. Below is an example for a human assembly:

```
> wget ftp://ftp.ensembl.org/pub/release-102/fasta/homo_sapiens/dna/Homo_sapiens.GRCh38.dna.primary_assembly.fa.gz
> gzip -d Homo_sapiens.GRCh38.dna.primary_assembly.fa.gz # unzip
> wget ftp://ftp.ensembl.org/pub/release-102/gtf/homo_sapiens/Homo_sapiens.GRCh38.102.gtf.gz
> gzip -d Homo_sapiens.GRCh38.102.gtf.gz # unzip
```

¹ Alexander Dobin, Carrie A. Davis, Felix Schlesinger, Jorg Drenkow, Chris Zaleski, Sonali Jha, Philippe Batut, Mark Chaisson, Thomas R. Gingeras, STAR: ultrafast universal RNA-seq aligner, *Bioinformatics*, Volume 29, Issue 1, January 2013, Pages 15–21, <https://doi.org/10.1093/bioinformatics/bts635>

NOTE: It's recommended to download the primary_assembly fasta file when possible (without the 'sm' or 'rm' tags). If not available, download the top_level assembly. For the *gtf*, download the one that does not have the 'chr' or 'abinitio' tags.

4.2.4.2 Use STAR to create an index for the genome assembly. Indicate the output folder name containing the index files using `--genomeDir` option:

```
> STAR --runMode genomeGenerate --genomeDir /path/to/genomeDir --genomeFastaFiles
Homo_sapiens.GRCh38.dna.primary_assembly.fa --sjdbGTFfile
Homo_sapiens.GRCh38.102.gtf --runThreadN 8
```

NOTES:

- The `--runThreadN` parameter can be modified depending on the number of cores available on your machine. The larger is this number, the more parallelized/fast will be the indexing.
- Depending on the genome assembly, STAR can use up to 32-40Gb of RAM. So, you should use a machine that has this RAM capacity.

4.2.5. Aligning to the reference genome and generation of count matrices

After the genome index is created, both R1 and R2 *fastq* files can be aligned to this reference genome. For this step, use the "solo" mode of STAR, which not only aligns the reads to the reference genome but also creates the gene read count and UMI (unique molecular identifier) count matrices.

The following parameters should be adjusted according to the sequencing information:

- `--soloCBwhitelist`: a text file with the list of barcodes (one barcode sequence per lane) which is used by STAR for demultiplexing. This file is provided according to version of the MERCURIUS kit used. Example of "[barcodes_96_MGI_V1A10_star.txt](#)":

```
> TGGATTAGCAAC
> CGATAAGTTCAC
> CCATCTTAACGG
> TTGCCTAAGTGA
> ACTCAGACGTAT
```

- `--soloCBstart`: Start position of the barcode in the R1 fastq file, equal to 1.
- `--soloCBlen`: Length of the barcode. This value should match the length of the barcode sequence in the file specified by `--soloCBwhitelist`. The barcode length depends on the version of the oligo-dT barcodes provided in the kit. For the barcodes plate set V5, the default value is 12.
- `--soloUMIstart`: Start position of the UMI, the default value is 15.
- `--soloUMIlen`: The length of UMI. This parameter depends on the version of the oligo-dT barcodes in the kit and number of sequencing cycles performed for Read1. For barcodes plate set V5 the default value is 10.
- `--readFilesIn`: name and path to the input *fastq* files.

The order of the fastq files provided in the script is important. The first *fastq* must contain genomic information, while the second the barcode and UMI content. Thus, files should be provided for STARsolo in the following order: `--readFilesIn mylibrary_R2 mylibrary_R1`.

- `--genomeDir`: a path to the genome indices directory generated before (`$genomeDir`).

Output count matrix parameters:

By default, STARsolo produces a UMI count matrix, i.e., containing unique non-duplicated reads per sample for each gene. This type of count data is a standard for single cell RNA-seq analysis. For bulk RNA-seq analysis a gene read count matrix is usually used. The following parameters will enable the generation of the output of interest.

`--soloUMI dedup NoDedup`, will generate a read count matrix output

`--soloUMI dedup NoDedup 1MM_All`, will generate both UMI and read count matrices in `mtx` format.

This step will output *bam* files and count matrices in the folder `$bamdir`.

```
> STAR --runMode alignReads --outSAMmapqUnique 60 --runThreadN 8 --outSAMunmapped
Within --soloStrand Forward --quantMode GeneCounts --outBAMsortingThreadN 8 --
genomeDir $genomeDir --soloType CB_UMI_Simple --soloCBstart 1 --soloCBlen 12 --
soloUMIstart 15 --soloUMIlen 10 --soloUMI dedup NoDedup 1MM_All --soloCellFilter
None --soloCBwhitelist barcodes.txt --soloBarcodeReadLength 0 --soloFeatures Gene
--outSAMattributes NH HI nM AS CR UR CB UB GX GN sS sQ sM --outFilterMultimapNmax
```

```
1 --readFilesCommand zcat --outSAMtype BAM SortedByCoordinate --outFileNamePrefix
  $bamdir --readFilesIn mylibrary_R2.fastq.gz mylibrary_R1.fastq.gz
```

The demultiplexing statistics can be found in the “*bamdir/Solo.out/Barcodes.stats*” file.

The alignment quality and performance metrics can be found in the “*bamdir/Log.final.out*” file.

NOTE: The most important statistic at this step is the proportion of “Uniquely mapped reads” which is expected to be greater than 70% (for human, mouse or drosophila).

4.2.6. Generating the count matrix from .mtx file

STARsolo will generate a count matrix (*matrix.mtx* file) located in the *bamdir/Solo.out/Gene/raw* folder. This file is a sparse matrix format that can be transformed into standard count matrix using an R script provided below:

```
> #Myscript.R
> library(data.table)
> library(Matrix)
> matrix_dir <- "$bamdir/Solo.out/Gene/raw"
> f <- file(paste0(matrix_dir, "matrix.mtx"), "r")
> mat <- as.data.frame(as.matrix(readMM(f)))
> close(f)
> feature.names = fread(paste0(matrix_dir, "features.tsv"), header = FALSE,
  stringsAsFactors = FALSE, data.table = F)
> barcode.names = fread(paste0(matrix_dir, "barcodes.tsv"), header = FALSE,
  stringsAsFactors = FALSE, data.table = F)
> colnames(mat) <- barcode.names$V1
> rownames(mat) <- feature.names$V1
> fwrite(mat, file = umi.counts.txt, sep = "\t", quote = F, row.names = T, col.names
  = T)
```

The resulting UMI/gene count matrix can be used for a standard expression analysis following conventional bioinformatic tools.

4.2.7. Demultiplexing bam files (Optional)

Generation of demultiplexed bam files, i.e., individual bam files for each sample, might be needed in some cases, for example, for submitting the raw data to an online repository that does not accept multiplexed data (for example, GEO or ArrayExpress), or for running an established bulk RNA-seq data analysis pipeline.

For this purpose, the Picard tool can be used with the following parameters:

- `$out_dir`, The output directory for demultiplexed bam files
- `$path_to_bam`, the path to multiplexed single bam file
- `$barcode_brb.txt`, tab-delimited file containing 2 columns: `sample_id` and barcode seq. Example of [barcode_96_MGI_V1A_brb.txt](#):

```
> Sample1 TACGTTATTCCGAA
> Sample2 AACAGGATAACTCC
> Sample3 ACTCAGGCACCTCC
> Sample4 ACGAGCAGATGCAG
```

NOTE: this file is different from the list of barcode files provided to STAR.

Run the following Picard script:

```
> #!/bin/bash
> demultiplexed_bam_out_dir=$out_dir
> input_bam=$path_to_bam
> barcode_info=$barcode_brb.txt
>
> while IFS=$'\t' read -r -a line
> do
>   sample_id="${line[0]}"
>   tag_value="${line[1]}"
>
>   java -jar /path/to/picard.jar FilterSamReads \
>     I=${input_bam} \
```

```
> O=${demultiplexed_bam_out_dir}/${sample_id}.bam \  
> TAG=CR TAG_VALUE=${tag_value} \  
> FILTER=includeTagValues  
> done < "$barcode_info"
```

NOTE: Please contact us at info@alitheagenomics.com in case you don't have the barcode sequences (in your email, please indicate the name of the barcode set and the PN of the barcode module)

4.2.8. Generating the read count matrix with per-sample stats (Optional)

After splitting (demultiplexing) the *bam* file into files for each sample, produce a read count matrix with per-sample statistics using the *featureCounts* tool with the following code:

```
> #!/bin/bash  
>  
> gtf=homo_sapience.gtf          ### GTF genome annotation file  
> output_name=read_counts.txt   ### Name of the final count output file  
> bam_dir=mypath/bam_demult     ### Directory with demultiplexed bam  
> files  
>  
> featureCounts [options] -t exon -g gene_id -s 1 -a $gtf -o $output_name  
> ${bam_dir}/*.bam
```

The resulting read count matrices can be used for subsequent analysis of gene expression using established pipelines and tools.

Appendix 1. MGI Adapter sequences

Adapter name	Barcode Name	Barcode 2 sequence in oligo	Barcode 2 sequence in the list
Adapter 1	MGI.AD.01	ATACTCACGC	GCGTGAGTAT
Adapter 2	MGI.AD.02	ATGCTCCGCG	CGCGGAGCAT
Adapter 3	MGI.AD.03	TGTGAACTTG	CAAGTTCACA
Adapter 4	MGI.AD.04	GAGAGGTGCT	AGCACCTCTC
Adapter 5	MGI.AD.05	TGCACTGTAA	TTACAGTGCA
Adapter 6	MGI.AD.06	GCCTAGGCAA	TTGCCTAGGC
Adapter 7	MGI.AD.07	CCATCATAGC	GCTATGATGG
Adapter 8	MGI.AD.08	CATGGTAATT	AATTACCATG

Table 4 MGI adapter sequences

Appendix 2. Library quantification with qPCR

To determine the optimal number of cycles, the following library quantification procedure using real-time PCR is recommended at step 2.6.3.

- After purification of the fragmented library set up the PCR amplification reaction and perform 5 cycles of library preamplification (Program 4_AMP).
- Put the tube on ice.
- Use a 5 μ L aliquot from the PCR reaction to prepare a qPCR reaction mix in the appropriate PCR tube or plate as follows:

Reagent	Per reaction, μ L	N +10%, μ L
5 cycles pre-amplified library	5.0	
SYBR 100x*	0.1	
LAM	2.5	
Water	2.4	
TOTAL	10.0	

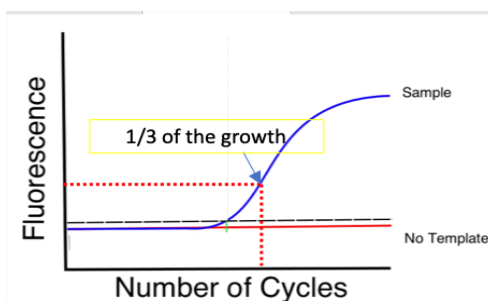
* Prepare 100x dilution with water from 10'000x stock

- Put it in the qPCR machine and run with the following program:

Step	Temperature, $^{\circ}$ C	Time	Cycles
Initial denaturation	98	1 min	
Denaturation	98	10 sec	
Annealing	63	30 sec	25
Extension + acquisition	72	1 min	

- Determine the cycle number depending on the growth curve in the multicomponent plot as in Figure 5. Of note, we recommend adding extra 4 cycles to the number corresponding to 1/3 of the growth curve (e.g., if a graph shows 10 cycles, perform PCR with 14 cycles).
- Perform PCR with a determined additional number of cycles with the tube containing the remaining 45 μ L of the pre-amplified library.

Figure 5 Determination of the additional number of amplification cycles with qPCR



Typically, 10 ng of cDNA is sufficient to obtain 60-80 ng of DNA library after 12 cycles of amplification. Table 5 shows the approximate amount of amplification cycles and the expected library yield.

Fragmented cDNA, ng	# PCR cycles	Expected library yield, ng/ μ L	Library purification (Right-side/Left-side)
1	15	3-6	
10	12	4-8	0.5x / 0.8x
20	11	4-8	

Table 5 Expected yield of BRB-seq libraries from different amounts of fragmented cDNA

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