# Supplementary Information

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### Introduction

In this experiment, we used quaddRAD library prep to prepare the sample DNA. This means that there were both two unique outer barcodes (typical Illumina barcodes) AND two unique inner barcodes (random barcode bases inside the adapters) for each sample - over 1700 to be exact!

The sequencing facility demultiplexes samples based on the outer barcodes (typically called 5nn and i7nn). Once this is done, each file still contains a mix of the inner barcodes. We will refer to these as "sublibraries" because they are sort of halfway demultiplexed. We separate them out bioinformatically later.

# Raw Data File Naming - Sublibraries

Here's a bit of information on the file name convention. The typical raw file looks like this:

AMH\_macro\_1\_1\_12px\_S1\_L001\_R1\_001.fastq.gz

These are author initials and "macro" stands for "Macrosystems". These are on every file.
 AMH\_macro

• The first number is the *i5nn* barcode for the given sublibrary. We know all these samples have a *i5nn* barcode "1", so that narrows down what they can be. The second number is the *i7nn* barcode for the given sublibrary. We know all these samples have a *i7nn* barcode "1", so that further narrows down what they can be.

1\_1

- This refers to how many samples are in the sublibrary. "12px" means 12-plexed, or 12 samples. In other words, we will use the inner barcodes to further distinguish 12 unique samples in this sublibrary.

  12px
- This is a unique sublibrary name. S1 = 1 i5nn and 1 i7nn.

S1

• This means this particular file came from lane 1 of the NovaSeq. There are four lanes. All samples should appear across all four lanes.

L001

• This is the first (R1) of two paired-end reads (R1 and R2).

R.1

The last part doesn't mean anything - it was just added automatically before the file suffix (fastq.gz)
 001.fastq.gz

#### A Note on File Transfers

There are three main systems at play for file transfer: the local machine, the sequencing facility's (GRCF) Aspera server, and MARCC. The Aspera server is where the data were/are stored immediately after sequencing. MARCC is where we plan to do preprocessing and analysis. Scripts and text files are easy for me to edit on my local machine. We used Globus to transfer these small files from my local machine to MARCC.

Midway through this analyses, we transitioned to another cluster, JHU's Rockfish. Scripts below, with the exception of file transfer from the Aspera server, should reflect the new filesystem, though you will have to adjust the file paths accordingly.

# Preprocessing

### Step 1 - Transfer Files

Files can be found in the O1\_transfer\_files/ directory.

01-aspera\_transfer\_n.txt

These are text files containing the names of fastq.gz files that we wanted to transfer from the sequencing facility's Aspera server to the computing cluster (MARCC). This was to maximize ease of transferring only certain files over at once, since transferring could take a long time. We definitely did this piecemeal. Possible file names shown in Aspera Transfer File Names. There are multiple of these files so that we could parallelize (replace n with the correct number in the command used below). This text file will need to be uploaded to your scratch directory in MARCC.

Files were then transferred using the following commands. Before starting, make sure you are in a data transfer node. Then, load the aspera module. Alternatively, you can install the Aspera transfer software and use that.

#### module load aspera

Initiate the transfer from within your scratch directory:

```
ascp -T -18G -i /software/apps/aspera/3.9.1/etc/asperaweb_id_dsa.openssh
--file-list=01-aspera_transfer_n.txt
--mode=recv --user=<aspera-user> --host=<aspera-IP> /scratch/users/<me>@jhu.edu
```

# Step 2 - Concatenate Files and Install Stacks

Files can be found in the O2\_concatenate\_and\_check/ directory.

#### Step 2a - Concatenate Files for each Sublibrary

We ran my samples across the whole flow cell of the NovaSeq, so results came in 8 files for each demultiplexed sublibrary (4 lanes \* paired reads). For example, for sublibrary 1\_1, we'd see the following 8 files:

```
AMH_macro_1_1_12px_S1_L001_R1_001.fastq.gz

AMH_macro_1_1_12px_S1_L001_R2_001.fastq.gz

AMH_macro_1_1_12px_S1_L002_R1_001.fastq.gz

AMH_macro_1_1_12px_S1_L002_R2_001.fastq.gz

AMH_macro_1_1_12px_S1_L003_R1_001.fastq.gz

AMH_macro_1_1_12px_S1_L003_R2_001.fastq.gz

AMH_macro_1_1_12px_S1_L004_R1_001.fastq.gz

AMH_macro_1_1_12px_S1_L004_R2_001.fastq.gz

AMH_macro_1_1_12px_S1_L004_R2_001.fastq.gz
```

The 02\_concatendate\_and\_check/02-concat\_files\_across4lanes.sh script finds all files in the working directory with the name pattern \*\_L001\_\*.fastq.gz and then concatenates across lanes 001, 002, 003, and 004 so they can be managed further. The "L001" part of the filename is then eliminated. For example the 8 files above would become:

```
AMH_macro_1_1_12px_S1_R1.fastq.gz
AMH_macro_1_1_12px_S1_R2.fastq.gz
```

Rockfish uses slurm to manage jobs. To run the script, use the sbatch command. For example:

```
sbatch ~/code/02-concat_files_across4lanes.sh
```

This command will run the script from within the current directory, but will look for and pull the script from the code directory. This will concatenate all files within the current directory that match the loop pattern.

#### Step 2b – Download and Install Stacks

On Rockfish, Stacks will need to be downloaded to each user's code directory. Stacks, and software in general, should be compiled in an interactive mode or loaded via module. For more information on interactive mode, see interact --usage.

```
interact -p debug -g 1 -n 1 -c 1 module load gcc
```

Now download Stacks. We used version 2.60.

```
wget http://catchenlab.life.illinois.edu/stacks/source/stacks-2.60.tar.gz
tar xfvz stacks-2.60.tar.gz
```

Next, go into the stacks-2.60 directory and run the following commands:

```
./configure --prefix=/home/<your_username>/code4-<PI_username>
make
make install
export PATH=$PATH:/home/<your_username>/code4-<PI_username>/stacks-2.60
```

The filesystem patterns on your cluster might be different, and you should change these file paths accordingly.

# Step 3 - Remove PCR Clones

Files can be found in the O3\_clone\_filter/ directory.

### Step 3a - Run PCR Clone Removal Script

The 03-clone\_filter.sh script runs clone\_filter from Stacks. The program was run with options --inline\_inline --oligo\_len\_1 4 --oligo\_len\_2 4. The --oligo\_len\_x 4 options indicate the 4-base pair degenerate sequence was included on the outside of the barcodes for detecting PCR duplicates. The script uses the file name prefixes listed for each single sub-pooled library in 03-clone\_filter\_file\_names.txt and loops to run clone\_filter on all of them. Possible file names shown in clone\_filter File Names.

### Step 3b - Parse PCR Clone Removal Results

If you want to extract descriptive statistics from the clone\_filter output, you can use the 03.5-parse\_clone\_filter.py script to do so. It can be run on your local terminal after transferring the clone\_filter.out logs to your local computer.



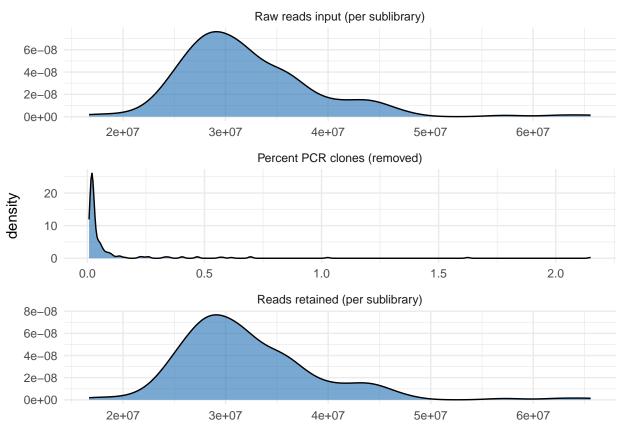


Figure 1: PCR clone removal statistics

## Step 4 - Demultiplexing and Sample Filtering

Files can be found in the O4\_demux\_filter/ directory.

#### Step 4a - Demultiplex and Filter

The 04-process\_radtags.sh script runs process\_radtags from Stacks. The program was run with options -c -q --inline\_inline --renz\_1 pstI --renz\_2 mspI --rescue --disable\_rad\_check. The script uses the same file prefixes as Step 3 - 03-clone\_filter.sh. Each sub-pooled library has a forward and reverse read file that was filtered in the previous step. Like the above section, the script uses the file name prefixes listed for each single sub-pooled library in 04-process\_radtags\_file\_names.txt and loops to run process\_radtags on all of them. Possible file names shown in clone\_filter File Names.

Each sub-pooled library also has a demultiplexing file (04-demux/ directory) that contains the sample names and inner(i5 and i7) barcodes. For example, the sublibrary 1\_1, we'd see the following barcode file:

```
ATCACG AGTCAA DS.BA.PIK.U.1
CGATGT
       AGTTCC DS.BA.PIK.U.2
TTAGGC ATGTCA DS.BA.PIK.U.3
TGACCA CCGTCC DS.BA.PIK.U.4
ACAGTG GTCCGC DS.BA.PIK.U.5
GCCAAT GTGAAA DS.BA.DHI.U.1
CAGATC GTGGCC DS.BA.DHI.U.2
ACTTGA GTTTCG DS.BA.DHI.U.3
GATCAG
       CGTACG DS.BA.DHI.U.4
TAGCTT
       GAGTGG DS.BA.DHI.U.5
GGCTAC ACTGAT DS.BA.GA.U.1
CTTGTA ATTCCT
              DS.BA.GA.U.2
```

The 'process\_radtags' command will demultiplex the data by separating out each sublibrary into the individual samples. It will then clean the data, and will remove low quality reads and discard reads where a barcode was not found.

### Step 4b - Organize files

In a new directory, make sure the files are organized by species. In the process\_radtags script, we specified that files be sent to ~/scratch/demux/\*sublibrary\_name\* (reasoning for this is in Step 4c), but files should manually be organized into species folders (i.e., ~/scratch/demux/\*SPP\*) after process\_radtags is performed. For example, the file "DS.MN.L01-DS.M.1.1.fq.gz" should be sent to the ~/scratch/demux/DS directory.

Note: this is not automated at this point but it would be nice to automate the file moving process so it's not forgotten at this point.

#### Step 4c - Assess the raw, processed, and cleaned data

In the script for Step 4, we have specified that a new output folder be created for each sublibrary. The output folder is where all sample files and the log file will be dumped for each sublibrary. It is important to specify a different output folder if you have multiple sublibraries because we will be assessing the output log for each sublibrary individually (and otherwise, the log is overwritten when the script loops to a new sublibrary).

The utility stacks-dist-extract can be used to extract data from the log file. First, we examined the library-wide statistics to identify sublibraries where barcodes may have been misentered or where sequencing error may have occurred. We used:

```
stacks-dist-extract process_radtags.log total_raw_read_counts
```

to pull out data on the total number of sequences, the number of low-quality reads, whether barcodes were found or not, and the total number of retained reads per sublibary. Look over these to make sure there are no outliers or sublibraries that need to be checked and rerun.

Next, we used:

to analyze how well each sample performed. There are three important statistics to consider for each sample.

- 1. The proportion of reads per sample for each sublibrary indicates the proportion that each individual was processed and sequenced within the overall library. This is important to consider as cases where a single sample dominates the sublibrary may indicate contamination.
- 2. The number of reads retained for each sample can be an indicator of coverage. It is most likely a good idea to remove samples with a very low number of reads. Where you decide to place the cutoff for low coverage samples is dependent on your dataset. For example, a threshold of 1 million reads is often used but this is not universal.
- 3. The proportion of reads retained for each sample can also indicate low-quality samples and will give an idea of the variation in coverage across samples.

Output for sublibraries for this step are summarized in process\_radtags-library\_output.csv.

Output for individual samples for this step are summarized in process\_radtags-sample\_output.csv.

The script 04c-process\_radtags\_stats.R was used to create many plots for easily assessing each statistic. Output from this step can be found in figures/process\_radtags/ where figures are organized by species.



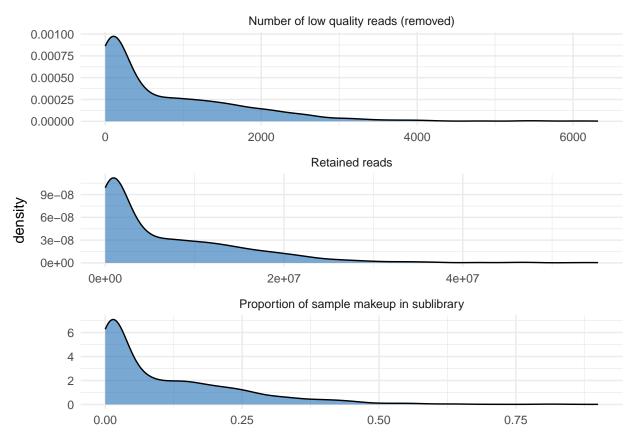


Figure 2: RAD tag processing statistics

### Step 4d - Identify low-coverage and low-quality samples from

#### downstream analysis

Using the same output log and the above statistics, we removed low-coverage and low-quality samples that may skew downstream analyses.

Samples were identified and removed via the following procedure:

- 1. First, samples that represented less than 1% of the sequenced sublibrary were identified and removed. These samples correlate to low-read and low-coverage samples.
- 2. Next, a threshold of **1** million retained reads per sample was used to remove any remaining low-read samples. Low-read samples correlate to low coverage and will lack enough raw reads to contribute to downstream analyses.

Good/kept samples are summarized in process\_radtags-kept\_samples.csv.

Discarded samples are summarized in process\_radtags-discarded\_samples.csv.

source("04\_demux\_filter/04c-radtags\_filter\_summary.R")
make\_manual\_discard\_plot()

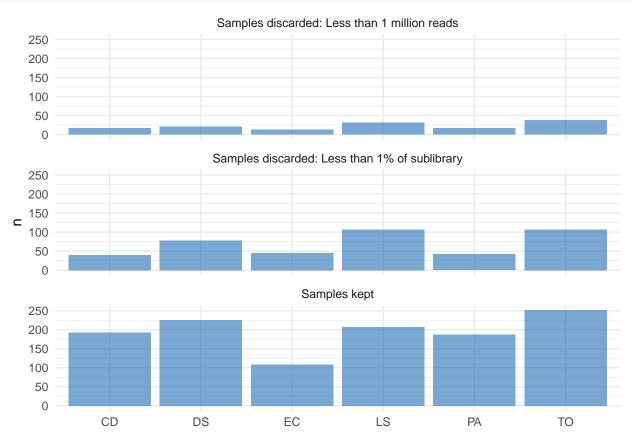


Figure 3: RAD tag manual filtering summary

Note: At this point, we started using Stacks 2.62 for its multi-threading capabilities. Functionality of the previous steps should be the same, however.

# Generating Stacks Catalogs and Calling SNPs

## Step 5 - Metapopulation Catalog Building and Parameter Search

Files can be found in the O5\_ustacks\_and\_params/ directory.

Going forward, when we use the term **metapopulation**, we are referring to the collection of all samples within species among all cities where the species was present.

It is important to conduct preliminary analyses that will identify an optimal set of parameters for the dataset (see Step 5a). Following the parameter optimization, the program ustacks can be run to generate a catalog of loci.

#### Step 5a - Run denovo\_map.sh

Stack assembly will differ based on several different aspects of the dataset(such as the study species, the RAD-seq method used, and/or the quality and quantity of DNA used). So it is important to use parameters that will maximize the amount of biological data obtained from stacks.

There are three main parameters to consider when doing this:

- 1. m = controls the minimum number of raw reads required to form a stack(implemented in ustacks)
- 2. M = controls the number of mismatches between stacks to to merge them into a putative locus (implemented in ustacks)
- 3. n = controls the number of mismatches allowed between stacks to merge into the catalog (implemented in cstacks)

There are two main ways to optimize parameterization:

- 1. an iterative method were you sequentially change each parameter while keeping the other parameters fixed (described in *Paris et al. 2017*), or
- 2. an iterative method were you sequentially change the values of M and n(keeping M = n) while fixing m = 3, and then test m = 2, 4 once the optimal M = n is determined (described in Rochette and Catchen 2017, Catchen 2020).

We performed the second method and used the denovo\_map.sh script to run the denovo\_map.pl command to perform iterations. This script requires that we first choose a subset of samples to run the iterations on. The samples should be representative of the overall dataset; meaning they should include all populations and have similar read coverage numbers. Read coverage numbers can be assessed by looking at the descriptive statistics produced from Step 4c.

Place these samples in a text file (popmap\_test\_samples.txt) with the name of the sample and specify that all samples belong to the same population. For example, popmap\_test\_samples.txt should look like...

```
DS.BA.GA.U.1 A
DS.PX.BUF.M.5 A
DS.BO.HC4.M.1 A
```

. . .

It is important to have all representative samples treated as one population because you will assess outputs found across 80% of the individuals. The script will read this text file from the --popmap argument.

The script also requires that you specify an output directory after  $\neg o$ . This should be unique to the parameter you are testing... for example, if you are testing M=3, then you could make a subdirectory labeled stacks.M3 where all outputs from denovo\_map.sh will be placed. Otherwise, for each iteration, the outputs will be overwritten and you will lose the log from the previous iteration. The denovo\_map.sh script also requires that you direct it toward where your samples are stored, which is your directory built in Step 4b. Make sure to run the  $\neg \neg \min \neg samples \neg per \neg pop 0.80$  argument.

To decide which parameters to use, examine the following from each iteration:

- 1. the average sample coverage: This is obtained from the summary log in the ustacks section of denovo\_map.log. If samples have a coverage <10x, you will have to rethink the parameters you use here.
- 2. the number of assembled loci shared by 80% of samples: This can be found in the haplotypes.tsv by counting the number of loci: cat populations.haplotypes.tsv | grep -v ^"#" | wc -l
- 3. the number of polymorphic loci shared by 80% of samples: This can be found in populations.sumstats.tsv or by counting populations.hapstats.tsv: cat populations.hapstats.tsv | grep -v "^#" | wc -1
- 4. the number of SNPs per locus shared by 80% of samples: found in denovo\_map.log or by counting the number of SNPs in populations.sumstats.tsv: populations.sumstats.tsv | grep -v ^"#" | wc -1

The script O5a-param\_opt-figures\_script.R was used to create plots for assessing the change in shared loci across parameter iterations.

Based on this optimization step, we used the following parameters:

Table 1: Final parameter optimization values for the Stacks pipeline.

Species	M (locus mismatches)	n (catalog mismatches)	m (minimum reads)
$\overline{\mathrm{CD}}$	8	8	3
DS	10	10	3
EC	8	8	3
LS	7	7	3
PA	5	5	3
TO	6	6	3

#### Step 5b - Run ustacks

ustacks builds de novo loci in each individual sample. We have designed the ustacks script so that the process requires three files:

- 05-ustacks\_n.sh: the shell script that executes ustacks
- 05-ustacks\_id\_n.txt : the sample ID number
- 05-ustacks\_samples\_n.txt: the sample names that correspond to the sample IDs

The sample ID should be derived from the order\_id column(first column) on the master spreadsheet. It is unique (1-1736) across all of the samples.

The sample name is the corresponding name for each sample ID in the spreadsheet. E.g., sample ID "9" corresponds to sample name "DS.BA.DHI.U.4". Sample naming convention is species.city.site.management type.replicate plant.

05-ustacks\_n.sh should have an out\_directory (-o option) that will be used for all samples (e.g., stacks/ustacks). Files can be processed piecemeal into this directory. There should be three files for every sample in the output directory:

- <samplename>.alleles.tsv.gz
- <samplename>.snps.tsv.gz
- <samplename>.tags.tsv.gz

Multiple versions of the O5-ustacks\_n.sh script can be run in parallel (simply replace n in the three files above with the correct number).

A small number of samples (13) were discarded at this stage as the ustacks tool was unable to form any primary stacks corresponding to loci. See output/ustacks-discarded samples.csv.

### Step 5c - Correct File Names

This step contains a script 05b-fix\_filenames.sh which uses some simple regex to fix filenames that are output in previous steps. Stacks adds an extra "1" at some point at the end of the sample name which is not meaningful. The following files:

- DS.MN.L02-DS.M.3.1.alleles.tsv.gz
- DS.MN.L03-DS.U.2.1.tags.tsv.gz
- DS.MN.L09-DS.U.1.1.snps.tsv.gz

#### become:

- DS.MN.L02-DS.M.3.alleles.tsv.gz
- DS.MN.L03-DS.U.2.tags.tsv.gz
- DS.MN.L09-DS.U.1.snps.tsv.gz

The script currently gives some strange log output, so it can probably be optimized/improved. The script should be run from the directory where the changes need to be made. Files that have already been fixed will not be changed.

### Step 5d - Choose catalog samples/files

In the next step, we will choose the files we want to go into the catalog. This involves a few steps:

- 1. Create a meaningful directory name. This could be the date (e.g., stacks\_22\_01\_25).
- 2. Copy the ustacks output for all of the files you want to use in the reference from Step 5b. Remember this includes three files per sample. So if you have 20 samples you want to include in the reference catalog, you will transfer  $3 \times 20 = 60$  files into the meaningful directory name. The three files per sample should follow this convention:
- <samplename>.alleles.tsv.gz
- <samplename>.snps.tsv.gz
- <samplename>.tags.tsv.gz
- 3. Remember the meaningful directory name. You will need it in Step 6.

### Step 6 - Metapopulation catalog with cstacks

Files can be found in the O6\_cstacks/ directory.

cstacks builds the locus catalog from all the samples specified. The accompanying script, cstacks\_SPECIES.sh is relatively simple since it points to the directory containing all the sample files. It follows this format to point to that directory:

```
cstacks -P ~/directory ...
```

Make sure that you use the meaningful directory from Step 5c and that you have copied all the relevant files over. Otherwise this causes problems downstream. For example, you might edit the code to point to ~/scratch/stacks/stacks\_22\_01\_25.

```
cstacks -P ~/scratch/stacks/stacks_22_01_25 ...
```

The tricky thing is ensuring enough compute memory to run the entire process successfully. There is probably space to optimize this process.

The cstacks method uses a "population map" file, which in this project is cstacks\_popmap\_SPECIES.txt. This file specifies which samples to build the catalog from and categorizes them into your 'populations', or in this case, cities using two tab-delimited columns, e.g.:

```
DS.BA.GA.U.1 Baltimore DS.BA.GA.U.2 Baltimore
```

```
DS.BA.GA.U.3 Baltimore
DS.BA.GA.U.4 Baltimore
DS.BA.GA.U.5 Baltimore
```

Make sure the samples in this file correspond to the input files located in e.g., ~/scratch/stacks/stacks\_22\_01\_25. cstacks builds three files for use in all your samples (in this pipeline run), mirroring the sample files output byustacks:

- catalog.alleles.tsv.gzcatalog.snps.tsv.gz
- catalog.tags.tsv.gz

Table 2: Subset of samples used in SNP catalog creation.

Sample	Species	City
DS.BA.PIK.U.1	DS	BA
DS.BA.GA.U.4	DS	BA
DS.BA.LH-1.M.4	DS	BA
DS.BA.LH-3.M.1	DS	BA
DS.BA.WB.U.2	DS	BA
DS.BA.LL-4.M.5	DS	BA
DS.BA.LH-2.M.5	DS	BA
DS.BA.TRC.U.3	DS	BA
DS.BA.W3.M.2	DS	BA
DS.BA.RG-1.M.1	DS	BA
DS.BA.LL-3.M.3	DS	BA
DS.BA.RG-2.M.4	DS	BA
DS.BO.HC1.M.3	DS	ВО
DS.BO.HC4.M.5	DS	ВО
DS.BO.LC1.M.3	DS	ВО
DS.BO.LC2.M.2	DS	ВО
DS.BO.LC3.M.5	DS	ВО
DS.BO.WL1.M.2	DS	ВО
DS.BO.WL2.M.1	DS	ВО
DS.BO.WL3.M.5	DS	ВО
DS.BO.I4.U.1	DS	ВО
DS.BO.R1.U.4	DS	BO
DS.BO.R2.U.2	DS	ВО
DS.BO.R4.U.4	DS	BO
DS.MN.L05-DS.M.3	DS	MN
DS.MN.L09-DS.M.3	DS	MN
DS.MN.L11-DS.M.1	DS	MN
DS.MN.L02-DS.U.1	DS	MN
DS.MN.L02-DS.M.4	DS	MN
DS.MN.L03-DS.U.3	DS	MN
DS.MN.L04-DS.U.5	DS	MN
DS.MN.L06-DS.U.3	DS	MN
DS.MN.L07-DS.U.3	DS	MN
DS.MN.L09-DS.U.3	DS	MN
DS.MN.L11-DS.U.1	DS	MN
DS.MN.L11-DS.U.5	DS	MN
DS.PX.BUF.M.1	DS	PX
DS.PX.PIE.M.2	DS	PX

Sample	Species	City
DS.PX.ALA.M.1	DS	PX
DS.PX.MTN.M.6	DS	PX
DS.PX.LAP.M.3	DS	PX
DS.PX.NUE.M.4	DS	PX
DS.PX.WES.M.2	DS	PX
DS.PX.DF1.M.1	DS	PX
DS.PX.ENC.M.1	DS	PX
DS.PX.DOW.M.1	DS	PX
DS.PX.DOW.M.4	DS	PX
DS.PX.DF2.M.3	DS	PX
CD.BA.LA.U.2	CD	BA
CD.BA.TRC.U.3	CD	BA
CD.BA.WGP.M.2	CD	BA
CD.BA.LH-2.M.2	CD	BA
CD.BA.LL-4.M.1	CD	BA
CD.BA.PIK.U.2	CD	BA
CD.BA.WB.U.2	CD	BA
CD.BA.CP.U.4	CD	BA
CD.BA.FH.U.1	CD	BA
CD.BA.PSP.M.4	CD	BA
CD.BA.AA.U.4	CD	BA
CD.BA.RG-1.M.2	CD	BA
CD.BA.W3.M.3	CD	BA BA
CD.BA.W3.M.3 CD.BA.GA.U.3	CD	BA BA
CD.BA.WBO.U.5	CD	BA BA
CD.LA.WHI.M.3	CD	LA
CD.LA.WHI.M.3 CD.LA.SEP.M.3	CD	LA LA
CD.LA.SEP.M.3 CD.LA.SEP.M.4	CD	LA LA
	CD	
CD.LA.ROS.M.5		LA
CD.LA.MR2.M.2	CD	LA
CD.LA.ALL.M.2	CD	LA
CD.LA.ALL.M.5	CD	LA
CD.LA.VAL.M.5	CD	LA
CD.LA.HAR.M.4	CD	LA
CD.LA.LUB.M.3	CD	LA
CD.LA.GLO.M.4	CD	LA
CD.LA.ZOO.M.3	CD	LA
CD.LA.NWH.M.5	CD	LA
CD.LA.KIN.M.3	CD	LA
CD.LA.KIN.M.5	CD	LA
CD.PX.CAM.U.5	CD	PX
CD.PX.MON.U.5	CD	PX
CD.PX.PKW.U.5	CD	PX
CD.PX.LAP.M.4	CD	PX
CD.PX.NES.U.4	CD	PX
CD.PX.PAL.M.3	CD	PX
CD.PX.ASU.M.1	CD	PX
CD.PX.NUE.M.5	CD	PX
CD.PX.WES.M.3	CD	PX
CD.PX.MAN.M.4	CD	PX
CD.PX.CLA.M.3	CD	PX
CD.PX.DF1.M.5	CD	PX

Sample	Species	City
CD.PX.COY.M.5	CD	PX
CD.PX.RPC.M.3	CD	PX
CD.PX.ENC.M.2	CD	PX
EC.BA.LH-2.M.2	EC	BA
EC.BA.WBO.U.4	EC	BA
EC.BA.WB.U.5	EC	BA
EC.BA.FH.U.3	EC	BA
EC.BA.CP.U.2	EC	BA
EC.BA.TRC.U.3	EC	BA
EC.BA.LL-4.M.4	EC	BA
EC.BA.WB.U.1	EC	BA
EC.BA.PIK.U.5	EC	BA
EC.BA.PSP.M.4	EC	BA
EC.BA.GA.U.2	EC	BA
EC.BA.LL-3.M.3	EC	BA
EC.BA.ML.U.1	EC	BA
EC.BA.TRC.U.5	EC	BA
EC.BA.ML.U.3	EC	BA
EC.LA.SGB.U.2	EC	LA
EC.LA.SGB.U.5	EC	LA
EC.LA.DUR.U.2	EC	LA
EC.LA.HOW.U.2	EC	LA
EC.LA.SAN.U.2	EC	LA
EC.LA.VER.U.1	EC	LA
EC.LA.VER.U.4	EC	LA
EC.LA.VB2.U.4	EC	LA
EC.LA. VB2.U.4 EC.LA. AC2.U.2	EC	LA
EC.LA.AC1.U.1	EC	$_{ m LA}$
EC.LA.VB1.U.1	EC	LA
EC.LA.VB1.U.3	EC	$_{ m LA}$
EC.LA.SGR.U.4	EC	$_{ m LA}$
EC.LA.SGR.U.5	EC	$_{ m LA}$
EC.LA.HOW.U.3	EC	$_{ m LA}$
EC.PX.BUF.M.1	EC	PX
EC.PX.BUF.M.3	EC	PX
EC.PX.ALA.M.3		
	EC	PX
EC.PX.MTN.M.2 EC.PX.WES.M.1	EC	PX
	EC	PX
EC.PX.WES.M.2	EC	PX
EC.PX.MAN.M.1	EC	PX
EC.PX.CLA.M.1	EC	PX
EC.PX.PSC.M.1	EC	PX
EC.PX.DF1.M.1	EC	PX
EC.PX.DOW.M.1	EC	PX
EC.PX.DOW.M.2	EC	PX
EC.PX.COY.M.2	EC	PX
EC.PX.COY.M.3	EC	PX
EC.PX.ALA.M.5	EC	PX
LS.BA.WB.U.1	LS	BA
LS.BA.WB.U.2	LS	BA
LS.BA.DHI.U.2	LS	BA
LS.BA.GA.U.1	LS	BA

Sample	Species	City
LS.BA.PIK.U.3	LS	BA
LS.BA.PIK.U.5	LS	BA
LS.BA.CP.U.2	LS	BA
LS.BA.ML.U.2	LS	BA
LS.BA.WBO.U.3	LS	BA
LS.BO.WL3.M.4	LS	ВО
LS.BO.II.U.1	LS	ВО
LS.BO.I1.U.1	LS	ВО
LS.BO.WL2.M.2	LS	ВО
LS.BO.R1.U.2	LS	ВО
LS.BO.R2.U.4	LS	ВО
LS.BO.R3.U.3	LS	ВО
LS.BO.HC4.M.3	LS	ВО
LS.BO.LC4.M.2	LS	ВО
LS.LA.VET.M.4	LS	LA
LS.LA.SSV.M.1	LS	LA
LS.LA.NAV.M.4	LS	LA
LS.LA.SHO.M.2	LS	LA
LS.LA.WES.M.3	LS	LA
LS.LA.GLO.M.3	LS	LA
LS.LA.HOW.U.5	LS	LA
LS.LA.SAN.U.2	LS	LA
LS.LA.ARR.U.2	LS	LA
LS.MN.L06-LS.U.2	LS	MN
LS.MN.L06-LS.U.5	LS	MN
LS.MN.L07-LS.U.4	LS	MN
LS.MN.L08-LS.U.5	LS	MN
LS.MN.L09-LS.U.3	LS	MN
LS.MN.L01-LS.M.4	LS	MN
LS.MN.L01-LS.U.3	LS	MN
LS.MN.L02-LS.U.1	LS	MN
LS.MN.L05-LS.U.2	LS	MN
LS.PX.MON.U.2	LS	PX
LS.PX.PKW.U.5	LS	PX
LS.PX.PIE.M.4	LS	PX
LS.PX.ALA.M.3	LS	PX
LS.PX.PAL.M.3	LS	PX
LS.PX.MAN.M.2	LS	PX
LS.PX.NUE.M.1	LS	PX
LS.PX.ENC.M.4	LS	PX
LS.PX.COY.M.3	LS	PX
PA.BA.PIK.U.1	PA	BA
PA.BA.LH-3.M.2	PA	BA
PA.BA.LH-3.M.3	PA	BA
PA.BA.WB.U.1	PA	BA
PA.BA.AA.U.1 PA.BA.WGP.M.3	PA DA	BA
PA.BA.LL-4.M.3	PA PA	BA BA
PA.BA.LA.U.2	PA PA	BA BA
PA.BA.LH-2.M.2	PA	BA
PA.BA.W3.M.3	PA	BA
PA.BA.RG-1.M.2	PA	BA
111.1511.1100-1.111.2	111	1011

Sample	Species	City
PA.BA.LL-3.M.5	PA	BA
PA.BO.I2.U.3	PA	ВО
PA.BO.HC1.M.4	PA	ВО
PA.BO.R3.U.2	PA	ВО
PA.BO.HC4.M.5	PA	ВО
PA.BO.R4.U.2	PA	ВО
PA.BO.WL2.M.5	PA	ВО
PA.BO.WL4.M.4	PA	ВО
PA.BO.LC4.M.4	PA	ВО
PA.BO.HC2.M.1	PA	ВО
PA.BO.R1.U.2	PA	ВО
PA.BO.WL1.M.1	PA	ВО
PA.BO.I1.U.5	PA	ВО
PA.LA.ALL.M.5	PA	LA
PA.LA.SEP.M.1	PA	LA
PA.LA.SEP.M.5	PA	LA
PA.LA.WHI.M.2	PA	LA
PA.LA.ROS.M.5	PA	LA
PA.LA.LUB.M.2	PA	LA
PA.LA.GLO.M.2	PA	LA
PA.LA.ZOO.M.4	PA	LA
PA.LA.ZOO.M.5	PA	LA
PA.LA.NWH.M.2	PA	LA
PA.LA.KIN.M.4	PA	LA
PA.LA.POP.M.4	PA	LA
PA.PX.BUF.M.3	PA	PX
PA.PX.PIE.M.4	PA	PX
PA.PX.LAP.M.5	PA	PX
PA.PX.ALA.M.1	PA	PX
PA.PX.PAP.M.2	PA	PX
PA.PX.PAP.M.5	PA	PX
PA.PX.DF1.M.2	PA	PX
PA.PX.RPP.U.3	PA	PX
PA.PX.ENC.M.4	PA	PX
PA.PX.ENC.M.5	PA	PX
PA.PX.COY.M.1	PA	PX
PA.PX.BUF.M.2	PA	PX
TO.BA.WBO.U.4	ТО	BA
TO.BA.CP.U.1	ТО	BA
TO.BA.FH.U.1	ТО	BA
TO.BA.LH-3.M.4	ТО	BA
TO.BA.WGP.M.3	ТО	BA
TO.BA.GA.U.4	ТО	BA
TO.BA.PIK.U.4	ТО	BA
TO.BA.PSP.M.1	TO	BA
TO.BA.RG-2.M.2	TO	BA
TO.BO.HC1.M.4	TO	ВО
TO.BO.HC2.M.5	TO	ВО
TO.BO.HC3.M.1	TO	ВО
TO.BO.HC4.M.5	TO	ВО
TO.BO.LC1.M.1	TO	ВО
TO.BO.LC2.M.5	TO	ВО

Sample	Species	City
TO.BO.LC3.M.1	ТО	ВО
TO.BO.WL2.M.1	TO	ВО
TO.BO.I2.U.3	TO	ВО
TO.LA.WHI.M.5	TO	LA
TO.LA.HAR.M.4	TO	LA
TO.LA.MR1.M.1	TO	LA
TO.LA.GLO.M.5	TO	LA
TO.LA.ZOO.M.1	TO	LA
TO.LA.NWH.M.4	TO	LA
TO.LA.VNS.M.2	TO	LA
TO.LA.PEP.M.5	TO	LA
TO.LA.COM.M.4	TO	LA
TO.MN.L11-TO.M.3	TO	MN
TO.MN.L02-TO.U.1	TO	MN
TO.MN.L04-TO.U.1	TO	MN
TO.MN.L06-TO.U.2	TO	MN
TO.MN.L08-TO.U.5	TO	MN
TO.MN.L09-TO.U.2	TO	MN
TO.MN.L11-TO.U.3	TO	MN
TO.MN.L05-TO.M.5	TO	MN
TO.MN.L08-TO.M.5	TO	MN
TO.PX.BUF.M.1	TO	PX
TO.PX.ALA.M.2	TO	PX
TO.PX.LAP.M.4	TO	PX
TO.PX.WES.M.1	TO	PX
TO.PX.CLA.M.1	TO	PX
TO.PX.DF1.M.1	TO	PX
TO.PX.DF2.M.1	TO	PX
TO.PX.COY.M.1	TO	PX
TO.PX.COY.M.6	ТО	PX

Step 7 - Metapopulation locus matching with sstacks

Files can be found in the O7\_sstacks/ directory.

All samples in the population (or all samples you want to include in the analysis) are matched against the catalog produced in [cstacks] (#step-6—cstacks) with sstacks, run in script stacks\_SPECIES.sh and stacks\_SPECIES\_additional.sh. It runs off of the samples based in the output directory and the listed samples in sstacks\_samples\_SPECIES.txt and sstacks\_samples\_SPECIES\_additional.txt (respectively), so make sure all your files (sample and catalog, etc.) are there and match. sstacks\_samples\_SPECIES.txt takes the form:

```
DS.BA.GA.U.1
DS.BA.GA.U.2
DS.BA.GA.U.3
DS.BA.GA.U.4
DS.BA.GA.U.5
```

There should be a new file produced at this step for every sample in the output directory:

• <samplename>.matches.tsv.gz

# Step 8 - Metapopulation oriented by locus tsv2bam

Files can be found in the O8\_tsv2bam/ directory.

tsv2bam and the proceeding programs in the pipeline use a populations map text file to specify which samples to include in the analysis. As such, a new population map (that differs from 06-cstacks\_popmap.txt) should be created that includes all samples (including those used to create your catalog) that you want to include in the analysis. This file will include the same samples specified in sstacks\_samples\_SPECIES.txt with a colomn specifying population. Here, this file is popmap\_SPECIES.txt.

We run tsv2bam using the script tsv2bam\_SPECIES.sh.

This is the step at which it's usually discovered that some samples are bad(don't have any useable matches to the catalog). These samples were excluded from popmap\_SPECIES.txt. For example we might simply cut out the following rows:

```
DS.MN.L10-DS.M.4 Minneapolis
DS.MN.L01-DS.M.4 Minneapolis
DS.BO.WL2.M.4 Boston
```

The following samples were discarded because they contained less than 300 sample loci matched to catalog loci:

Table 3: Samples discarded at the tsv2bam stage of the Stacks pipeline.

Sample	City
CD.BA.RG-1.M.4	Baltimore
CD.BA.RG-1.M.5	Baltimore
CD.BA.DHI.U.2	Baltimore
CD.BA.DHI.U.3	Baltimore
DS.MN.L04-DS.U.2	Minneapolis
DS.BO.WL3.M.4	Boston
DS.BO.WL1.M.4	Boston
DS.BO.LC1.M.2	Boston
DS.BO.HC4.M.4	Boston
EC.BO.R4.U.1	Boston
LS.PX.PAL.M.5	Phoenix
LS.PX.PAL.M.2	Phoenix
LS.PX.PAL.M.1	Phoenix
LS.MN.L01-LS.M.1	Minneapolis
LS.PX.PKW.U.3	Phoenix
LS.PX.ENC.M.2	Phoenix
LS.MN.L01-LS.U.1	Minneapolis
LS.LA.ARR.U.4	Los Angeles
LS.BO.WL2.M.3	Boston
LS.BO.WL2.M.1	Boston
LS.BO.R4.U.4	Boston
LS.BO.R4.U.2	Boston
LS.BO.R4.U.1	Boston
LS.BO.R3.U.2	Boston
LS.BO.R2.U.1	Boston
LS.BO.LC4.M.5	Boston
LS.BO.LC2.M.1	Boston
LS.BO.I4.U.1	Boston
LS.BO.HC4.M.4	Boston
LS.BO.HC4.M.2	Boston

Sample	City
LS.BA.WB.U.5	Baltimore
PA.BA.AA.U.3	Baltimore
PA.BA.AA.U.4	Baltimore
PA.BA.LH-3.M.1	Baltimore
PA.BA.LH-3.M.4	Baltimore
PA.BA.LL-4.M.1	Baltimore
PA.BA.RG-1.M.1	Baltimore
PA.BO.HC2.M.4	Boston
PA.BO.LC2.M.3	Boston
PA.BO.LC2.M.4	Boston
PA.BO.R3.U.3	Boston
PA.PX.ALA.M.2	Phoenix
PA.PX.ALA.M.3	Phoenix
PA.PX.RPP.U.1	Phoenix
PA.PX.RPP.U.2	Phoenix
TO.BA.DHI.U.5	Baltimore
TO.BA.TRC.U.1	Baltimore
TO.BA.TRC.U.2	Baltimore
TO.BA.TRC.U.3	Baltimore
TO.BO.R2.U.2	Boston
TO.BO.R4.U.1	Boston
TO.BO.R4.U.2	Boston

# Step 9 - Metapopulation SNP calling with gstacks

Files can be found in the O9\_gstacks/ directory.

The script gstacks\_SPECIES.sh also uses the population map specified in Step 8, popmap\_SPECIES.txt. The gstacks program aligns the paired-end reads and assembles the paired-end contigs and then calls SNPs.

Produces the following:

- catalog.fa.gz: consensus catalog loci, contains the consensus sequence for each locus as produced by gstacks in a standard FASTA file
- catalog.calls: per-nucleotide genotypes, contains the output of

### Step 10 - Metapopulation summaries with populations

Files can be found in the 10\_populations/ directory.

The populations program will use the script <code>species\_populations.sh</code> and the population maps specified in <code>Step 9</code> (popmap\_SPECIES.txt) to calculate population-level summary statistics. Specifically, the script iterates through all species and several levels of the parameter <code>--min-samples-overall</code>, the minimum percentage of individuals across populations required to process a locus

You will most likely run the populations program multiple times if you are looking at different 'sub-populations'. A new directory should be created and the population program should run out of that directory for each iteration of the population program. Alternativley, you can specify a new directory as the output folder in the script using the command -0.

Ultimately, the key parameters we used for running populations were as follows:

- --write-random-snp: restrict data analysis to one random SNP per locus
- --min-samples-overall: 20 locus must be in 20% of individuals

• --min-maf: 0.05 - minimum minor allele frequency required to process a nucleotide site at a locus

### Step 11 - Examine Within-city Catalogs and Populations

Files can be found in the 11\_city\_catalogs/ directory.

For any given species within city, there is likely to be a slightly different set of SNPs compared to the whole metapopulation of five cities. We examined 24 sets of species-city combinations. Within the folder 11\_city\_catalogs there are 24 folders:

```
CD_BA_22_09_14
CD_LA_22_09_14
CD_PX_22_09_14
DS_BA_22_09_14
DS_B0_22_09_14
DS_MN_22_09_14
DS_PX_22_09_14
EC_BA_22_09_14
EC_LA_22_09_14
EC_PX_22_09_14
LS_BA_22_09_14
LS BO 22 09 14
LS_LA_22_09_14
LS MN 22 09 14
LS_PX_22_09_14
PA_BA_22_09_14
PA_B0_22_09_14
PA_LA_22_09_14
PA_PX_22_09_14
TO_BA_22_09_14
TO_BO_22_09_14
TO LA 22 09 14
TO_MN_22_09_14
TO_PX_22_09_14
```

All folders contain a script and set of samples used to build the species-city catalog. Because parameter search had already been performed at the metapopulation level, we ran all species-city combinations using denovo map.pl. Input samples came from step 4. For example, input files should look like this:

```
CD.BA.AA.U.1.1.fq.gz
CD.BA.AA.U.1.2.fq.gz
CD.BA.AA.U.1.rem.1.fq.gz
CD.BA.AA.U.1.rem.2.fq.gz
```

A population map is also included within each directory to ensure only appropriate samples (i.e., ok coverage) are included in the catalog.

## Step 11b - City Level Population Analysis

The city-level populations program will use the script 11-city\_catalogs/11-city\_populations.sh. The goal of this script is to run the Stacks function populations on each city-species combination while toggling the --min-samples-overall option. Toggling this option allows us to hone in on a reasonable number of SNPs while also getting rid of SNPs with a lot of missing data, therefore creating a more robust population structure snapshot. As described in step 11, each city-species combination with adequate data is represented by a folder. The 11-city\_populations.sh script iterates through folders, within which it runs several --min-samples-overall levels and outputs each parameter permutation to its own new directory. This script

uses the 11-city\_catalogs/11-city\_catalog\_names.txt to iterate rather than doing all folders by default. This is convenient if you only want to iterate through a subset of the folders (city-species combinations).

# Appendix

### SessionInfo()

```
sessionInfo()
## R version 4.2.2 (2022-10-31)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS Big Sur 11.7
##
## Matrix products: default
           /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
## attached base packages:
                 graphics grDevices utils
## [1] stats
                                               datasets methods
                                                                    base
##
## other attached packages:
## [1] dplyr_1.0.10
                      magrittr_2.0.3 tidyr_1.2.1
                                                     ggplot2_3.4.0
##
## loaded via a namespace (and not attached):
  [1] highr_0.9
##
                          pillar_1.8.1
                                            compiler_4.2.2
                                                               formatR_1.12
  [5] tools_4.2.2
                          bit_4.0.5
                                            digest_0.6.30
                                                               evaluate_0.18
## [9] lifecycle_1.0.3
                          tibble_3.1.8
                                            gtable_0.3.1
                                                               pkgconfig_2.0.3
                          cli_3.4.1
## [13] rlang_1.0.6
                                            DBI_1.1.3
                                                               rstudioapi_0.14
## [17] parallel_4.2.2
                          yam1_2.3.6
                                            xfun_0.35
                                                               fastmap_1.1.0
## [21] withr_2.5.0
                          stringr_1.4.1
                                            knitr_1.41
                                                               systemfonts_1.0.4
## [25] hms_1.1.2
                          generics_0.1.3
                                            vctrs_0.5.1
                                                               bit64_4.0.5
## [29] grid_4.2.2
                          tidyselect_1.2.0
                                            glue_1.6.2
                                                               R6_2.5.1
## [33] textshaping_0.3.6 fansi_1.0.3
                                            vroom_1.6.0
                                                               rmarkdown_2.18
## [37] farver 2.1.1
                          tzdb 0.3.0
                                            readr 2.1.3
                                                               purrr 0.3.5
## [41] ellipsis_0.3.2
                          scales_1.2.1
                                                               assertthat_0.2.1
                                            htmltools_0.5.3
## [45] colorspace_2.0-3
                          labeling_0.4.2
                                                               utf8_1.2.2
                                            ragg_1.2.4
## [49] stringi_1.7.8
                          munsell_0.5.0
                                            crayon_1.5.2
```

### File Organization

All data files for the Macrosystems project are permanently stored under Meghan Avolio's group resources in the Johns Hopkins University Rockfish computing cluster. Files are stored under the 'data' directory under the following subdirectories:

- 01-raw\_data: This folder contains the raw, unprocessed data files that were obtained directly from the sequencing server. There are eight fastq.gz files per sublibrary that correspond to the four sequencing lanes for each read direction.
- 02-concatenated\_data: This folder contains the concatenated, unprocessed files for each sublibrary (i.e., the files containing the sequences for each lane were combined to create one file per read direction).
- 03-pcr\_filtered\_data: Here, you will find the resulting data files from the clone\_filter program,

where per replicates/clones have been removed from the raw sequences. There are two fq.gz files per sublibrary.

- 04-process\_radtags: This folder contains various subdirectories that correspond to the process\_radtags program that demultiplexes and cleans the data. The demux\_txt\_files folder contains the .txt files used to identify barcodes and separate out the individual samples from each sublibrary. The resulting data files from the process-radtags program are separated by individual and can be found in the relevant species folder(i.e., CD, DS, EC, LS, PA, TE, TO). Each individual sample has four data files; sampleID.1.fq.gz and sampleID.2.fq.gz correspond to the forward and reverse reads for each sample and sampleID.rem,1/2.fq.gz contain the remainder reads that were cleaned and removed from the data sequence.
- 05-ustacks-denovo\_data: This folder contains species subdirectories that store the resulting data files from the ustacks program for each individual. There are three files per individual; sampleID.allelles.tsv.gz, sampleID.snps.tsv.gz, and, sampleID.tags.tsv.gz. These files should be permanently stored here and copied to a new directory for any new catalogs and/or when a group of samples are being aligned to a new catalog.
- catalogs\_by\_city: For any given species within city, there is likely to be a slightly different set of SNPs compared to the whole metapopulation of five cities. We examined 24 sets of species-city combinations. These catalogs are permanently stored here.
- catalogs\_by\_species: Metapopulation catalogs are stored within this folder for each species. The metapopulation catalog was created using samples from all populations to create a national catalog.

Some notes about catalog directories:

- Catalogs contain three files; catalog.alleles.tsv.gz, catalog.snps.tsv.gz, and catalog.tafs.tsv.gz. If you would like to use the catalog on a new project, you will need to copy all three files to a new project folder.
- You can determine which individuals were used to create the catalog by looking at the cstacks\_popmap.txt found within each folder. Specifically for the metapopulation catalogs, this information is also found in the cstacks-metapop-catalog\_samples-included.csv
- You can determine which individuals were subsequently aligned to the catalog and used in the subsequent stacks analysis by looking at the popmap\*.txt found within each folder.
- Each folder also contains the relevant ustacks and stacks pipeline scripts and output files (i.e., from cstacks, gstacks, stacks, tsv2bam, and populations),

## Aspera Transfer File Names

```
/Hoffman macrosystems/AMH macro 1 1 12px S1 L001 R1 001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_1_12px_S1_L001_R2_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_1_12px_S1_L002_R1_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_1_12px_S1_L002_R2_001.fastq.gz
/Hoffman macrosystems/AMH macro 1 1 12px S1 L003 R1 001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_1_12px_S1_L003_R2_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_1_12px_S1_L004_R1_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_1_12px_S1_L004_R2_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_10_8px_S10_L001_R1_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_10_8px_S10_L001_R2_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_10_8px_S10_L002_R1_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_10_8px_S10_L002_R2_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_10_8px_S10_L003_R1_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_10_8px_S10_L003_R2_001.fastq.gz
/Hoffman_macrosystems/AMH_macro_1_10_8px_S10_L004_R1_001.fastq.gz
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## clone filter File Names

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AMH macro 1 11 8px S11
AMH_macro_1_12_8px_S12
AMH macro 1 13 8px S13
AMH_macro_1_14_8px_S14
AMH macro 1 2 12px S2
AMH_macro_1_3_12px_S3
AMH_macro_1_4_12px_S4
AMH_macro_1_5_8px_S5
AMH_macro_1_6_8px_S6
AMH_macro_1_7_8px_S7
AMH_macro_1_8_8px_S8
AMH_macro_1_9_8px_S9
AMH_macro_10_1_8px_S127
AMH_macro_10_10_12px_S136
AMH_macro_10_11_12px_S137
AMH_macro_10_12_12px_S138
AMH macro 10 13 8px S139
AMH macro 10 14 8px S140
AMH_macro_10_2_8px_S128
AMH_macro_10_3_8px_S129
AMH_macro_10_4_8px_S130
AMH macro 10 5 8px S131
AMH_macro_10_6_8px_S132
AMH_macro_10_7_8px_S133
AMH_macro_10_8_8px_S134
AMH_macro_10_9_12px_S135
AMH_macro_11_1_8px_S141
AMH_macro_11_10_12px_S150
AMH_macro_11_11_12px_S151
AMH_macro_11_12_12px_S152
AMH_macro_11_13_8px_S153
AMH_macro_11_14_8px_S154
AMH_macro_11_2_8px_S142
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AMH\_macro\_11\_3\_8px\_S143

- AMH macro 11 4 8px S144
- AMH\_macro\_11\_5\_8px\_S145
- AMH macro 11 6 8px S146
- AMH\_macro\_11\_7\_8px\_S147
- AMH\_macro\_11\_8\_8px\_S148
- AMH macro 11 9 12px S149
- AMH macro 12 1 8px S155
- AMH\_macro\_12\_10\_12px\_S164
- AMH macro 12 11 12px S165
- AMH\_macro\_12\_12\_12px\_S166
- AMH\_macro\_12\_13\_8px\_S167
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- AMH\_macro\_12\_4\_8px\_S158
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- AMH\_macro\_12\_8\_8px\_S162
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- AMH macro 2 4 12px S18

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- AMH\_macro\_2\_9\_8px\_S23
- AMH\_macro\_3\_1\_12px\_S29
- AMH macro 3 10 8px S38
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- AMH\_macro\_5\_1\_8px\_S57
- AMH\_macro\_5\_10\_8px\_S66
- AMH\_macro\_5\_11\_8px\_S67
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- AMH\_macro\_5\_14\_8px\_S70
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- AMH\_macro\_5\_8\_12px\_S64
- AMH\_macro\_5\_9\_8px\_S65
- AMH\_macro\_6\_1\_8px\_S71
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- AMH\_macro\_7\_13\_8px\_S97
- AMH\_macro\_7\_14\_8px\_S98
- AMH\_macro\_7\_2\_8px\_S86
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- AMH\_macro\_7\_9\_8px\_S93
- AMH\_macro\_8\_1\_8px\_S99
- AMH\_macro\_8\_10\_8px\_S108
- AMH macro 8 11 8px S109
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- AMH\_macro\_8\_13\_8px\_S111
- AMH\_macro\_8\_14\_8px\_S112
- AMH\_macro\_8\_2\_8px\_S100
- AMH\_macro\_8\_3\_8px\_S101
- AMH\_macro\_8\_4\_8px\_S102
- AMH\_macro\_8\_5\_12px\_S103
- AMH\_macro\_8\_6\_12px\_S104
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