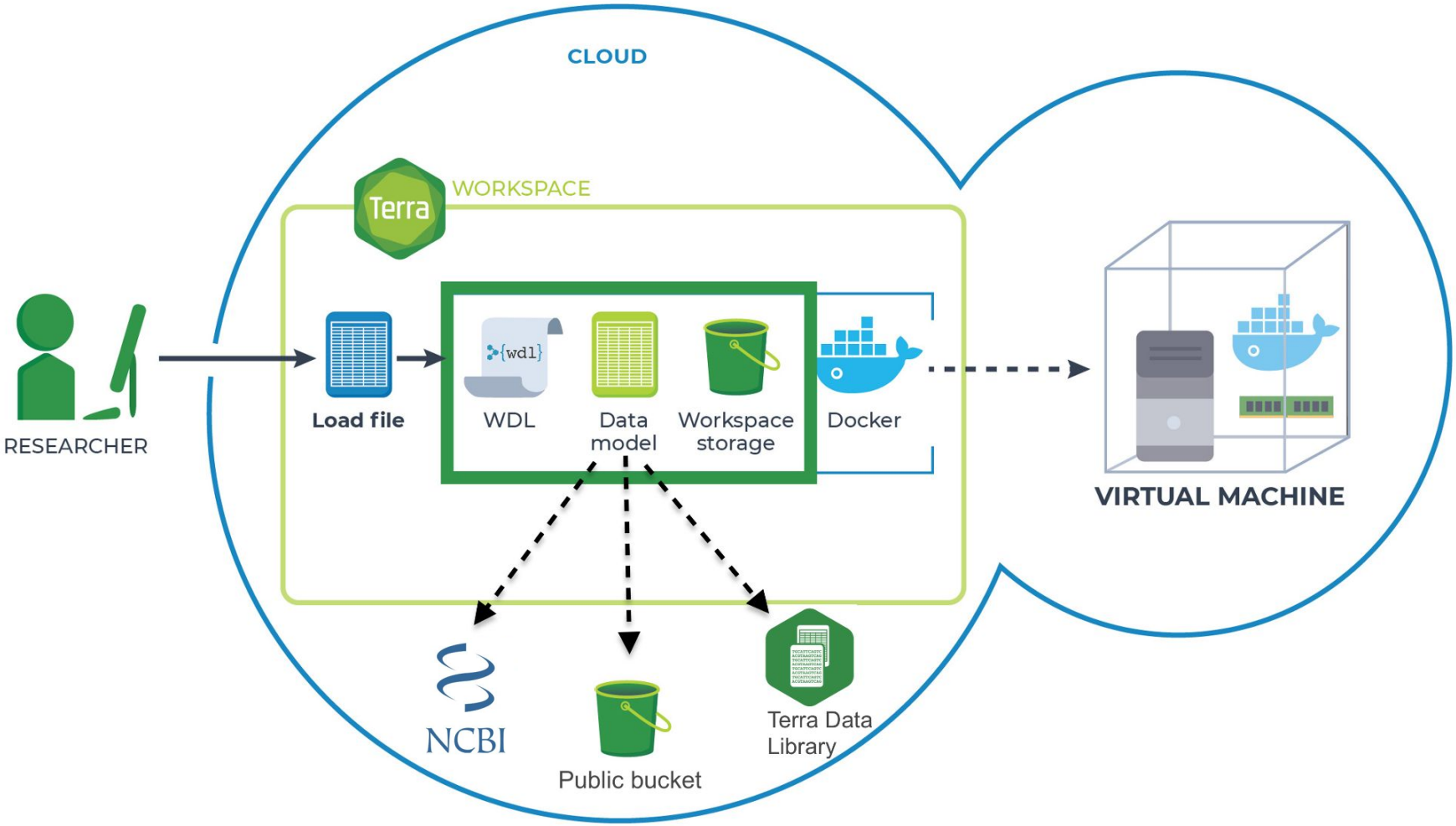
Introducing the Malaria Plasmodium Illumina Amplicon Workspace

In Terra


CLOUD
Terra
WORKSPACE
RESEARCHER
Load file
{wdl}
WDL
Data model
Workspace storage
Docker
VIRTUAL MACHINE
NCBI
Public bucket
Terra Data Library

STABLE VERSIONING WITH:

Workflows:

- **https://github.com/broadinstitute/malaria**

Dockerfiles and Code:

- **https://github.com/broadinstitute/malaria_ampseq**
- **https://github.com/broadinstitute/malaria_mhap**

```
FROM condaforge/mambaforge:23.3.1-0

RUN mamba config \
    --add channels defaults \
    --add channels bioconda \
    --add channels conda-forge && \
    mamba create -n ampseq_env python=3.7.10 -y && \
    mamba install -n ampseq_env \
    r-base=4.1 \
    pandas=1.3.0 \
    biopython=1.79 \
    bbmap=39.01 \
    trim-galore=0.6.6 \
    cutadapt=3.4 \
    muscle=3.8.1551 \
    bioconductor-dada2=1.20.0 \
    bioconductor-limma=3.48.0 \
    r-data.table=1.14.0 \
    r-viridisLite=0.4.0 \
    r-argparse=2.0.3 \
    r-seqinr=4.2_5 \
    r-stringdist=0.9.8 \
    r-rmarkdown=2.22 \
    r-gridextra=2.3 \
    r-gt=0.9.0 \
    r-tidyverse=2.0.0 \
    -c conda-forge -c bioconda && \
    mamba clean --all -f -y && \
    echo "source activate ampseq_env" > ~/.bashrc

ENV PATH /opt/conda/envs/ampseq_env/bin:$PATH
ENV PATH /opt/conda/envs/ampseq_env/bin/python:$PATH
SHELL ["conda", "run", "-n", "ampseq_env", "/bin/bash", "-c"]
```

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon ›
Dashboard

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Rate: $0.00 per hour

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Overview of Workflows

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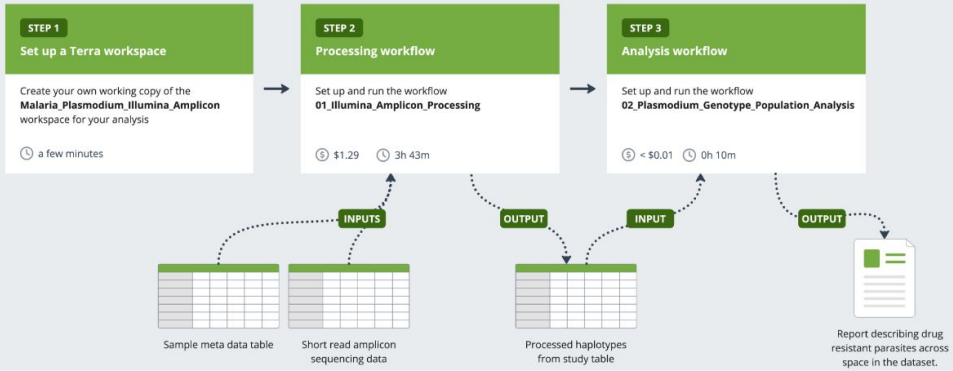


WORKSPACE INFORMATION

Last Updated	9/14/2024
Creation Date	5/7/2024
Access Level	Writer

CLOUD INFORMATION

Cloud Name	Google Cloud
Location	us-central1 (Iowa)
Google Project ID	terra-37936ad7
Bucket Name	fc-41ecac47-1f1a-484f-8...
Estimated Storage Cost Updated on 9/14/2024	$0.00
Bucket Size Updated on 9/14/2024	82.5 MiB

Open bucket in browser
Open project in Google Cloud Console

OWNERS

cloreth@broadinstitute.org
pbretsch@broadinstitute.org

TAGS

Terra for Public Health Genomics is not intended to host personally identifiable information.

Add a tag

pathogen genomics × malaria ×

WORKSPACE

01_Illumina_Amplicon_Processing

In Terra

01_Illumina_Amplicon_Processing

File Preparation → Adaptor and Primer Removal → Denoising → ASV Filtering

Takes a:

1. Bed file with coordinate. specifications for an Amplicon Panel.
2. Reference Genome.

And builds:

1. Reference multifasta with ASVs sequences.
2. (Also other internal files necessary to run pipeline).

Adaptor and Primer Removal:

- cutadapt v3.4
- trim-galore v0.0.6

Workflow performs denoising with DADA2.

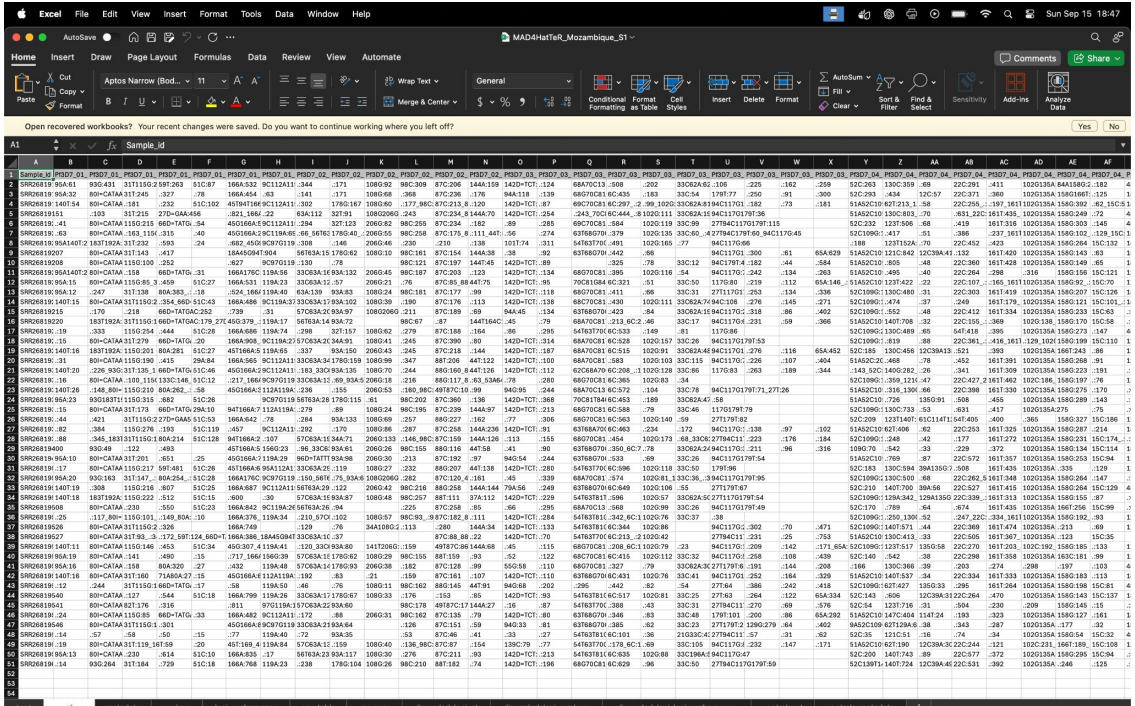
ASV filtered based on criteria:

- Homopolymer mask.
- Off-target products.
- Erroneous calls removal.
- Minimum read coverage.
- Bimera removal.

https://github.com/broadinstitute/malaria_ampseq

EASILY BROWSABLE OUTPUT IN EXCEL FORMAT

- Gt
- Metadata
- Markers
- Loci_Performance
- ASV_Table
- ASV_Seqs
- Discarder_Loci_Markers
- Discarded_Loci_Loci_Performance
- Controls_gt
- Control_Metadata



WORKSPACE

02_Plasmodium_Genotype_Population_Analysis

In Terra

02_Plasmodium_Genotype_Population_Analysis

Integrate Metadata	Report	Layout
Takes input from first workflow in Excel format.	1. Number of samples per location that yielded usable data. 2. Dataset completeness. 3. Genotype Frequency	Layout report in html format.

https://github.com/broadinstitute/malaria_mhap

Malaria_Plasmodium_Illumina | Genotyping Report | Job Manager

storage.googleapis.com/fc-77fc09e7-98aa-42c5-a876-e65049608fe8/submissions/fb51c352-9356-406a-9178-1e03a2c5280f/report_layouting/99454df3-e597-4c50-8723-b40e20e1...

New Chrome available

Genotyping Report

Code

- Performance Summary
- Genotype Frequency
- Prevalence of resistant marker

Performance Summary

This report summarizes data processed with the 01_Illumina_Amplicon_Processing workflow. It details the performance of amplicons and samples and the occurrence of mutations associated with resistance to different antimalarial drugs.

Show

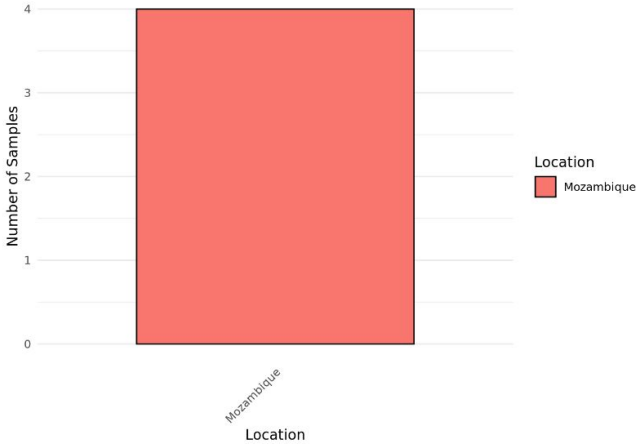


Figure 1: Number of samples per location that yielded usable data.

Show

WORKSPACE

03_Plasmodium_Genotyping_PCA

In Terra - Currently not exposed as of June 6th/2025

03_Plasmodium_Genotyping_PCA

Integrate Metadata	Report	Layout
Takes input from first workflow in Excel format.	1. IBS - PCA 2. PCA components table 3. COI 4. IBD - PCA	Layout report in html format.

https://github.com/broadinstitute/malaria_mhap

PCA

Code

MHap Analysis Report: PCoA of Genetic Relatedness (IBS)

Neafsey Lab

The genetic relatedness between individual parasite haplotypes and among parasite populations has several practical uses in the study of malaria. For example, relatedness information can help determine the geographic origin of imported infections, define the extent to which parasites are dispersing or are contained within landscapes, and identify whether specific strains are being selected for over time. Relatedness information is also very helpful in understanding longitudinal (within-individual) infection dynamics. In the case of *P. vivax*, for example, it can distinguish whether infection represents newly acquired parasites, recrudescence after treatment, or relapse from longer-lasting hypnozoite reservoirs. Relatedness information can also help resolve polyclonality signals, i.e., clarify the number of different haplotypes co-infecting individual patients.

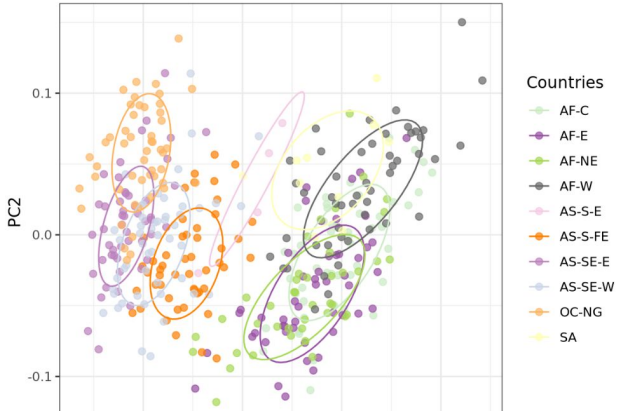
Relatedness is defined as the probability that, at any locus in the genome, the alleles sampled from two different individuals are identical by descent (IBD). Genetic markers used for this purpose include SNPs, microsatellites, and (increasingly) amplicon micro-haplotypes (MHAP). Relatedness can be estimated using a Hidden Markov Model approach implemented in the R package paneljudge (see mathematical framework in AR Taylor et al. 2019). In this package, relatedness (r) is estimated as a function of the haplotype of the two sampled parasites ($Y^{(i)}$ and $Y^{(j)}$, where i and j denote two different sampled genotypes from the population), the frequency of the alleles in the population ($f_t(g)$, where t denotes locus), the physical distance (d_t, in base-pairs) between successively analyzed loci ($t-1$ and t), the recombination rate (ρ), a switching rate of the Markov chain (k), and a constant genotyping error rate (ε).

Show

PCA

PCA plot summarizing the genetic relatedness between samples are constructed.

Show



General guidelines

- All of today's slides and other materials will be available after the workshop.
- If you haven't already:
  - Sign up in Terra at https://publichealth.terra.bio/
  - Set up billing by sending us your Google Email account.
- Terra works best on Chrome.

You will learn about:

Theoretical component:

- What Terra is and why it's on the cloud.
- What our panel agnostic workflow can do for you.

Practical component:

- How to:
  - Interact with the Terra Interface.
  - Run Workflows.
  - Access logs.
  - Download Results.

Not covered today:

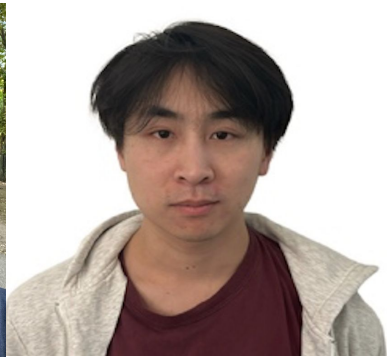
- Data upload.
- Workflow development.

Today’s program

1. How to log in.
2. How to clone the workspace.
3. How to launch the data. processing workflow.
4. How to monitor your process.
5. How to launch the genotyping workflow.
6. How to download output files.

Don’t hesitate to ask for assistance

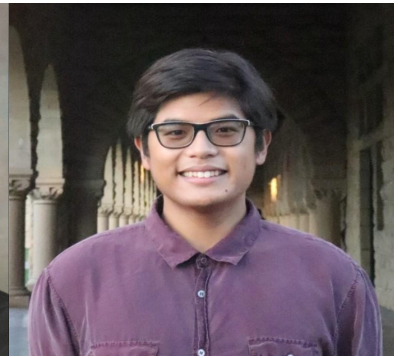
Paulo Manrique



Wesley Wong

Christine Loreth

Jonn Smith



Raphael Brosula

How to log in

Terra for Public Health Genom

publichealth.terra.bio

New Chrome available

Public Health Genomics

Terra for Public Health Genomics

Terra is a secure cloud-based data platform enabling pathogen genomic data analysis in public health, clinical, and academic settings.

Malaria Resources on Terra

Theiagen Workflow Repository (Dockstore)

Terra Cloud Costs FAQs

Contact us

Terra Support

Image credit
Lydia Krasilnikova

My Workspaces

Combine your own data and workflows with publicly available data and workflows to power your analyses in a secure environment.

Public Workspaces

Curated example workspaces to help users understand common pathogen genomic datasets and workflows.

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Agree Reject

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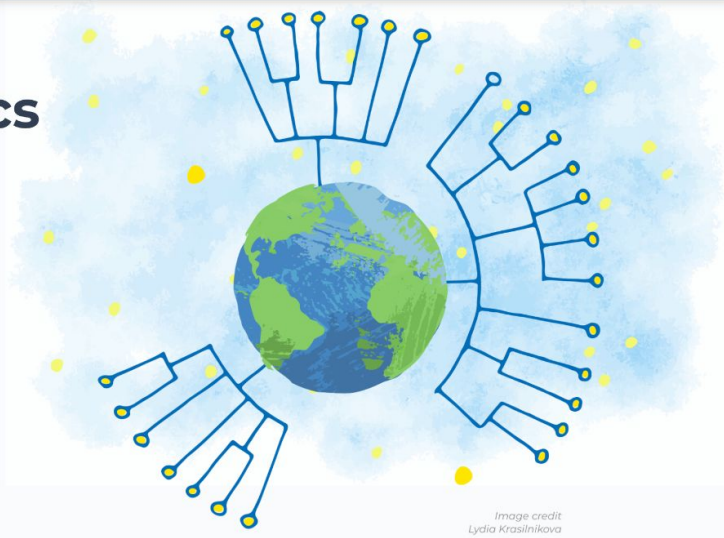

Image credit
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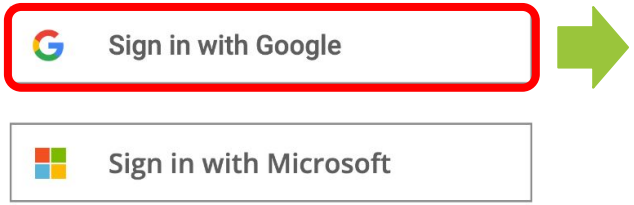
Agree Reject



If necessary, login with the account you used to register.

Terra for Public Health Genom | Malaria_Resources_Overview

publichealth.terra.bio/#workspaces/malaria-featured-workspaces/Malaria_Resources_Overview

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Public Health Genomics WORKSPACES

Workspaces › malaria-featured-workspaces/Malaria_Resources_Overview ›
Dashboard

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Rate: $0.00 per hour

ABOUT THE WORKSPACE

Welcome to the Malaria Resources Overview page on Terra

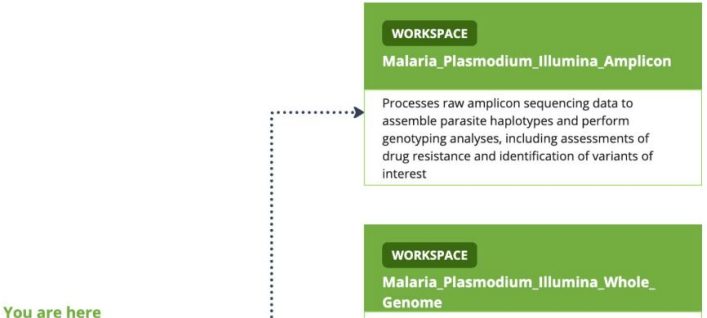
Here you will find a growing collection of validated tools (or "workflows") to perform common data processing and analysis of common malaria genomic data types.

The workflows are available in Terra "workspaces"—dedicated spaces where workflows and data are combined together to perform analyses in the cloud.

You can explore these workflows in the following workspaces:.

Malaria_Plasmodium_Illumina_Amplicon: This workspace allows users to process Illumina-based amplicon sequencing data to filter PCR and sequencing errors, and to perform a variety of downstream analyses, including interpretation of polymorphisms associated with drug resistance.

Malaria_Plasmodium_Illumina_Whole_Genome: This workspace allows users to processes short read whole genome sequencing data using GATK best practices and produces a dataset of high confidence SNP calls for downstream analyses, including drug resistance calls



WORKSPACE INFORMATION

Last Updated	9/13/2024
Creation Date	8/19/2024
Access Level	Reader

CLOUD INFORMATION

OWNERS

TAGS

NOTIFICATIONS

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon

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Public Health Genomics WORKSPACES

Workspaces › malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon ›
Dashboard

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

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Overview of Workflows

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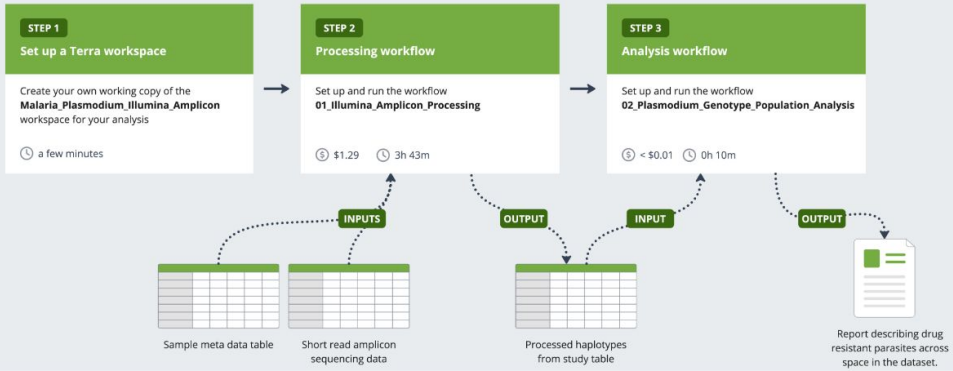

WORKSPACE INFORMATION

Last Updated	9/14/2024
Creation Date	5/7/2024
Access Level	Writer

CLOUD INFORMATION

Cloud Name	Google Cloud
Location	us-central1 (Iowa)
Google Project ID	terra-37936ad7
Bucket Name	fc-41ecac47-1f1a-484f-8...
Estimated Storage Cost Updated on 9/14/2024	$0.00
Bucket Size Updated on 9/14/2024	82.5 MiB

Open bucket in browser
Open project in Google Cloud Console

OWNERS

cloreth@broadinstitute.org
pbretsch@broadinstitute.org

TAGS

Terra for Public Health Genomics is not intended to host personally identifiable information.

Add a tag

pathogen genomics × malaria ×

How to clone the workspace

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon

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Public Health Genomics WORKSPACES

Workspaces › malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon ›
Dashboard

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

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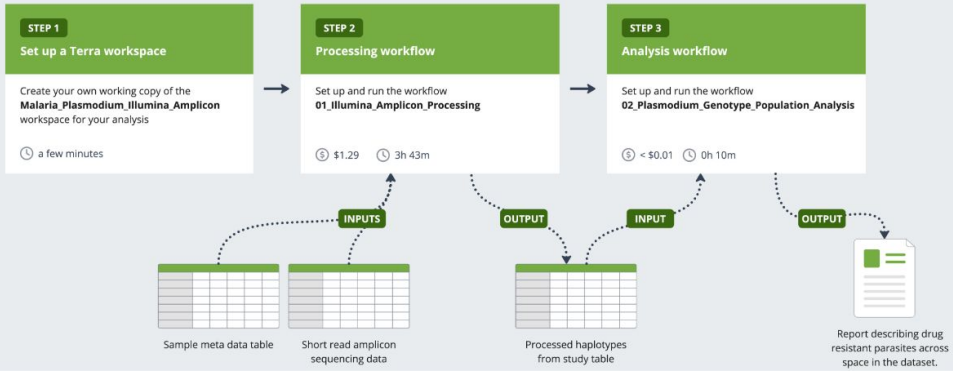

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pathogen genomics × malaria ×

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon

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Public Health Genomics WORKSPACES

Workspaces › malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon ›
Dashboard

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Settings
Clone
Share
Lock
Leave
Delete

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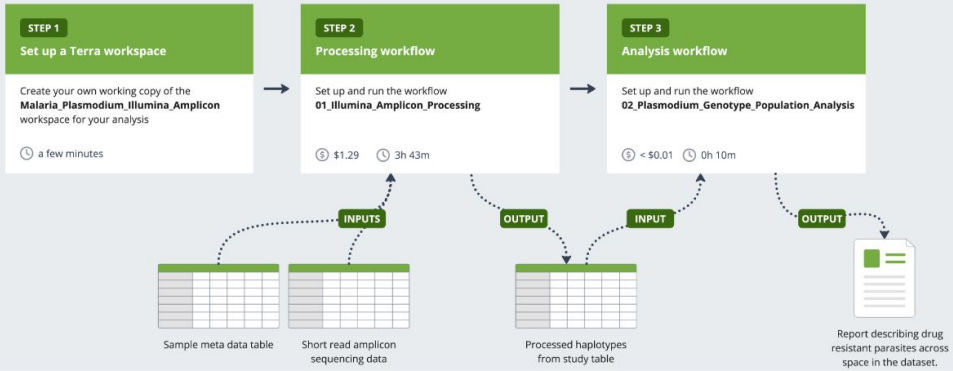

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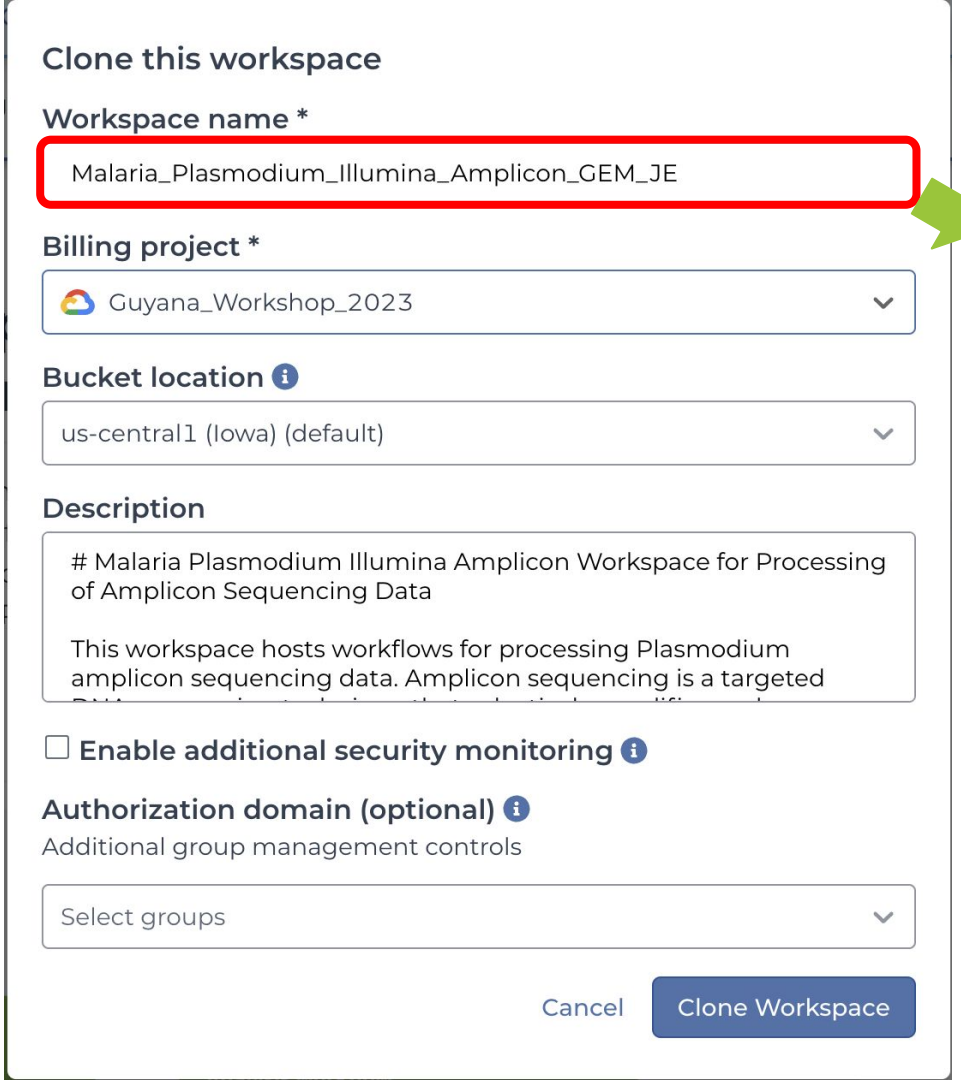
pathogen genomics × malaria ×



- **No two workspaces can have the same name.**
- **Give a unique name to your workspace.**
- **Recommendation _GEM_[INITIALS]**

Clone this workspace

Workspace name *

Malaria_Plasmodium_Illumina_Amplicon_GEM_JE

Billing project *

Guyana_Workshop_2023

Bucket location

us-central1 (Iowa) (default)

Description

Malaria Plasmodium Illumina Amplicon Workspace for Processing of Amplicon Sequencing Data

This workspace hosts workflows for processing Plasmodium amplicon sequencing data. Amplicon sequencing is a targeted

☐ **Enable additional security monitoring**

Authorization domain (optional)

Additional group management controls

Select groups

Cancel | Clone Workspace

Select Billing Project: gates-malaria.

Clone this workspace

Workspace name *

Malaria_Plasmodium_Illumina_Amplicon_GEM_JE

Billing project *

Guyana_Workshop_2023

Bucket location

us-central1 (Iowa) (default)

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Authorization domain (optional)

Additional group management controls

Select groups

Cancel | Clone Workspace

Cloning workspace

Please stand by...

Creating and provisioning your workspace.

This may take a few minutes.

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE

New Chrome available

Public Health Genomics WORKSPACES

Workspaces : Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE

Dashboard

This means the workspace was cloned successfully.

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

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Overview of Workflows

Process Illumina Amplicon sequencing data

STEP 1 Set up a Terra workspace
Create your own working copy of the **Malaria_Plasmodium_Illumina_Amplicon** workspace for your analysis
a few minutes

→

STEP 2 Processing workflow
Set up and run the workflow **01_Illumina_Amplicon_Processing**
$1.29 3h 43m

→

STEP 3 Analysis workflow
Set up and run the workflow **02_Plasmodium_Genotype_Population_Analysis**
< $0.01 0h 10m

INPUTS: Sample meta data table, Short read amplicon sequencing data

OUTPUT: Processed haplotypes from study table

INPUT

OUTPUT: Report describing drug resistant parasites across space in the dataset.

WORKSPACE INFORMATION

Last Updated	9/14/2024
Creation Date	9/14/2024
Access Level	Project Owner

CLOUD INFORMATION

OWNERS

TAGS

NOTIFICATIONS

Rate: $0.00 per hour

How to launch the data processing workflow

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/data

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Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

Search all tables

MAD4HatTeR_Mo... (50)

MAD4HatTeR_Moza... (2)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Edit | Open With... | Export | Settings | 0 rows selected | Advanced Search | Search

Rate: $0.00 per hour

MAD4H...	Country	Geo_Level	Latitude	Longitude
SRR26819135	Mozambique	NA	-25.58	32.35
SRR26819139	Mozambique	NA	-25.58	32.35
SRR26819141	Mozambique	NA	-25.58	32.35
SRR26819151	Mozambique	NA	-25.58	32.35
SRR26819200	Mozambique	NA	-25.58	32.35
SRR26819202	Mozambique	NA	-25.58	32.35
SRR26819206	Mozambique	NA	-25.58	32.35
SRR26819207	Mozambique	NA	-25.58	32.35
SRR26819208	Mozambique	NA	-25.58	32.35
SRR26819211	Mozambique	NA	-25.58	32.35
SRR26819212	Mozambique	NA	-25.58	32.35
SRR26819213	Mozambique	NA	-25.58	32.35
SRR26819214	Mozambique	NA	-25.58	32.35
SRR26819215	Mozambique	NA	-25.58	32.35

1 - 50 of 50 « ‹ 1 › » Items per page: 100

https://publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/data

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/data

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

Edit | Open With... | Export | Settings | 0 rows selected | Advanced Search | Search

Rate: $0.00 per hour

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moz... (2)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

MAD4H...	MAD4HatTeR_Mozambiques
MAD4HatTeR_...	SRR26819135, SRR26... (4 entities)
MAD4HatTeR_...	SRR26819135, SRR2... (50 entities)

1 - 2 of 2 « ‹ 1 › » Items per page: 100

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/data

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moza... (2)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Edit | Download TSV | 0 rows selected

Search

Rate: $0.00 per hour

Key	Value	Description
BackUp_ASVs	M4H_Mozambique_DS_TestSet6_n32_1-32.xlsx	MAD4HAtter BackUp ASVs
ForwardPrimersMAD4Hatter	MAD4HatTer_fwd_v4.2.fasta	Forward primers for MAD4Hatter Amplicon panel
MAD4Hatter_BED	MAD4Hatter_bed.bed	MAD4Hatter BED file
MAD4Hatter_Mozambique_Metadata	MAD4Hatter_Mozambique_Metadata.csv	Metadata for MAD4Hatter Mozambique
Markers	MAD4HAtTer_v4_MarkersTable.csv	Markers of resistance for Genotyping Analysis
PlasmoDB-59_Pfalciparum3D7Genome	PlasmoDB-59_Pfalciparum3D7_Genome.fasta	Genome of Pfalciparum3D7 in fasta format
PlasmoDB-59_Pfalciparum3D7Gff	PlasmoDB-59_Pfalciparum3D7.gff	Gff file of Pfalciparum3D7
reference_genomes	PkPfPmPoPv.fasta	Reference genomes file
ReferenceSeq_MAD4Hatter	MAD4HatTer_refseqs_v4.fasta	Reference sequences for MAD4HAtter amplicon panel
ReversePrimersMAD4Hatter	MAD4HatTer_rvs_v4.2.fasta	Reverse primers for MAD4Hatter Amplicon panel
Selected_Checkboxes	selected_checkboxes.csv	Selected data points
WHO_Drug_Resistance_Markers	drug_alleles_who.csv	WHO Markers of resistance for Genotyping Analysis

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon/workflows

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Public Health Genomics WORKSPACES

Workspaces › malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon ›
Workflows

DASHBOARD DATA ANALYSES WORKFLOWS SUBMISSION HISTORY

Rate: $0.00 per hour

WORKFLOWS

SEARCH WORKFLOWS Sort By: Alphabetical

Find a Workflow

01_Illumina_Amplicon_Processing
V. main
Source: Dockstore

02_Plasmodium_Genotype_Population_Analysis
V. main
Source: Dockstore

03_Plasmodium_Genotyping_PCA
V. main
Source: Dockstore

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/workflows/malaria-featured-workspaces/01_Illumina_Amplicon_Processing

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE › workflows ›
01_Illumina_Amplicon_Processing

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Back to list

01_Illumina_Amplicon_Processing

Version: main

Source: github.com/broadinstitute/malaria/AmpSeq:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data — No data selected

- ☑ Use call caching
- ☐ Use reference disks
- ☐ Ignore empty outputs
- ☐ Delete intermediate outputs
- ☐ Retry with more memory
- ☐ Resource monitoring

SCRIPT | INPUTS | OUTPUTS | Run Analysis

Rate: $0.00 per hour

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
ampseq	fastq1s	Array[File]	this.MAD4HatTeR_Mozambiques.fastq1
ampseq	fastq2s	Array[File]	this.MAD4HatTeR_Mozambiques.fastq2
ampseq	forward_primers_file	File	workspace.ForwardPrimersMAD4Hatter
ampseq	reference_amplicons	File	workspace.ReferenceSeq_MAD4Hatter
ampseq	reference_genome	File	workspace.reference_genomes

https://dockstore.org/workflows/github.com/broadinstitute/malaria/AmpSeq:main

Select Data

Create a new MAD4HatTeR_Mozambique_set from selected MAD4HatTeR_Mozambiques

Choose specific MAD4HatTeR_Mozambique_sets to process

elect MAD4HatTeR_Mozambique_sets to process | Settings | 0 rows selected | Advanced Search | Search

MAD4H...	MAD4HatTeR_Mozambiques
MAD4HatTeR_...	SRR26819135, SRR2... (4 entities)
MAD4HatTeR_...	SRR26819135,... (50 entities)

Choose this box then click OK

1 - 2 of 2 | Items per page: 100

cel | OK

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/workflows/malaria-featured-workspaces/01_Illumina_Amplicon_Processing

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE › workflows ›
01_Illumina_Amplicon_Processing

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Back to list

01_Illumina_Amplicon_Processing

Version: main

Source: github.com/broadinstitute/malaria/AmpSeq:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data | 1 selected MAD4HatTeR_Mozambique_set

- ☑ Use call caching
- ☐ Use reference disks
- ☐ Ignore empty outputs
- ☐ Delete intermediate outputs
- ☐ Retry with more memory
- ☐ Resource monitoring

SCRIPT | INPUTS | OUTPUTS | Run Analysis

Rate: $0.00 per hour

This means you successfully chose your dataset.

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
ampseq	fastq1s	Array[File]	this.MAD4HatTeR_Mozambiques.fastq1
ampseq	fastq2s	Array[File]	this.MAD4HatTeR_Mozambiques.fastq2
ampseq	forward_primers_file	File	workspace.ForwardPrimersMAD4Hatter
ampseq	reference_amplicons	File	workspace.ReferenceSeq_MAD4Hatter
ampseq	reference_genome	File	workspace.reference_genomes

State of the default parameters as of June 6th/2025

Make sure the R1 and R2 files are referenced correctly

Task name ↓	Variable	Type	Input value
ampseq	fastq1s	Array[File]	this.Mad4Hatter_Mozambiques.fastq1
ampseq	fastq2s	Array[File]	this.Mad4Hatter_Mozambiques.fastq2
ampseq	panel_info	File	workspace.MAD4Hatter_PanelInfo
ampseq	reference_genome	File	workspace.Reference_Genomes
ampseq	sample_metadata	File	workspace.MAD4Hatter_Mozambique_Metadata

Make sure the correct Panel Info and reference genome is in use

Available panels and reference genomes as of June 6th/2025

Panel	Panel Info File	Reference Genome
Mad4Hatter	workspace.MAD4Hatter_PanelInfo	workspace.Reference_Genomes
AMPLseq	workspace.AMPLseq_PanelInfo	workspace.Reference_Genomes
SIMPLseq	workspace.SIMPLseq_PanelInfo	workspace.Reference_Genomes
SIMPLseq + CI	workspace.SIMPLseqCI_PanelInfo	workspace.Reference_Genomes
Spotmalaria	workspace.SpotMalaria_PanelInfo	workspace.Reference_Genomes
PvGTseq	workspace.PvGTSeq_PanelInfo	workspace.Reference_Genome_pvivax

State of the default parameters as of June 6th/2025

Task name ↓	Variable	Type	Input value
ampseq	fastq1s	Array[File]	this.Mad4Hatter_Mozambiques.fastq1
ampseq	fastq2s	Array[File]	this.Mad4Hatter_Mozambiques.fastq2
ampseq	panel_info	File	workspace.MAD4Hatter_PanelInfo
ampseq	reference_genome	File	workspace.Reference_Genomes
ampseq	sample_metadata	File	workspace.MAD4Hatter_Mozambique_Metadata

Provide metadata in the correct format

Format of the metadata file

Metadata must be provided in a CSV file with the following four mandatory fields columns (extra columns may be provided).

- Sample_id -> Name of the sample including the _S* suffix.
- Country -> The country of origin of the sample. “Placeholder” can be used if the country is unknown.
- Latitude and Longitude -> Numeric coordinates.

The metadata may contain more samples than found in the dataset, but not less.

```
Sample_id,Country,Latitude,Longitude
N1928295_4_S22,Placeholder,0,0
N1933388_5_S115,Placeholder,0,0
N1933391_5_S197,Placeholder,0,0
N1933401_1_S120,Placeholder,0,0
N1933402_8_S194,Placeholder,0,0
N1933403_5_S54,Placeholder,0,0
N1933568_1_S57,Placeholder,0,0
N1933569_8_S60,Placeholder,0,0
N1933571_1_S116,Placeholder,0,0
```

SIMPLseq + CI (special case 1)

Additional primer files must be provided to execute the SIMPLseq + CI workflows as shown below.

Barcodes index: A comma separated file with three columns corresponding to Filename,Forward_primer,Reverse_primer.

Primer files: A special primer file containing primer with Inline Barcodes.

ampseq	*barcodes_index*	*File*	workspace_Barcodes_index
ampseq	*forward_primers_file*	*File*	workspace.SIMPLseqCI_forward_primers
ampseq	*path_to_snv*	*File*	Optional
ampseq	*reference_amplicons*	*File*	Optional
ampseq	*reference_amplicons_2*	*File*	Optional
ampseq	*reverse_primers_file*	*File*	workspace.SIMPLseqCI_reverse_primers

Barcodes_index

```
sample_id,Forward,Reverse
0276C-UV1_S1,CGACTTGG,TACCGGAC
Placeholder_1,GTGGCTGCT,TACCGGAC
Placeholder_2,GCAGTTACAG,TACCGGAC
0371R-enroll_S2,CACGATGACTA,TACCGGAC
Placeholder_4,CGTGGTAA,TACCGGAC
0419X-Day98_S3,ATAATTCTG,TACCGGAC
0291V-Day42_S4,CTTGGCAT,TACCGGAC
0407H-Day140_S5,ATGTTGTACAG,TACCGGAC
Placeholder_8,CTGGTTCA,TACCGGAC
Placeholder_9,GTCCATATG,TACCGGAC
0242N-Day112_S6,GCGAGTTGAC,TACCGGAC
0306P-Day154_S7,GCCCTCCGTAC,TACCGGAC
0291V-Day154_S8,CGACTTGG,GTGGCTGCT
Negative-CIS43LS1_S9,GTGGCTGCT,GTGGCTGCT
0272X-Day112_S10,GCAGTTACAG,GTGGCTGCT
Placeholder_15,CACGATGACTA,GTGGCTGCT
Placeholder_16,CGTGGTAA,GTGGCTGCT
0387K-Day42_S11,ATAATTCTG,GTGGCTGCT
0412Q-Day126_S12,CTTGGCAT,GTGGCTGCT
0226T-UV1_S13,ATGTTGTACAG,GTGGCTGCT
0321F-enroll_S14,CTGGTTCA,GTGGCTGCT
```

Please refer to the files in the workspace for further details

Primers with CIs

```
>CSP
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTAAGGAACAAGAAGGATAATACCA
>TRAP
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCCAGCACATGCGAGTAAAG
>SERA8
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACGAATTGTATTTCTCCTAATATGTGCA
>WD
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGTCTACACGCGTATTTCATAGCT
>SURFIN
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCCAAAAAGGAGATCAGCAAAG
>KELT_A1
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGACTTGGAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A2
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTGGCTGCTAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A3
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAGTTACAGAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A4
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCACGATGACTAAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A5
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGTGGTAAAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A6
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATAATTCTGAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A7
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTTGGCATAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A8
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATGTTGTACAGAGAAAATAACAAGAGAATCAGGGCAA
>KELT_A9
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGGTTCAAGAAAATAACAAGAGAATCAGGGCAA
```

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/workflows/malaria-featured-workspaces/01_Illumina_Amplicon_Processing

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE › workflows ›
01_Illumina_Amplicon_Processing

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Back to list

01_Illumina_Amplicon_Processing

Version: main

Source: github.com/broadinstitute/malaria/AmpSeq:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data — 1 selected MAD4HatTeR_Mozambique_set

- ☑ Use call caching
- ☐ Use reference disks
- ☐ Ignore empty outputs
- ☐ Delete intermediate outputs
- ☐ Retry with more memory
- ☐ Resource monitoring

Rate: $0.00 per hour

SCRIPT | INPUTS | OUTPUTS | Run Analysis

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
ampseq	fastq1s	Array[File]	this.MAD4HatTeR_Mozambiques.fastq1
ampseq	fastq2s	Array[File]	this.MAD4HatTeR_Mozambiques.fastq2
ampseq	forward_primers_file	File	workspace.ForwardPrimersMAD4Hatter
ampseq	reference_amplicons	File	workspace.ReferenceSeq_MAD4Hatter
ampseq	reference_genome	File	workspace.reference_genomes

Confirm launch

Output files will be saved as workspace data in:

us-central1 (Iowa)

Running workflows will generate cloud charges.

How much does my workflow cost?

Set up budget alert

Describe your submission (optional):

Enter comment for the submission

This will launch **1** analysis.

Cancel Launch

Add a comment if wanted.

Click Launch

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/aefe4cc8-8d60-45b7-ae66-3af1c136b088

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission aefe4cc8-8d60-45b7-ae66-3af1c136b088

Rate: $0.00 per hour

Workflow Statuses
Submitted: 1

Workflow Configuration
malaria-featured-workspaces/01_Illumina_Amplicon_P...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 2:34 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
aefe4cc8-8d60-45b7-ae66-3af1c136b088

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 2:34 PM	Launching	N/A			

Downsampling feature

Pre set to True

t_001_validate_fastqs	*use_validated_fastqs*	*Boolean*	Optional
t_002_cutadapters	*downsample_fraction*	*Int*	40000

Preset to 40000. Set to 0 to avoid downsampling.

How to monitor your process

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/aefe4cc8-8d60-45b7-ae66-3af1c136b088

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Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission aefe4cc8-8d60-45b7-ae66-3af1c136b088

Rate: $0.00 per hour

Workflow Statuses
Succeeded: 1

Workflow Configuration
malaria-featured-workspaces/01_Illumina_Amplicon_P...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 2:34 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
aefe4cc8-8d60-45b7-ae66-3af1c136b088

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 2:56 PM	Succeeded	N/A		cf614e79-8738-4386-b2c3-243d0002041a	

This may look different if your process hasn't finished.

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/aefe4cc8-8d60-45b7-ae66-3af1c136b088

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission aefe4cc8-8d60-45b7-ae66-3af1c136b088

Rate: $0.00 per hour

Workflow Statuses
Succeeded: 1

Workflow Configuration
malaria-featured-workspaces/01_Illumina_Amplicon_P...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 2:34 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
aefe4cc8-8d60-45b7-ae66-3af1c136b088

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

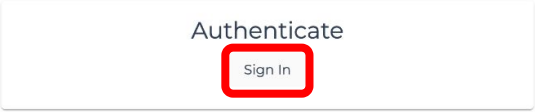
Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 2:56 PM	Succeeded	N/A		cf614e79-8738-4386-b2c3-243d0002041a	

Job Manager



You may be asked to authenticate again.

Job Manager

job-manager.dsde-prod.broadinstitute.org/jobs/abe4d8f1-92e2-4d2c-8ae5-4b546

To exit full screen, press (fn) F

New Chrome available

Job Manager

SIGN OUT

ampseq

ID: abe4d8f1-92e2-4d2c-8ae5-4b54676a2796

workspace-id: **27bd93a4-1599-45a8-a11e-6484605e407b** submission-id: **5f661457-a97f-4a7c-a6f6-b2e001ad3747**

Status: Succeeded

Tasks: 4 succeeded, 0 failed, 0 currently being processed

Submitted: Sep 14, 3:54 PM

Started: Sep 14, 3:54 PM

Ended: Sep 14, 4:36 PM (0h 42m)

LIST VIEW | INPUTS | OUTPUTS | LABELS | TIMING DIAGRAM

Job Summary

Task Name	Status	Start	Duration	Inputs	Outputs	Links	Attempts
prepare_files	✓	Sep 14, 3:57 PM	0h 4m				2
amplicon_no_demultiplexi...	✓	Sep 14, 4:02 PM	0h 17m				1
amplicon_denoising	✓	Sep 14, 4:19 PM	0h 12m				1
asv_filtering	✓	Sep 14, 4:31 PM	0h 4m				1

Access to log and Google Bucket

How to launch the genotyping workflow

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/aefe4cc8-8d60-45b7-ae66-3af1c136b088

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission aefe4cc8-8d60-45b7-ae66-3af1c136b088

Rate: $0.00 per hour

Workflow Statuses
Succeeded: 1

Workflow Configuration
malaria-featured-workspaces/01_Illumina_Amplicon_P...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 2:34 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
aefe4cc8-8d60-45b7-ae66-3af1c136b088

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 2:56 PM	Succeeded	N/A		cf614e79-8738-4386-b2c3-243d0002041a	

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/data

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moz... (2)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Edit | Open With... | Export | Settings | 0 rows selected | Advanced Search | Search

Rate: $0.00 per hour

MAD4H...	MAD4HatTeR_Mozambiques	ampseq_object_f
MAD4HatTeR_...	SRR26819135, SRR2... (4 entities)	MAD4HatTeR_Mozambique_Minim...
MAD4HatTeR_...	SRR26819135, SRR... (50 entities)	

Result is stored in a new column

1 - 2 of 2 « ‹ 1 › » Items per page: 100

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon/workflows

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › malaria-featured-workspaces/Malaria_Plasmodium_Illumina_Amplicon ›
Workflows

DASHBOARD DATA ANALYSES WORKFLOWS SUBMISSION HISTORY

Rate: $0.00 per hour

WORKFLOWS

SEARCH WORKFLOWS Sort By: Alphabetical

Find a Workflow

01_Illumina_Amplicon_Processing
V. main
Source: Dockstore

02_Plasmodium_Genotype_Population_Analysis
V. main
Source: Dockstore

03_Plasmodium_Genotyping_PCA
V. main
Source: Dockstore

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/workflows/malaria-featured-workspaces/02_Plasmodium_Genotype_Popu...

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE › workflows ›
02_Plasmodium_Genotype_Population_Analysis

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Back to list

02_Plasmodium_Genotype_Population_Analysis

Version: main

Source: github.com/broadinstitute/malaria/MHap:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data — No data selected

- ☑ Use call caching
- ☐ Use reference disks
- ☐ Ignore empty outputs
- ☐ Delete intermediate outputs
- ☐ Retry with more memory
- ☐ Resource monitoring

SCRIPT | INPUTS | OUTPUTS | Run Analysis

Rate: $0.00 per hour

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name	Variable	Type	Input value
report_layouting	ampseq_excelfile	File	this.ampseq_object_f
report_layouting	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
report_layouting	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
report_layouting	reference_alleles	File	workspace.WHO_Drug_Resistance_Markers
report_layouting	selected_checkboxes	File	workspace.Selected_Checkboxes

Select Data

Create a new MAD4HatTeR_Mozambique_set from selected MAD4HatTeR_Mozambiques

Choose specific MAD4HatTeR_Mozambique_sets to process

elect MAD4HatTeR_Mozambique_sets to process Settings 1 row selected Advanced Search Search

MAD4H...	ampseq_object_f	MAD4HatTeR_Mozambiques
MAD4HatTeR_...	MAD4HatTeR_Mozambique_Minim...	SRR26819135, SRR2... (4 entities)
MAD4HatTeR_...		SRR26819135, SRR... (50 entities)

Choose this box then click OK

1 - 2 of 2 Items per page: 100

cel OK

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/workflows/malaria-featured-workspaces/02_Plasmodium_Genotype_Popu...

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE › workflows ›
02_Plasmodium_Genotype_Population_Analysis

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Back to list

02_Plasmodium_Genotype_Population_Analysis

Version: main

Source: github.com/broadinstitute/malaria/MHap:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data | 1 selected MAD4HatTeR_Mozambique_set

- ☑ Use call caching
- ☐ Use reference disks
- ☐ Ignore empty outputs
- ☐ Delete intermediate outputs
- ☐ Retry with more memory
- ☐ Resource monitoring

SCRIPT • INPUTS • OUTPUTS • Run Analysis

Rate: $0.00 per hour

This means you successfully choose your dataset.

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
report_layouting	ampseq_excelfile	File	this.ampseq_object_f
report_layouting	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
report_layouting	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
report_layouting	reference_alleles	File	workspace.WHO_Drug_Resistance_Markers
report_layouting	selected_checkboxes	File	workspace.Selected_Checkboxes

State of the default parameters as of June 6th/2025

Task name ↓	Variable	Type	Input value
report_layouting	ampseq_excelfile	File	this.ampseq_object_f
report_layouting	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
report_layouting	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
report_layouting	reference_alleles	File	workspace.WHO_Drug_Resistance_Markers
report_layouting	selected_checkboxes	File	workspace.Selected_Checkboxes

Selected checkboxes

Selected checkboxes is a file used to parametrize sample selection during the reporting workflow

```
Selected_Checkboxes
gene_names__
DHFR
MDR1
CRT
DHPS
Kelch13
gene_ids__
PF3D7_0417200
PF3D7_0523000
PF3D7_0709000
PF3D7_0810800
PF3D7_1343700
Country__
Placeholder
Run__
Run1
```

Genes to be displayed

The categories must coincide with columns provided in the metadata. The category must be indicated by providing the name followed by two underscores (__).

Categories

At the least, one category present in the metadata must be provided. The category Run is optional.

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/workflows/malaria-featured-workspaces/02_Plasmodium_Genotype_Popu...

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE › workflows ›
02_Plasmodium_Genotype_Population_Analysis

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Back to list

02_Plasmodium_Genotype_Population_Analysis

Version: main

Source: github.com/broadinstitute/malaria/MHap:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data — 1 selected MAD4HatTeR_Mozambique_set

- ☑ Use call caching
- ☐ Use reference disks
- ☐ Ignore empty outputs
- ☐ Delete intermediate outputs
- ☐ Retry with more memory
- ☐ Resource monitoring

Rate: $0.00 per hour

SCRIPT | INPUTS | OUTPUTS | Run Analysis

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
report_layouting	ampseq_excelfile	File	this.ampseq_object_f
report_layouting	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
report_layouting	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
report_layouting	reference_alleles	File	workspace.WHO_Drug_Resistance_Markers
report_layouting	selected_checkboxes	File	workspace.Selected_Checkboxes

Confirm launch

Output files will be saved as workspace data in:

us-central1 (Iowa)

Running workflows will generate cloud charges.

How much does my workflow cost?

Set up budget alert

Describe your submission (optional):

Enter comment for the submission

Add a comment if wanted.

This will launch **1** analysis.

Cancel Launch

Click Launch

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/fb51c352-9356-406a-9178-1e03a2c5280f

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission fb51c352-9356-406a-9178-1e03a2c5280f

Rate: $0.00 per hour

Workflow Statuses
Submitted: 1

Workflow Configuration
malaria-featured-workspaces/02_Plasmodium_Genoty...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 3:01 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
fb51c352-9356-406a-9178-1e03a2c5280f

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 3:01 PM	Queued	N/A			

Select Data

Create a new MAD4HatTeR_Mozambique_set from selected MAD4HatTeR_Mozambiques

Choose specific MAD4HatTeR_Mozambique_sets to process

elect MAD4HatTeR_Mozambique_sets to process Settings 1 row selected Advanced Search Search

MAD4H...	ampseq_object_f	MAD4HatTeR_Mozambiques
MAD4HatTeR_...	MAD4HatTeR_Mozambique_Minim...	SRR26819135, SRR2... (4 entities)
MAD4HatTeR_...		SRR26819135, SRR... (50 entities)

Choose this box then click OK

1 - 2 of 2 Items per page: 100

cel OK

How to launch the connectivity and COI workflow - Not exposed as of June6th/2025

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/aefe4cc8-8d60-45b7-ae66-3af1c136b088

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission aefe4cc8-8d60-45b7-ae66-3af1c136b088

Rate: $0.00 per hour

Workflow Statuses
Succeeded: 1

Workflow Configuration
malaria-featured-workspaces/01_Illumina_Amplicon_P...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 2:34 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
aefe4cc8-8d60-45b7-ae66-3af1c136b088

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 2:56 PM	Succeeded	N/A		cf614e79-8738-4386-b2c3-243d0002041a	

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/data

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moz... (2)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Edit | Open With... | Export | Settings | 0 rows selected | Advanced Search | Search

Rate: $0.00 per hour

	MAD4H...	MAD4HatTeR_Mozambiques	ampseq_object_f
	MAD4HatTeR_...	SRR26819135, SRR2... (4 entities)	MAD4HatTeR_Mozambique_Minim...
	MAD4HatTeR_...	SRR26819135, SRR... (50 entities)	

Result is stored in a new column

1 - 2 of 2 « ‹ 1 › » Items per page: 100

Terra WORKSPACES

Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Clone › workflows ›
03_Plasmodium_Genotyping_PCA

DASHBOARD | DATA | ANALYSES | WORKFLOWS | SUBMISSION HISTORY

Rate: $0.00 per hour

← Back to list

03_Plasmodium_Genotyping_PCA

Version: main

Source: github.com/broadinstitute/malaria/PCA:main

Synopsis:

No documentation provided

○ Run workflow with inputs defined by file paths

◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data | No data selected

Runtime options:

- [x] Use call caching
- [ ] Use reference disks
- [ ] Ignore empty outputs
- [ ] Delete intermediate outputs
- [ ] Retry with more memory
- [ ] Resource monitoring

SCRIPT • • INPUTS • • OUTPUTS • • Launch

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
plot_pca	ampseq_excelfiles	Array[File]	this.ampseq_obj
plot_pca	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
plot_pca	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
plot_pca	selected_checkboxes	File	workspace.Selected_Checkboxes
plot_pca	*preserve_samples*	*File*	workspace.Preserve_Samples
plot_pca	*reference_samples*	*File*	workspace.AMPLseq_RefWorldwideSet

WORKSPACES

Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Clone › workflows ›
03_Plasmodium_Genotyping_PCA

DASHBOARD | DATA | ANALYSES | WORKFLOWS | SUBMISSION HISTORY

Back to list

03_Plasmodium_Genotyping_PCA

Version: main

Source: github.com/broadinstitute/malaria/PCA:main

Synopsis:

No documentation provided

- Run workflow with inputs defined by file paths
- Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data | 1 selected MAD4HatTeR_Mozambique_set

Runtime options:

- [x] Use call caching
- [ ] Use reference disks
- [ ] Ignore empty outputs
- [ ] Delete intermediate outputs
- [ ] Retry with more memory
- [ ] Resource monitoring

SCRIPT • • INPUTS • • OUTPUTS • • Launch

Rate: $0.00 per hour

This means you successfully choose your dataset.

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name	Variable	Type	Input value
plot_pca	ampseq_excelfiles	Array[File]	this.ampseq_obj
plot_pca	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
plot_pca	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
plot_pca	selected_checkboxes	File	workspace.Selected_Checkboxes
plot_pca	*preserve_samples*	*File*	workspace.Preserve_Samples
plot_pca	*reference_samples*	*File*	workspace.AMPLseq_RefWorldwideSet
t_001_pca_process	*hap_color_palette*	*String*	Optional

Rate: **$0.00** per hour

← Back to list

03_Plasmodium_Genotyping_PCA

Version: main

Source: github.com/broadinstitute/malaria/PCA:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Moz...

Step 2

Select Data — 1 selected MAD4HatTeR_Mozambique_set

Runtime options:

- [x] Use call caching
- [ ] Use reference disks
- [ ] Ignore empty outputs
- [ ] Delete intermediate outputs
- [ ] Retry with more memory
- [ ] Resource monitoring

SCRIPT • • INPUTS • • OUTPUTS • • Launch

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
plot_pca	ampseq_excelfiles	Array[File]	this.ampseq_obj
plot_pca	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
plot_pca	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
plot_pca	selected_checkboxes	File	workspace.Selected_Checkboxes
plot_pca	*preserve_samples*	*File*	workspace.Preserve_Samples
plot_pca	*reference_samples*	*File*	workspace.AMPLseq_RefWorldwideSet
t_001_pca_process	*hap_color_palette*	*String*	Optional

app.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Teaching_Clone/workflows/malaria-featured-workspa...

Finish update

WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Teaching_Clone › workflows ›
02_Plasmodium_Genotype_PCA_Analysis

DASHBOARD | DATA | ANALYSES | WORKFLOWS | SUBMISSION HISTORY

Back to list

02_Plasmodium_Genotype_PCA_Analysis

Version: main

Source: github.com/broadinstitute/malaria/PCA:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Mo...

Step 2

Select Data | No data selected

Runtime options:

- [x] Use call caching
- [ ] Use reference disks
- [ ] Ignore empty outputs
- [ ] Delete intermediate outputs
- [ ] Retry with more memory
- [ ] Resource monitoring

SCRIPT | INPUTS | OUTPUTS | Launch

Rate: $0.00 per hour

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name	Variable	Type	Input value
plot_pca	ampseq_excelfiles	Array[File]	this.ampseq_obj
plot_pca	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
plot_pca	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
plot_pca	selected_checkboxes	File	workspace.Selected_Checkboxes_Worldwide_Level2
plot_pca	*preserve_samples*	*File*	Optional
plot_pca	*reference_samples*	*File*	workspace.AMPLseq_RefWorldwideSet

Select reference sample set (Optional).

t_001_pca_process	*metadata_variable1_name*	*String*	"Subnational_level2"

Select the level of the analysis. Default is country.

app.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Teaching_Clone/workflows/malaria-featured-workspa...

Finish update

WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Teaching_Clone › workflows ›
02_Plasmodium_Genotype_PCA_Analysis

DASHBOARD | DATA | ANALYSES | WORKFLOWS | SUBMISSION HISTORY

Back to list

02_Plasmodium_Genotype_PCA_Analysis

Version: main

Source: github.com/broadinstitute/malaria/PCA:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Mo...

Step 2

Select Data | No data selected

Runtime options:

- [x] Use call caching
- [ ] Use reference disks
- [ ] Ignore empty outputs
- [ ] Delete intermediate outputs
- [ ] Retry with more memory
- [ ] Resource monitoring

SCRIPT | INPUTS | OUTPUTS | Launch

Rate: $0.00 per hour

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
plot_pca	ampseq_excelfiles	Array[File]	this.ampseq_obj
plot_pca	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
plot_pca	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
plot_pca	selected_checkboxes	File	workspace.Selected_Checkboxes_Worldwide_Level2
plot_pca	*preserve_samples*	*File*	Optional
plot_pca	*reference_samples*	*File*	workspace.AMPLseq_RefWorldwideSet

Select filter criteria

Selected_Checkboxes

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

☐	ReversePrimersPvGTseq	PvGTSeq249_rvs.fasta	Reverse primers for PvGTseq Amplicon panel
☐	Selected_Checkboxes	selected_checkboxes.csv	Selected data points
☐	Selected_Checkboxes_Country_Level	selected_checkboxes_southamerica.csv	Selected data points country level
☐	Selected_Checkboxes_ExtMethod_Level2	selected_checkboxes_extmethods_level2.csv	Selected data points country level for extmethod
☐	Selected_Checkboxes_Gates_Level	selected_checkboxes_gates_level2.csv	Selected data points country level for gates
☐	Selected_Checkboxes_SouthAmerica_Country_Level	selected_checkboxes_southamerica.csv	Selected data points country level for SouthAmerica
☐	Selected_Checkboxes_SouthAmerica_Level2	selected_checkboxes_southamerica_level2.csv	Selected data points subnational level for SouthAmerica
☐	Selected_Checkboxes_Worldwide_Country_Level	selected_checkboxes_worldwide.csv	Selected data points country level for Worldwide
☐	Selected_Checkboxes_Worldwide_Level2	selected_checkboxes_worldwide_level2.csv	Selected data points subnational level for Worldwide

File Details

Filename

selected_checkboxes_extmethods_level2.csv

File size

237 B

View this file in the Google Cloud Storage Browser

Download For < $0.01*

Terminal download command

Download to:

- Current Directory
- New Subdirectory

```
gcloud storage cp 'gs://broad-malaria-public/BogotaTraining/selected_che
```

> More Information

* Estimated. Download cost may be higher in China or Australia.

File Preview

```
Selected_Checkboxes
gene_names__
DHFR
MDR1
CRT
DHPS
Kelch13
gene_ids__
PF3D7_0417200
PF3D7_0523000
PF3D7_0709000
PF3D7_0810800
PF3D7_1343700
Subnational_level2__
Buenaventura
Guapi
Imputed_Colombia
Quibdo
Rio Quito
Tumaco
Run__
Run1
Ref
```

Done

app.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Teaching_Clone/workflows/malaria-featured-workspa...

Finish update

WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_Bogota_Teaching_Clone › workflows ›
02_Plasmodium_Genotype_PCA_Analysis

DASHBOARD | DATA | ANALYSES | WORKFLOWS | SUBMISSION HISTORY

Back to list

02_Plasmodium_Genotype_PCA_Analysis

Version: main

Source: github.com/broadinstitute/malaria/PCA:main

Synopsis:

No documentation provided

- ○ Run workflow with inputs defined by file paths
- ◉ Run workflow(s) with inputs defined by data table

Step 1

Select data table: MAD4HatTeR_Mo...

Step 2

Select Data | No data selected

Runtime options:

- ☑ Use call caching
- ☐ Use reference disks
- ☐ Ignore empty outputs
- ☐ Delete intermediate outputs
- ☐ Retry with more memory
- ☐ Resource monitoring

SCRIPT | INPUTS | OUTPUTS | Launch

Rate: $0.00 per hour

Hide optional inputs

Download json | Drag or click to upload json | Clear inputs | SEARCH INPUTS

Task name ↓	Variable	Type	Input value
plot_pca	ampseq_excelfiles	Array[File]	this.ampseq_obj
plot_pca	ref_fasta	File	workspace.PlasmoDB-59_Pfalciparum3D7Genome
plot_pca	ref_gff	File	workspace.PlasmoDB-59_Pfalciparum3D7Gff
plot_pca	selected_checkboxes	File	workspace.Selected_Checkboxes_Worldwide_Level2
plot_pca	*preserve_samples*	*File*	Optional
plot_pca	*reference_samples*	*File*	workspace.AMPLseq_RefWorldwideSet

Select list of samples to preserve (Optional).

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moza... (2)

reference_genomes

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

PlasmoDB-59_Pfalciparum3D7Genome	PlasmoDB-59_Pfalciparum3D7_Genome.fasta	Genome of Pfalciparum3D7 in fasta format	
PlasmoDB-59_Pfalciparum3D7Gff	PlasmoDB-59_Pfalciparum3D7.gff	Gff file of Pfalciparum3D7	
Preserve_all_samples	preserve_samples_all.csv	All samples	
Preserve_exmethod_samples	preserve_samples_extmethod.csv	ExMethod Samples	
Preserve_exmethod_samples_nonimputed	preserve_samples_extmethod_nonimputed.csv	ExMethod Samples Non imputed	
Preserve_gates_samples	preserve_samples_gates.csv	Gates Samples	
Preserve_worldwide_samples	preserve_samples_worldwide.csv	Worldwide Samples	
reference_genomes	PkPfPmPoPv.fasta	Reference genomes file	
ReferenceSeq_MAD4Hatter	MAD4HatTer_refseqs_v4.fasta	Reference sequences for MAD4HAtter amplicon panel	
ReferenceSeq_PvGTseq	PvGTSeq249_refseqs.fasta	Reference sequences PvGTseq for amplicon panel	
ReversePrimersAMPLseq	AMPLseq_rvs_v1.fasta	Reverse primers for AMPLseq Amplicon panel	

File Details

Filename

preserve_samples_extmethod_nonimputed.csv

File size

615 B

View this file in the Google Cloud Storage Browser

Download For < $0.01*

Terminal download command

Download to:

- Current Directory
- New Subdirectory

```
gcloud storage cp 'gs://broad-malaria-public/Workspace_Data/preserve_sam
```

> More Information

* Estimated. Download cost may be higher in China or Australia.

File Preview

```
B11-CH
B11-KF
B11-PL
B11-QIA
B12-CH
B12-KF
B12-PL
B12-QIA
B16-CH
B16-KF
B16-PL
B16-QIA
GA03-CH
GA03-KF
GA03-PL
GA03-QIA
GA32-CH
GA32-KF
GA32-PL
GA32-QIA
GA35-CH
GA35-KF
GA35-PL
GA35-QIA
GE32-CH
GE32-KF
GE32-PL
GE32-QIA
GE35-CH
```

Done

Confirm launch

Output files will be saved as workspace data in:

us-central1 (Iowa)

Running workflows will generate cloud charges.

How much does my workflow cost?

Set up budget alert

Describe your submission (optional):

Enter comment for the submission

Add a comment if wanted.

This will launch **1** analysis.

Cancel Launch

Click Launch

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/fb51c352-9356-406a-9178-1e03a2c5280f

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission fb51c352-9356-406a-9178-1e03a2c5280f

Rate: $0.00 per hour

Workflow Statuses
Submitted: 1

Workflow Configuration
malaria-featured-workspaces/02_Plasmodium_Genoty...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 3:01 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
fb51c352-9356-406a-9178-1e03a2c5280f

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 3:01 PM	Queued	N/A			

How to download output files

Malaria_Plasmodium_Illumina

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/job_history/fb51c352-9356-406a-9178-1e03a2c5280f

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Job History

DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY

Job History › Submission fb51c352-9356-406a-9178-1e03a2c5280f

Rate: $0.00 per hour

Workflow Statuses
Succeeded: 1

Workflow Configuration
malaria-featured-workspaces/02_Plasmodium_Genoty...

Submitted by
jamayaro@broadinstitute.org
Sep 14, 2024, 3:01 PM

Total Run Cost
N/A

Data Entity
MAD4HatTeR_Mozambique_Minimal
MAD4HatTeR_Mozambique_set

Submission ID
fb51c352-9356-406a-9178-1e03a2c5280f

Call Caching
Enabled

Comment

Delete Intermediate Outputs
Disabled

Use Reference Disks
Disabled

Retry with More Memory
Disabled

WORKFLOWS INPUTS OUTPUTS

Search workflows | Completion status | Download TSV

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
MAD4HatTeR_Mozambique_Minimal (MAD4HatTeR_Moza...	Sep 14, 2024, 3:07 PM	Succeeded	N/A		99454df3-e597-4c50-8723-b40e20e1c8cc	

Malaria_Plasmodium_Illumina | Job Manager

job-manager.dsde-prod.broadinstitute.org/jobs/99454df3-e597-4c50-8723-b40e20e1c8cc

New Chrome available

Job Manager SIGN OUT

report_layouting

ID: 99454df3-e597-4c50-8723-b40e20e1c8cc

workspace-id: **77fc09e7-98aa-42c5-a876-e65049608fe8** submission-id: **fb51c352-9356-406a-9178-1e03a2c5280f**

Status: Succeeded

Tasks: 1 succeeded, 0 failed, 0 currently being processed

Submitted: Today, 3:01 PM

Started: Today, 3:01 PM

Ended: Today, 3:06 PM (0h 5m)

LIST VIEW | INPUTS | OUTPUTS | LABELS | TIMING DIAGRAM

Job Summary

Task Name	Status	Start	Duration	Inputs	Outputs	Links	Attempts
report_layouting_process	✓	Today, 3:01 PM	0h 5m				1

Access to log and Google Bucket

Malaria_Plasmodium_Illumina | Job Manager

publichealth.terra.bio/#workspaces/Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE/data

New Chrome available

Public Health Genomics WORKSPACES

Workspaces › Guyana_Workshop_2023/Malaria_Plasmodium_Illumina_Amplicon_GEM_JE ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moz... (2)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Edit | Open With... | Export | Settings | 0 rows selected | Advanced Search | Search

Rate: $0.00 per hour

MAD4H...	MAD4HatTeR_Mozambiques	ampseq_object_f	drs_minimal_report_f
MAD4HatTeR_...	SRR26819135, SRR2... (4 entities)	MAD4HatTeR_Mozambique_Minim...	MHap_Profile_DRS_Minimal_Report...
MAD4HatTeR_...	SRR26819135, SRR... (50 entities)		

1 - 2 of 2 « ‹ 1 › » Items per page: 100

Result is stored in a new column

File Details

Filename

MHap_Profile_DRS_Minimal_Report.html

File size

1.45 MB

View this file in the Google Cloud Storage Browser

Download For < $0.01*

Terminal download command

Download to:

- Current Directory
- New Subdirectory

```
gcloud storage cp 'gs://fc-77fc09e7-98aa-42c5-a876-e6504
```

> More Information

* Estimated. Download cost may be higher in China or Australia.

File Preview

Code

- Show All Code
- Hide All Code

Genotyping Report

- Performance Summary
- Genotype Frequency
- Prevalence of resistant marker

Performance Summary

This report summarizes data processed with the 01_Illumina_Amplicon_Processing workflow. It details the performance of amplicons and samples and the occurrence of mutations associated with resistance to different antimalarial drugs.

```
samples_by_location
```

Done

Depending on the configuration of your computer, you may have to right click the Download button and click “Save Link as…”

Malaria_Plasmodium_Illumina | Genotyping Report | Job Manager

storage.googleapis.com/fc-77fc09e7-98aa-42c5-a876-e65049608fe8/submissions/fb51c352-9356-406a-9178-1e03a2c5280f/report_layouting/99454df3-e597-4c50-8723-b40e20e1...

New Chrome available

Genotyping Report

Code

- Performance Summary
- Genotype Frequency
- Prevalence of resistant marker

Performance Summary

This report summarizes data processed with the 01_Illumina_Amplicon_Processing workflow. It details the performance of amplicons and samples and the occurrence of mutations associated with resistance to different antimalarial drugs.

Show

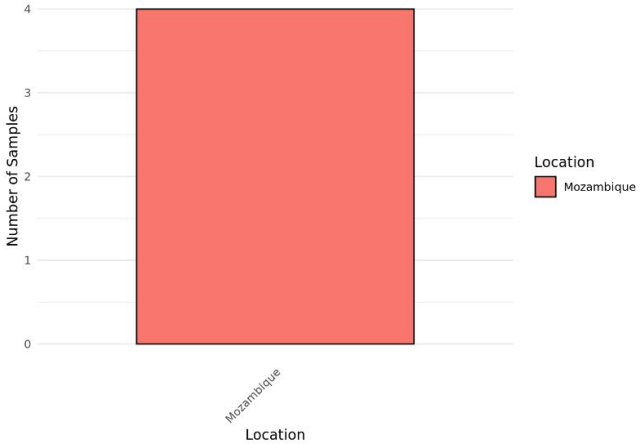


Figure 1: Number of samples per location that yielded usable data.

Show

Cost estimates

These are cost from previous runs.

Panel	Number of Samples	Workflow	Cost
AMPLseq	60 Samples	1	0.48
Mad4HAtter	50 Samples	1	0.27
SpotMalaria	4 Samples	1	0.03
SIMPLseq	5 Samples	1	0.04
SIMPLseq + CI	4 Samples	1	0.02
PvGTseq	5 Samples	1	0.11
AMPLseq	200 Samples (downsampling to 5000 reads)	1	1.79
AMPLseq	34 Samples	2	0.01
Mad4Hatter	50 Samples	2	0.01
SIMPLseq + CI	741 Samples	1	1.24

Alternative Log In Path

Terra for Public Health Genom

publichealth.terra.bio

New Chrome available

Public Health Genomics

Jorge Eduardo Amaya...

Workspaces

Library

Support

r Public Health Genomics

d-based data platform enabling pathogen
is in public health, clinical, and academic

erra

pository (Dockstore)

Image credit
Lydia Krasilnikova

Public Workspaces

Curated example workspaces to help users understand common pathogen genomic datasets and workflows.

Built on: 9/12/2024, 10:19:51 AM

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Terra for Public Health Genom

publichealth.terra.bio

New Chrome available

Public Health Genomics

Jorge Eduardo Amaya...

Workspaces

Library

Support

r Public Health Genomics

d-based data platform enabling pathogen
is in public health, clinical, and academic

erra

pository (Dockstore)

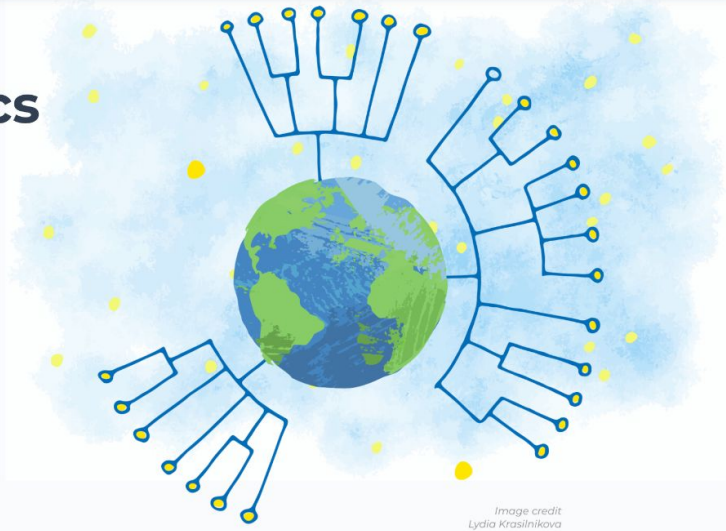

Image credit
Lydia Krasilnikova

Public Workspaces

Curated example workspaces to help users understand common pathogen genomic datasets and workflows.

Built on: 9/12/2024, 10:19:51 AM

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Workspaces

publichealth.terra.bio/#workspaces?tab=public&filter=Malaria_Plasmodium_Illumina_Amplicon

New Chrome available

Public Health Genomics WORKSPACES

Workspaces

Dedicated spaces for you and your collaborators to access and analyze data together. Learn more about workspaces.

Recently Viewed

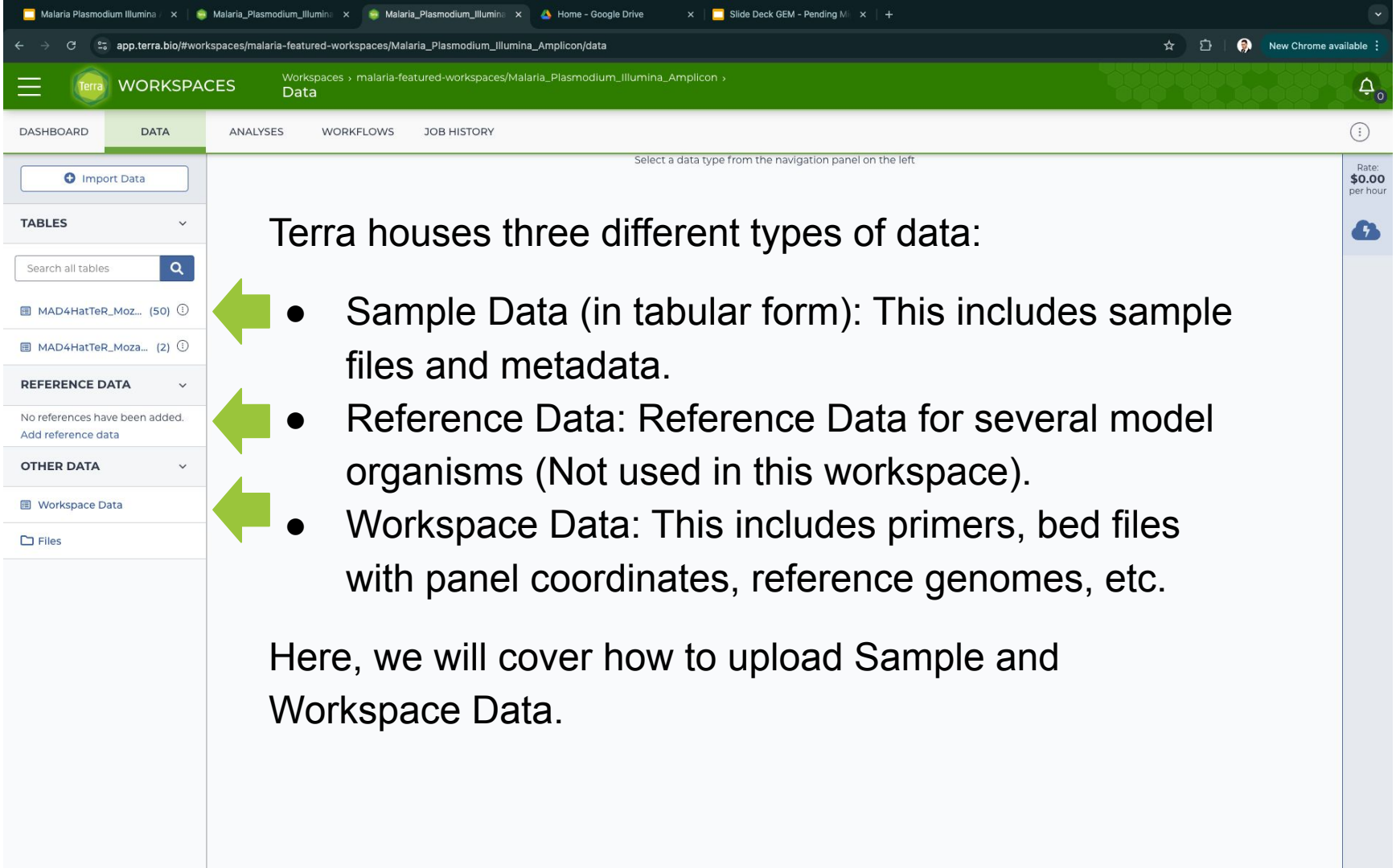
- Malaria_Plasmodium_Illumina_Amplicon_Jor... — *Viewed Sep 14, 2024, 2:13 PM*
- Malaria_Plasmodium_Illumina_Amplicon — *Viewed Sep 14, 2024, 1:28 PM*
- Malaria_Plasmodium_Illumina_Amplicon — *Viewed Sep 13, 2024, 12:54 PM*
- Malaria_Plasmodium_Illumina_Amplicon_Jor... — *Viewed Sep 11, 2024, 4:34 PM*

Malaria_Plasmodium_Illumina_Amplicon | Tags | Access levels | Billing project | Cloud platform

MY WORKSPACES (11) | NEW AND INTERESTING (0) | FEATU (0) | PUBLIC (1)

Name	Last Modified	Created By	Access Level
Malaria_Plasmodium_Illumina_Amplicon This workspace hosts workflows for processing Plasmodium amplicon sequencing data. Am...	Sep 14, 2024	cloreth@broadinstitute.org	Writer

Uploading data to Terra



Terra houses three different types of data:

- Sample Data (in tabular form): This includes sample files and metadata.
- Reference Data: Reference Data for several model organisms (Not used in this workspace).
- Workspace Data: This includes primers, bed files with panel coordinates, reference genomes, etc.

Here, we will cover how to upload Sample and Workspace Data.

Note: The workspace has been pre-populated data to ease familiarisation with Terra functionalities. The following steps to upload data will work the same in an empty or pre-populated workspaces. These functionalities also allow to upload new sets of samples on a workspace that has been used previously; therefore, there is no need to create new clones of the workspace as your number of samples grows!

Uploading Sample Data with the Data Uploader Application

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina

app.terra.bio/#workspaces/gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone

New Chrome available

WORKSPACES

Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone ›
Dashboard

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Rate: $0.00 per hour

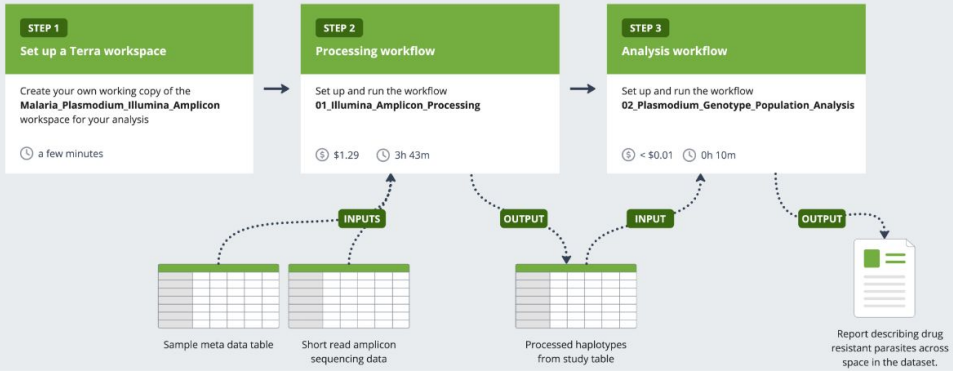
ABOUT THE WORKSPACE

Malaria Plasmodium Illumina Amplicon Workspace for Processing of Amplicon Sequencing Data

This workspace hosts workflows for processing Plasmodium amplicon sequencing data. Amplicon sequencing is a targeted DNA sequencing technique that selectively amplifies and sequences specific regions of interest within a genome. The workflow will perform detection of contamination resulting from improper sequencing protocols (in development), removal of erroneous SNPs calls caused by sequencing errors (denoising), and reporting of Drug Resistant Genotypes in the dataset. This is a standardized, panel agnostic workflow, capable of processing amplicon sequencing data produced with any amplicon panel.

Overview of Workflows

Process Illumina Amplicon sequencing data



WORKSPACE INFORMATION

Last Updated	9/24/2024
Creation Date	9/24/2024
Access Level	Project Owner

CLOUD INFORMATION

OWNERS

TAGS

NOTIFICATIONS

Malaria Plasmodium Illumina / Malaria_Plasmodium_Illumina

app.terra.bio/#workspaces/gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone/data

New Chrome available

WORKSPACES

Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

No tables have been uploaded.
Upload TSV

REFERENCE DATA

No references have been added.
Add reference data

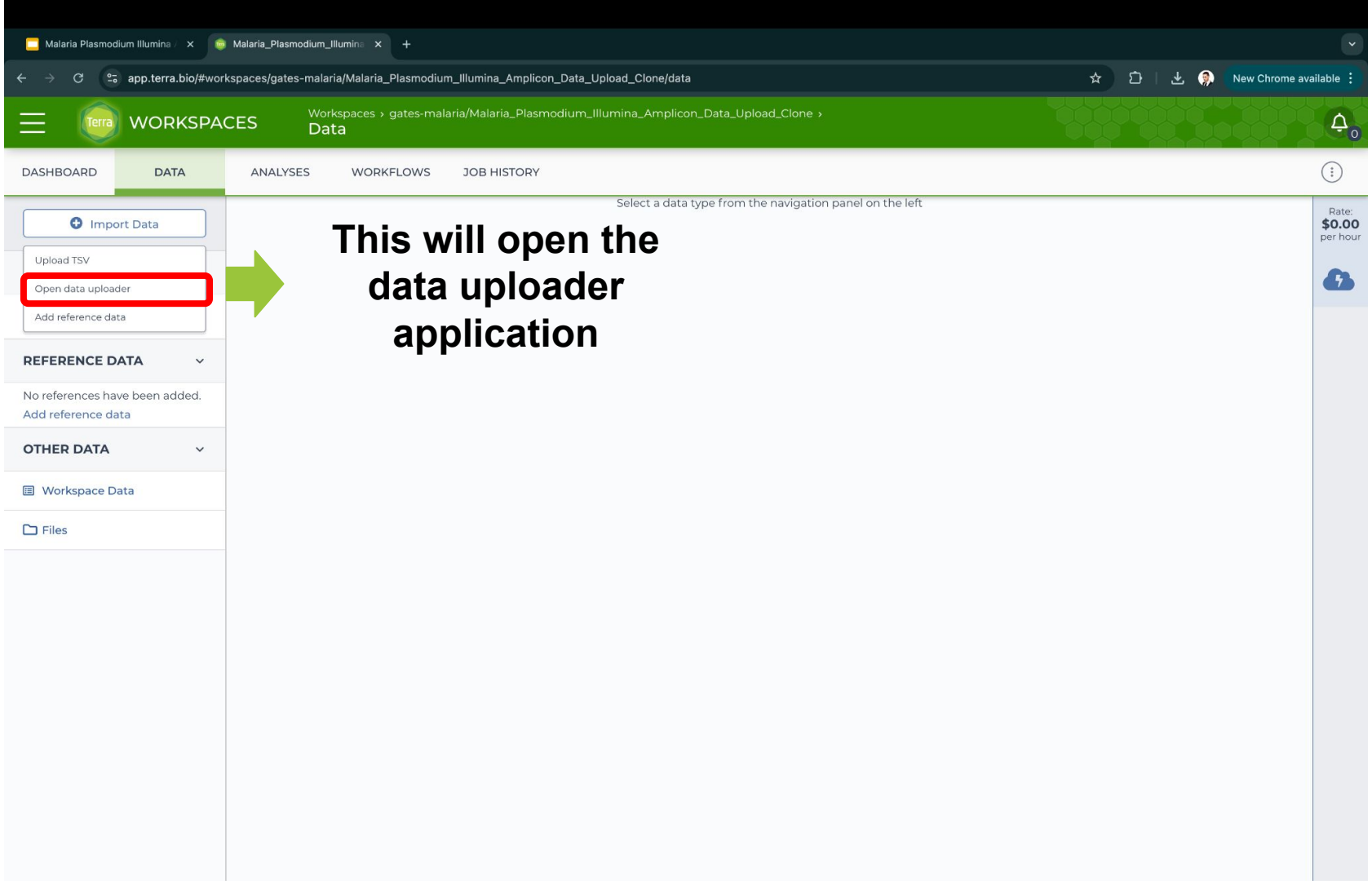
OTHER DATA

Workspace Data

Files

Select a data type from the navigation panel on the left

Rate:
$0.00
per hour


Malaria Plasmodium Illumina
Malaria_Plasmodium_Illumina
app.terra.bio/#workspaces/gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone/data
New Chrome available
WORKSPACES
Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone ›
Data
DASHBOARD
DATA
ANALYSES
WORKFLOWS
JOB HISTORY
Select a data type from the navigation panel on the left
Rate:
$0.00
per hour
Import Data
Upload TSV
Open data uploader
Add reference data
REFERENCE DATA
No references have been added.
Add reference data
OTHER DATA
Workspace Data
Files
This will open the data uploader application

Malaria Plasmodium Illumina | Upload

app.terra.bio/#upload?workspace=8c366203-217a-4b27-98c8-9843bd5760d5

New Chrome available

Terra DATA UPLOADER

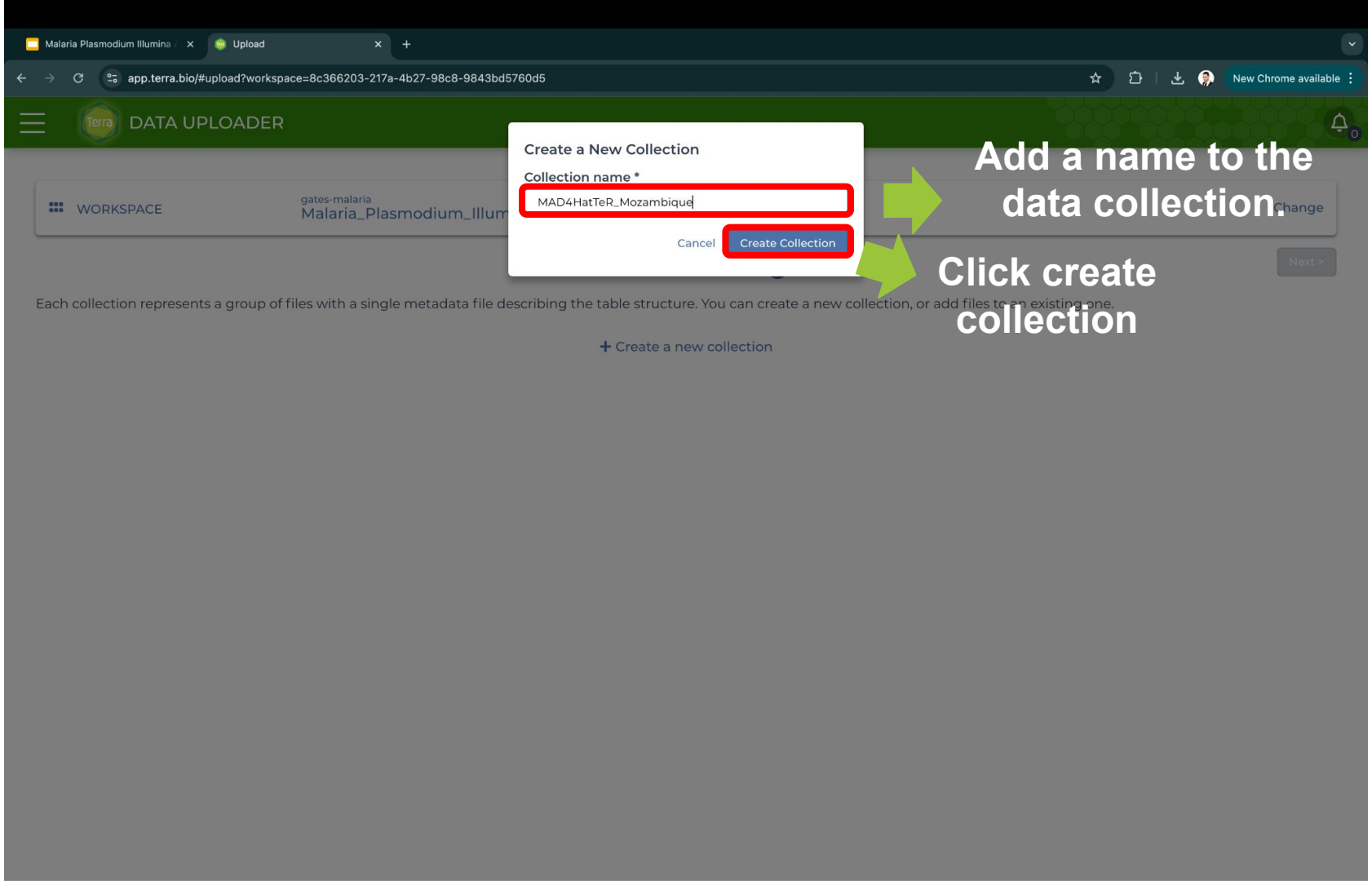
WORKSPACE gates-malaria Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone Change

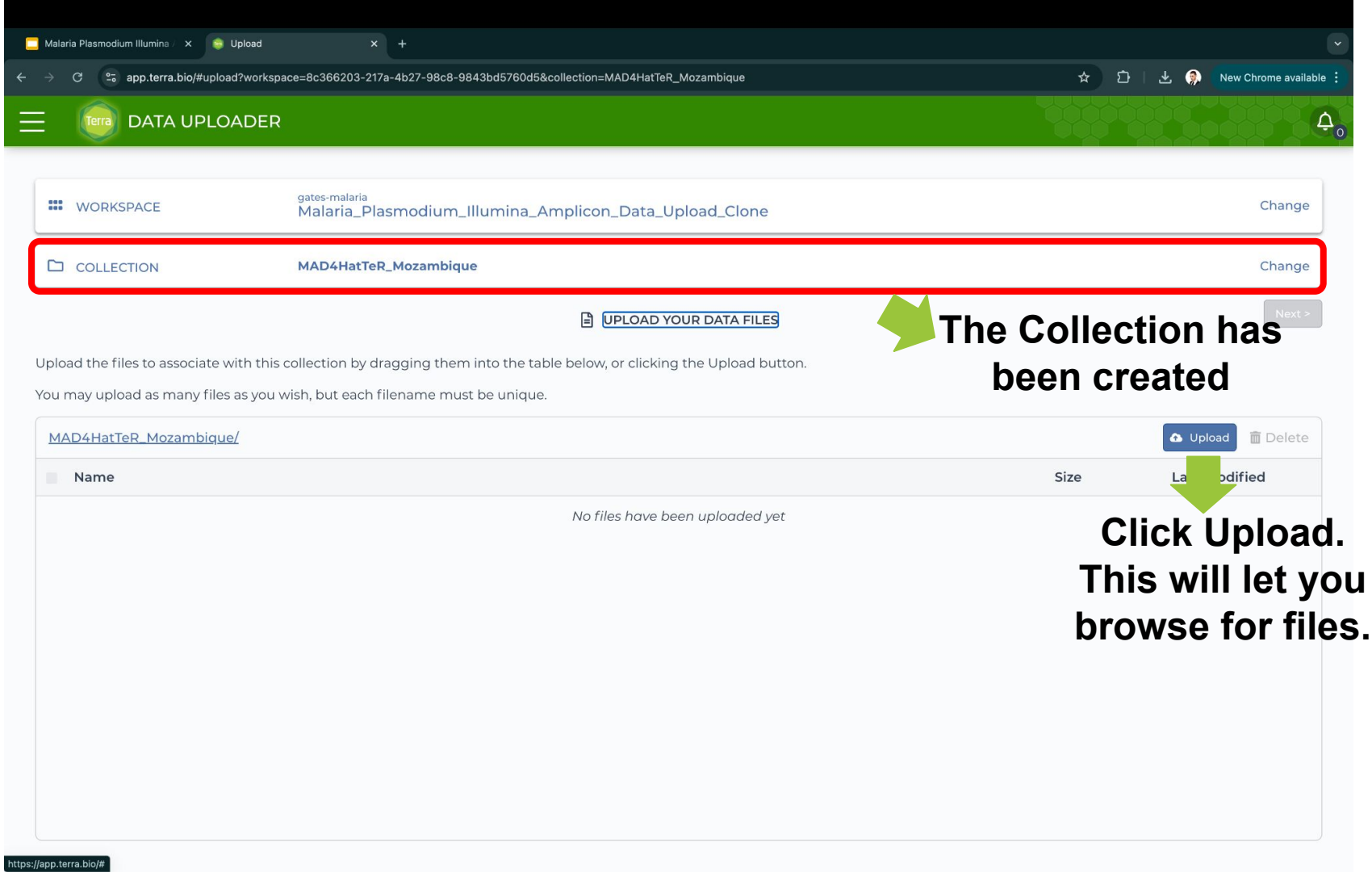
Next >

SELECT A COLLECTION

Each collection represents a group of files with a single metadata file describing the table structure. You can create a new collection, or add files to an existing one.

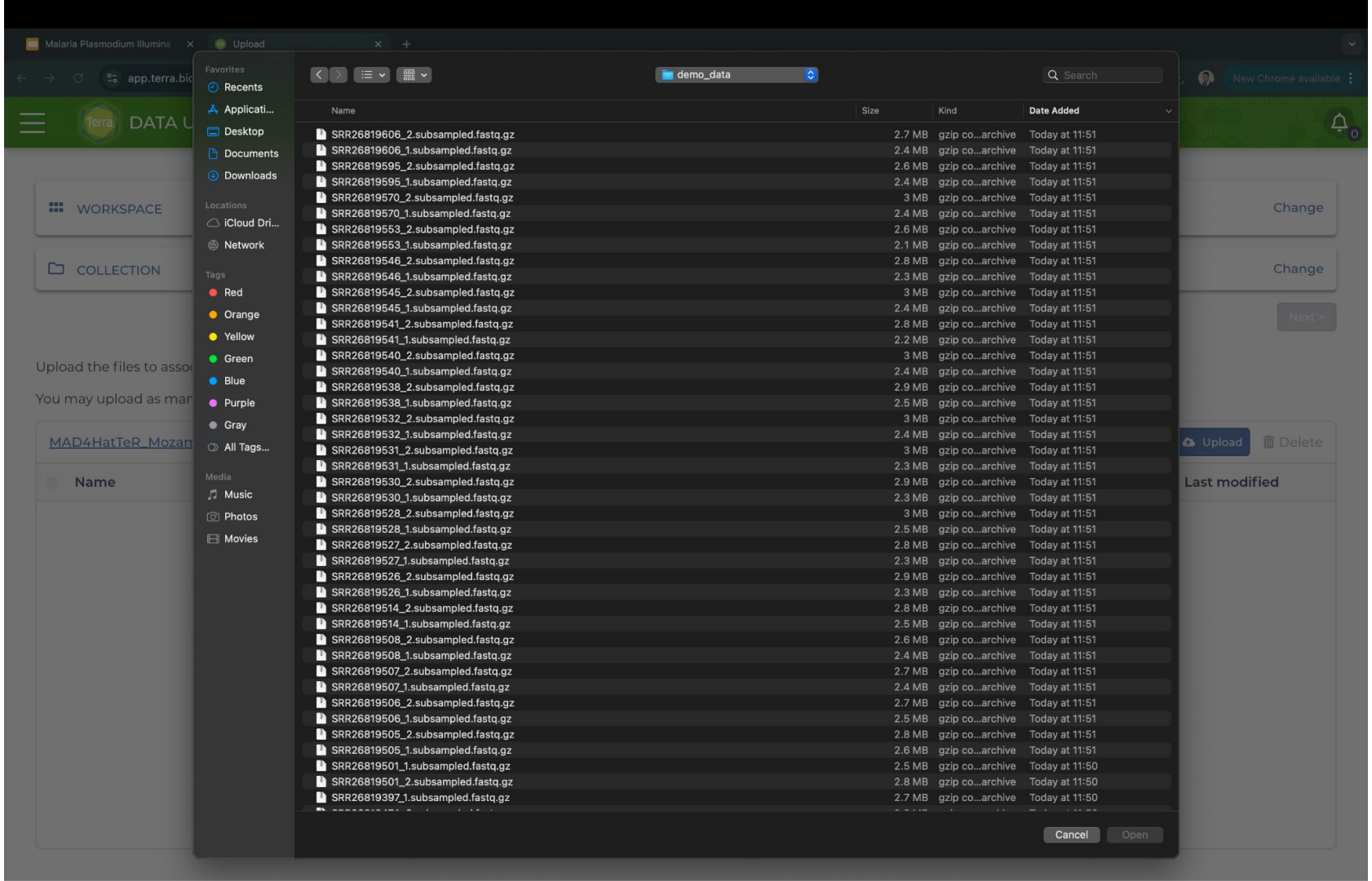
+ Create a new collection

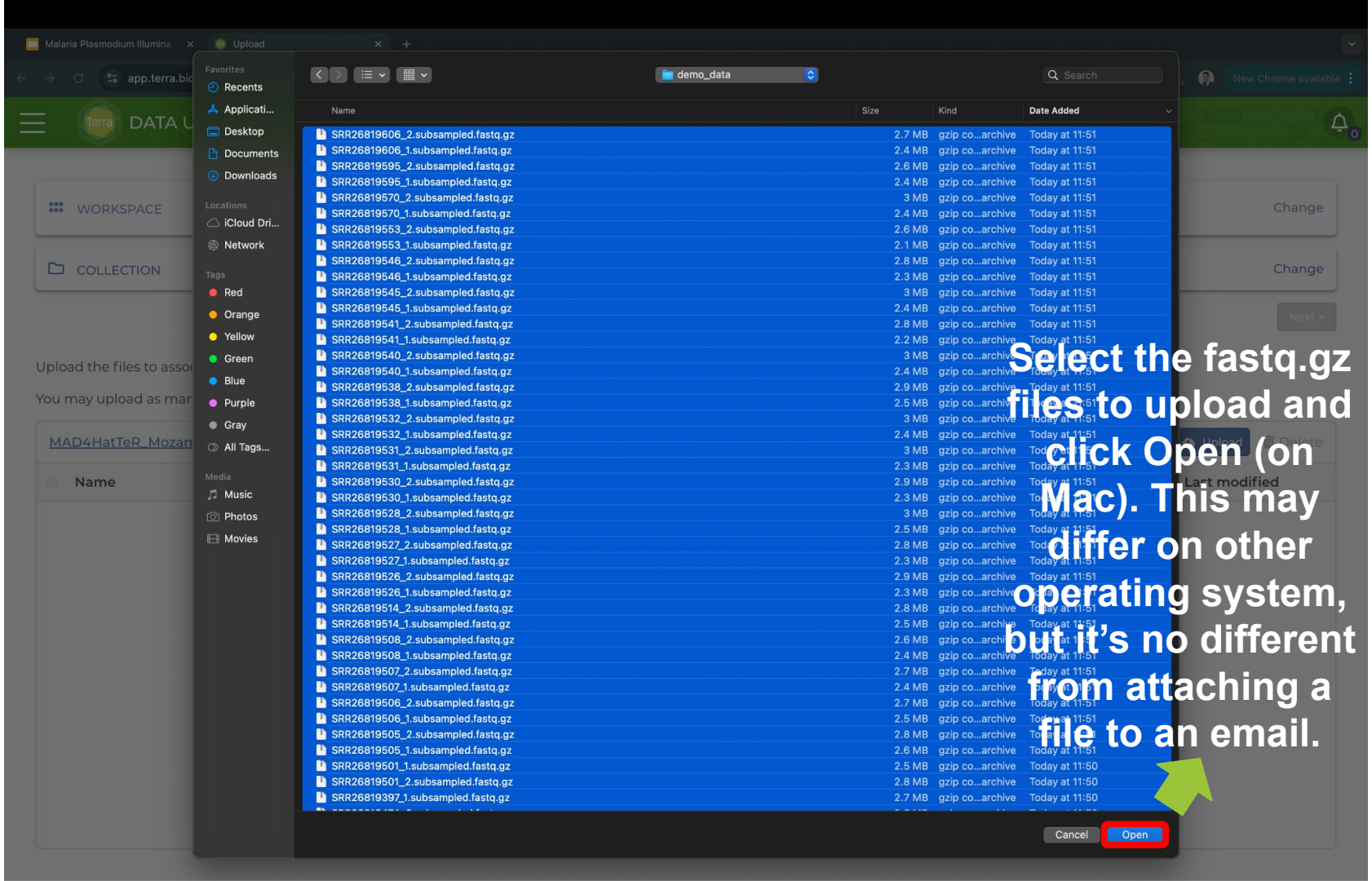

Malaria Plasmodium Illumina
Upload
app.terra.bio/#upload?workspace=8c366203-217a-4b27-98c8-9843bd5760d5
New Chrome available
DATA UPLOADER
WORKSPACE
gates-malaria
Malaria_Plasmodium_Illum
Change
Next >
Create a New Collection
Collection name *
MAD4HatTeR_Mozambique
Cancel
Create Collection
Add a name to the data collection.
Click create collection
Each collection represents a group of files with a single metadata file describing the table structure. You can create a new collection, or add files to an existing one.
+ Create a new collection



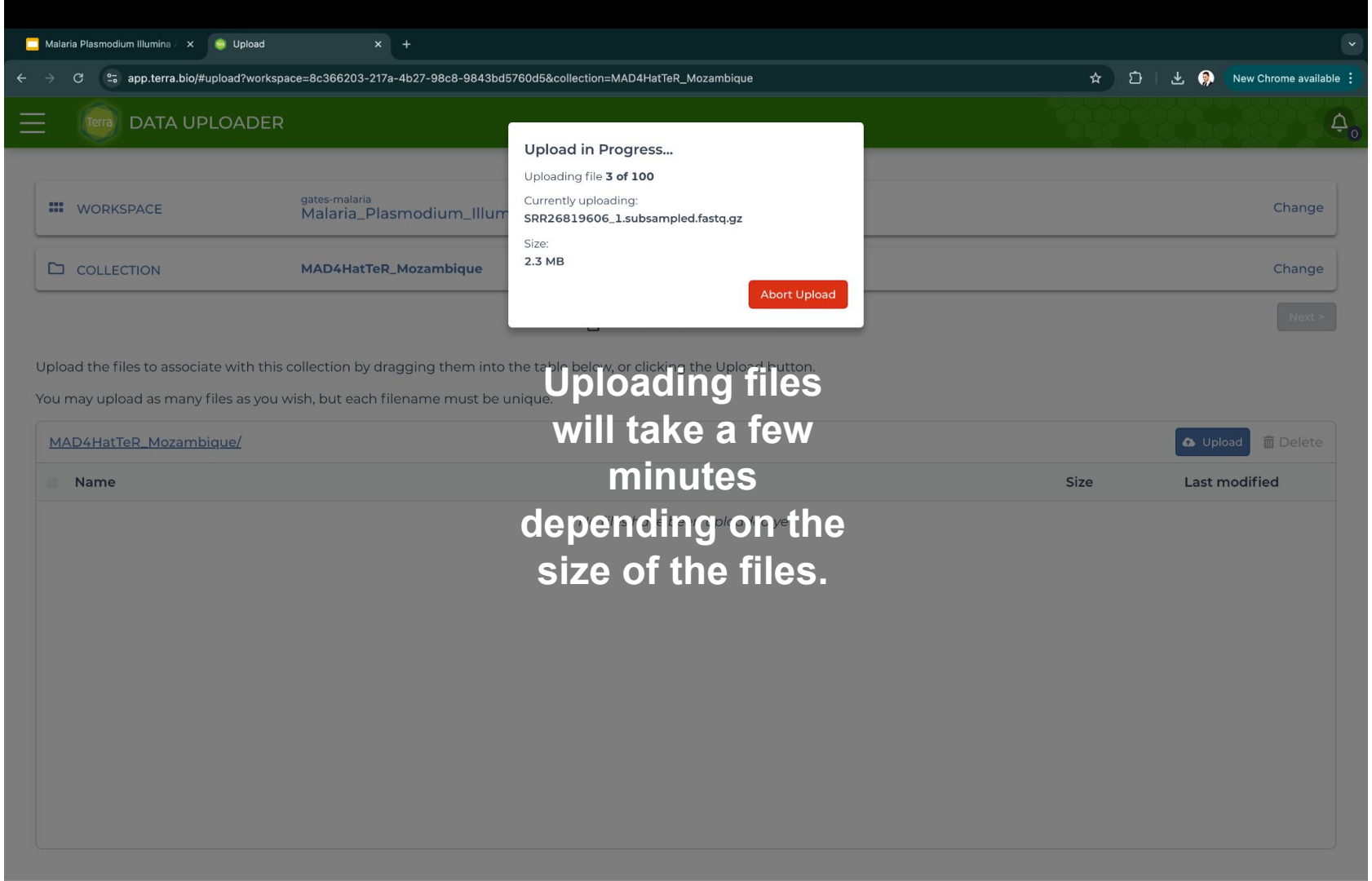
The Collection has been created

Click Upload. This will let you browse for files.


Malaria Plasmodium Illumina
Upload
app.terra.bio
New Chrome available
DATA U
WORKSPACE
Change
COLLECTION
Change
Next >
Upload the files to asso
You may upload as mar
MAD4HatTeR_Mozam
Upload
Delete
Name
Last modified
Favorites
Recents
Applicati...
Desktop
Documents
Downloads
Locations
iCloud Dri...
Network
Tags
Red
Orange
Yellow
Green
Blue
Purple
Gray
All Tags...
Media
Music
Photos
Movies
demo_data
Search
Name
Size
Kind
Date Added
SRR26819606_2.subsampled.fastq.gz 2.7 MB gzip co...archive Today at 11:51
SRR26819606_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819595_2.subsampled.fastq.gz 2.6 MB gzip co...archive Today at 11:51
SRR26819595_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819570_2.subsampled.fastq.gz 3 MB gzip co...archive Today at 11:51
SRR26819570_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819553_2.subsampled.fastq.gz 2.6 MB gzip co...archive Today at 11:51
SRR26819553_1.subsampled.fastq.gz 2.1 MB gzip co...archive Today at 11:51
SRR26819546_2.subsampled.fastq.gz 2.8 MB gzip co...archive Today at 11:51
SRR26819546_1.subsampled.fastq.gz 2.3 MB gzip co...archive Today at 11:51
SRR26819545_2.subsampled.fastq.gz 3 MB gzip co...archive Today at 11:51
SRR26819545_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819541_2.subsampled.fastq.gz 2.8 MB gzip co...archive Today at 11:51
SRR26819541_1.subsampled.fastq.gz 2.2 MB gzip co...archive Today at 11:51
SRR26819540_2.subsampled.fastq.gz 3 MB gzip co...archive Today at 11:51
SRR26819540_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819538_2.subsampled.fastq.gz 2.9 MB gzip co...archive Today at 11:51
SRR26819538_1.subsampled.fastq.gz 2.5 MB gzip co...archive Today at 11:51
SRR26819532_2.subsampled.fastq.gz 3 MB gzip co...archive Today at 11:51
SRR26819532_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819531_2.subsampled.fastq.gz 3 MB gzip co...archive Today at 11:51
SRR26819531_1.subsampled.fastq.gz 2.3 MB gzip co...archive Today at 11:51
SRR26819530_2.subsampled.fastq.gz 2.9 MB gzip co...archive Today at 11:51
SRR26819530_1.subsampled.fastq.gz 2.3 MB gzip co...archive Today at 11:51
SRR26819528_2.subsampled.fastq.gz 3 MB gzip co...archive Today at 11:51
SRR26819528_1.subsampled.fastq.gz 2.5 MB gzip co...archive Today at 11:51
SRR26819527_2.subsampled.fastq.gz 2.8 MB gzip co...archive Today at 11:51
SRR26819527_1.subsampled.fastq.gz 2.3 MB gzip co...archive Today at 11:51
SRR26819526_2.subsampled.fastq.gz 2.9 MB gzip co...archive Today at 11:51
SRR26819526_1.subsampled.fastq.gz 2.3 MB gzip co...archive Today at 11:51
SRR26819514_2.subsampled.fastq.gz 2.8 MB gzip co...archive Today at 11:51
SRR26819514_1.subsampled.fastq.gz 2.5 MB gzip co...archive Today at 11:51
SRR26819508_2.subsampled.fastq.gz 2.6 MB gzip co...archive Today at 11:51
SRR26819508_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819507_2.subsampled.fastq.gz 2.7 MB gzip co...archive Today at 11:51
SRR26819507_1.subsampled.fastq.gz 2.4 MB gzip co...archive Today at 11:51
SRR26819506_2.subsampled.fastq.gz 2.7 MB gzip co...archive Today at 11:51
SRR26819506_1.subsampled.fastq.gz 2.5 MB gzip co...archive Today at 11:51
SRR26819505_2.subsampled.fastq.gz 2.8 MB gzip co...archive Today at 11:51
SRR26819505_1.subsampled.fastq.gz 2.6 MB gzip co...archive Today at 11:51
SRR26819501_1.subsampled.fastq.gz 2.5 MB gzip co...archive Today at 11:50
SRR26819501_2.subsampled.fastq.gz 2.8 MB gzip co...archive Today at 11:50
SRR26819397_1.subsampled.fastq.gz 2.7 MB gzip co...archive Today at 11:50
Cancel
Open



Select the fastq.gz files to upload and click Open (on Mac). This may differ on other operating system, but it's no different from attaching a file to an email.



Uploading files will take a few minutes depending on the size of the files.

Malaria Plasmodium Illumina | Upload

app.terra.bio/#upload?workspace=8c366203-217a-4b27-98c8-9843bd5760d5&collection=MAD4HatTeR_Mozambique

New Chrome available

DATA UPLOADER

WORKSPACE gates-malaria Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone Change

COLLECTION MAD4HatTeR_Mozambique Change

Next >

UPLOAD YOUR DATA FILES

Upload the files to associate with this collection by dragging them into the table below, or clicking the Upload button.

You may upload as many files as you wish, but each filename must be unique.

Files have been uploaded

MAD4HatTeR_Mozambique/ Upload Delete

Name	Size	Last modified
SRR26819135_1.subsampled.fastq.gz	3 MB	Today
SRR26819135_2.subsampled.fastq.gz	3 MB	Today
SRR26819139_1.subsampled.fastq.gz	3 MB	Today
SRR26819139_2.subsampled.fastq.gz	3 MB	Today
SRR26819141_1.subsampled.fastq.gz	3 MB	Today
SRR26819141_2.subsampled.fastq.gz	3 MB	Today
SRR26819151_1.subsampled.fastq.gz	2 MB	Today
SRR26819151_2.subsampled.fastq.gz	2 MB	Today
SRR26819200_1.subsampled.fastq.gz	2 MB	Today

Malaria Plasmodium Illumina | Upload

app.terra.bio/#upload?workspace=8c366203-217a-4b27-98c8-9843bd5760d5&collection=MAD4HatTeR_Mozambique

New Chrome available

DATA UPLOADER

WORKSPACE	gates-malaria Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone	Change
COLLECTION	**MAD4HatTeR_Mozambique**	Change
DATA FILES	Includes **100** files	Change

UPLOAD YOUR METADATA FILES

Upload a tab-separated file describing your table structures.

- Any columns which reference files should include just the filenames, which will be matched up to the data files in this collection.
- The first column must contain the unique identifiers for each row. The name of the first column must start with `entity:` followed by the table name, followed by `_id`.

For example, if the first column is named `entity:sample_id`, a table named "sample" will be created with "sample_id" as its first column. There are no restrictions on other columns.

Drag and drop your metadata .tsv or .txt file here

Workspace_Data_ampseq_demo_terra

Possible Data Loss Some features might be lost if you save this workbook in the text (.txt) format. To preserve these features, save it in an Excel file format.

C14 NA

	A	B	C	D	E	F	G	H	I
1	entity:MAD4HatTeR_Mozambique_id	Country	Geo_Level	Latitude	Longitude	Temp_Level	fastq1	fastq2	run_id
2	SRR26819303	Mozambique	NA	-25.58	32.35	NA	SRR26819303_1.subsampled.fastq.gz	SRR26819303_2.subsampled.fastq.gz	ampseq_demo
3	SRR26819141	Mozambique	NA	-25.58	32.35	NA	SRR26819141_1.subsampled.fastq.gz	SRR26819141_2.subsampled.fastq.gz	ampseq_demo
4	SRR26819531	Mozambique	NA	-25.58	32.35	NA	SRR26819531_1.subsampled.fastq.gz	SRR26819531_2.subsampled.fastq.gz	ampseq_demo
5	SRR26819135	Mozambique	NA	-25.58	32.35	NA	SRR26819135_1.subsampled.fastq.gz	SRR26819135_2.subsampled.fastq.gz	ampseq_demo
6	SRR26819139	Mozambique	NA	-25.58	32.35	NA	SRR26819139_1.subsampled.fastq.gz	SRR26819139_2.subsampled.fastq.gz	ampseq_demo
7	SRR26819398	Mozambique	NA	-25.58	32.35	NA	SRR26819398_1.subsampled.fastq.gz	SRR26819398_2.subsampled.fastq.gz	ampseq_demo
8	SRR26819246	Mozambique	NA	-25.58	32.35	NA	SRR26819246_1.subsampled.fastq.gz	SRR26819246_2.subsampled.fastq.gz	ampseq_demo
9	SRR26819397	Mozambique	NA	-25.58	32.35	NA	SRR26819397_1.subsampled.fastq.gz	SRR26819397_2.subsampled.fastq.gz	ampseq_demo
10	SRR26819570	Mozambique	NA	-25.58	32.35	NA	SRR26819570_1.subsampled.fastq.gz	SRR26819570_2.subsampled.fastq.gz	ampseq_demo
11	SRR26819214	Mozambique	NA	-25.58	32.35	NA	SRR26819214_1.subsampled.fastq.gz	SRR26819214_2.subsampled.fastq.gz	ampseq_demo
12	SRR26819300	Mozambique	NA	-25.58	32.35	NA	SRR26819300_1.subsampled.fastq.gz	SRR26819300_2.subsampled.fastq.gz	ampseq_demo
13	SRR26819212	Mozambique	NA	-25.58	32.35	NA	SRR26819212_1.subsampled.fastq.gz	SRR26819212_2.subsampled.fastq.gz	ampseq_demo
14	SRR26819213	Mozambique	NA	-25.58	32.35	NA	SRR26819213_1.subsampled.fastq.gz	SRR26819213_2.subsampled.fastq.gz	ampseq_demo
15	SRR26819545	Mozambique	NA	-25.58	32.35	NA	SRR26819545_1.subsampled.fastq.gz	SRR26819545_2.subsampled.fastq.gz	ampseq_demo
16	SRR26819211	Mozambique	NA	-25.58	32.35	NA	SRR26819211_1.subsampled.fastq.gz	SRR26819211_2.subsampled.fastq.gz	ampseq_demo
17	SRR26819528	Mozambique	NA	-25.58	32.35	NA	SRR26819528_1.subsampled.fa		
18	SRR26819538	Mozambique	NA	-25.58	32.35	NA	SRR26819538_1.subsampled.fa		
19	SRR26819530	Mozambique	NA	-25.58	32.35	NA	SRR26819530_1.subsampled.fa		
20	SRR26819532	Mozambique	NA	-25.58	32.35	NA	SRR26819532_1.subsampled.fa		
21	SRR26819553	Mozambique	NA	-25.58	32.35	NA	SRR26819553_1.subsampled.fa		
22	SRR26819215	Mozambique	NA	-25.58	32.35	NA	SRR26819215_1.subsampled.fa		
23	SRR26819400	Mozambique	NA	-25.58	32.35	NA	SRR26819400_1.subsampled.fa		
24	SRR26819540	Mozambique	NA	-25.58	32.35	NA	SRR26819540_1.subsampled.fa		
25	SRR26819208	Mozambique	NA	-25.58	32.35	NA	SRR26819208_1.subsampled.fa		
26	SRR26819220	Mozambique	NA	-25.58	32.35	NA	SRR26819220_1.subsampled.fa		
27	SRR26819526	Mozambique	NA	-25.58	32.35	NA	SRR26819526_1.subsampled.fa		

Workspace_Data_ampseq_demo_terr

Ready Accessibility: Unavailable

The metadata file is a TSV file with metadata for each sample. Notice as well the two columns with the name of the forward and reverse fastq.gz files

```
entity:MAD4HatTeR_Mozambique_id Country Geo_Level       Latitude        Longitude       Temp_Level      fastq1  fastq2  run_id
SRR26819303     Mozambique      NA      -25.58  32.35   NA      SRR26819303_1.subsampled.fastq.gz       SRR26819303_2.subsampled.fastq.gz       ampseq_demo
SRR26819141     Mozambique      NA      -25.58  32.35   NA      SRR26819141_1.subsampled.fastq.gz       SRR26819141_2.subsampled.fastq.gz       ampseq_demo
SRR26819531     Mozambique      NA      -25.58  32.35   NA      SRR26819531_1.subsampled.fastq.gz       SRR26819531_2.subsampled.fastq.gz       ampseq_demo
SRR26819135     Mozambique      NA      -25.58  32.35   NA      SRR26819135_1.subsampled.fastq.gz       SRR26819135_2.subsampled.fastq.gz       ampseq_demo
SRR26819139     Mozambique      NA      -25.58  32.35   NA      SRR26819139_1.subsampled.fastq.gz       SRR26819139_2.subsampled.fastq.gz       ampseq_demo
SRR26819398     Mozambique      NA      -25.58  32.35   NA      SRR26819398_1.subsampled.fastq.gz       SRR26819398_2.subsampled.fastq.gz       ampseq_demo
SRR26819246     Mozambique      NA      -25.58  32.35   NA      SRR26819246_1.subsampled.fastq.gz       SRR26819246_2.subsampled.fastq.gz       ampseq_demo
SRR26819397     Mozambique      NA      -25.58  32.35   NA      SRR26819397_1.subsampled.fastq.gz       SRR26819397_2.subsampled.fastq.gz       ampseq_demo
SRR26819570     Mozambique      NA      -25.58  32.35   NA      SRR26819570_1.subsampled.fastq.gz       SRR26819570_2.subsampled.fastq.gz       ampseq_demo
SRR26819214     Mozambique      NA      -25.58  32.35   NA      SRR26819214_1.subsampled.fastq.gz       SRR26819214_2.subsampled.fastq.gz       ampseq_demo
SRR26819300     Mozambique      NA      -25.58  32.35   NA      SRR26819300_1.subsampled.fastq.gz       SRR26819300_2.subsampled.fastq.gz       ampseq_demo
SRR26819212     Mozambique      NA      -25.58  32.35   NA      SRR26819212_1.subsampled.fastq.gz       SRR26819212_2.subsampled.fastq.gz       ampseq_demo
SRR26819213     Mozambique      NA      -25.58  32.35   NA      SRR26819213_1.subsampled.fastq.gz       SRR26819213_2.subsampled.fastq.gz       ampseq_demo
SRR26819545     Mozambique      NA      -25.58  32.35   NA      SRR26819545_1.subsampled.fastq.gz       SRR26819545_2.subsampled.fastq.gz       ampseq_demo
SRR26819211     Mozambique      NA      -25.58  32.35   NA      SRR26819211_1.subsampled.fastq.gz       SRR26819211_2.subsampled.fastq.gz       ampseq_demo
SRR26819528     Mozambique      NA      -25.58  32.35   NA      SRR26819528_1.subsampled.fastq.gz       SRR26819528_2.subsampled.fastq.gz       ampseq_demo
SRR26819538     Mozambique      NA      -25.58  32.35   NA      SRR26819538_1.subsampled.fastq.gz       SRR26819538_2.subsampled.fastq.gz       ampseq_demo
SRR26819530     Mozambique      NA      -25.58  32.35   NA      SRR26819530_1.subsampled.fastq.gz       SRR26819530_2.subsampled.fastq.gz       ampseq_demo
SRR26819532     Mozambique      NA      -25.58  32.35   NA      SRR26819532_1.subsampled.fastq.gz       SRR26819532_2.subsampled.fastq.gz       ampseq_demo
SRR26819553     Mozambique      NA      -25.58  32.35   NA      SRR26819553_1.subsampled.fastq.gz       SRR26819553_2.subsampled.fastq.gz       ampseq_demo
SRR26819215     Mozambique      NA      -25.58  32.35   NA      SRR26819215_1.subsampled.fastq.gz       SRR26819215_2.subsampled.fastq.gz       ampseq_demo
SRR26819400     Mozambique      NA      -25.58  32.35   NA      SRR26819400_1.subsampled.fastq.gz       SRR26819400_2.subsampled.fastq.gz       ampseq_demo
SRR26819540     Mozambique      NA      -25.58  32.35   NA      SRR26819540_1.subsampled.fastq.gz       SRR26819540_2.subsampled.fastq.gz       ampseq_demo
SRR26819208     Mozambique      NA      -25.58  32.35   NA      SRR26819208_1.subsampled.fastq.gz       SRR26819208_2.subsampled.fastq.gz       ampseq_demo
SRR26819220     Mozambique      NA      -25.58  32.35   NA      SRR26819220_1.subsampled.fastq.gz       SRR26819220_2.subsampled.fastq.gz       ampseq_demo
SRR26819526     Mozambique      NA      -25.58  32.35   NA      SRR26819526_1.subsampled.fastq.gz       SRR26819526_2.subsampled.fastq.gz       ampseq_demo
SRR26819202     Mozambique      NA      -25.58  32.35   NA      SRR26819202_1.subsampled.fastq.gz       SRR26819202_2.subsampled.fastq.gz       ampseq_demo
SRR26819505     Mozambique      NA      -25.58  32.35   NA      SRR26819505_1.subsampled.fastq.gz       SRR26819505_2.subsampled.fastq.gz       ampseq_demo
SRR26819206     Mozambique      NA      -25.58  32.35   NA      SRR26819206_1.subsampled.fastq.gz       SRR26819206_2.subsampled.fastq.gz       ampseq_demo
SRR26819200     Mozambique      NA      -25.58  32.35   NA      SRR26819200_1.subsampled.fastq.gz       SRR26819200_2.subsampled.fastq.gz       ampseq_demo
SRR26819324     Mozambique      NA      -25.58  32.35   NA      SRR26819324_1.subsampled.fastq.gz       SRR26819324_2.subsampled.fastq.gz       ampseq_demo
SRR26819365     Mozambique      NA      -25.58  32.35   NA      SRR26819365_1.subsampled.fastq.gz       SRR26819365_2.subsampled.fastq.gz       ampseq_demo
SRR26819507     Mozambique      NA      -25.58  32.35   NA      SRR26819507_1.subsampled.fastq.gz       SRR26819507_2.subsampled.fastq.gz       ampseq_demo
SRR26819606     Mozambique      NA      -25.58  32.35   NA      SRR26819606_1.subsampled.fastq.gz       SRR26819606_2.subsampled.fastq.gz       ampseq_demo
SRR26819228     Mozambique      NA      -25.58  32.35   NA      SRR26819228_1.subsampled.fastq.gz       SRR26819228_2.subsampled.fastq.gz       ampseq_demo
SRR26819501     Mozambique      NA      -25.58  32.35   NA      SRR26819501_1.subsampled.fastq.gz       SRR26819501_2.subsampled.fastq.gz       ampseq_demo
SRR26819506     Mozambique      NA      -25.58  32.35   NA      SRR26819506_1.subsampled.fastq.gz       SRR26819506_2.subsampled.fastq.gz       ampseq_demo
SRR26819514     Mozambique      NA      -25.58  32.35   NA      SRR26819514_1.subsampled.fastq.gz       SRR26819514_2.subsampled.fastq.gz       ampseq_demo
SRR26819546     Mozambique      NA      -25.58  32.35   NA      SRR26819546_1.subsampled.fastq.gz       SRR26819546_2.subsampled.fastq.gz       ampseq_demo
SRR26819207     Mozambique      NA      -25.58  32.35   NA      SRR26819207_1.subsampled.fastq.gz       SRR26819207_2.subsampled.fastq.gz       ampseq_demo
SRR26819345     Mozambique      NA      -25.58  32.35   NA      SRR26819345_1.subsampled.fastq.gz       SRR26819345_2.subsampled.fastq.gz       ampseq_demo
SRR26819313     Mozambique      NA      -25.58  32.35   NA      SRR26819313_1.subsampled.fastq.gz       SRR26819313_2.subsampled.fastq.gz       ampseq_demo
SRR26819356     Mozambique      NA      -25.58  32.35   NA      SRR26819356_1.subsampled.fastq.gz       SRR26819356_2.subsampled.fastq.gz       ampseq_demo
SRR26819240     Mozambique      NA      -25.58  32.35   NA      SRR26819240_1.subsampled.fastq.gz       SRR26819240_2.subsampled.fastq.gz       ampseq_demo
SRR26819474     Mozambique      NA      -25.58  32.35   NA      SRR26819474_1.subsampled.fastq.gz       SRR26819474_2.subsampled.fastq.gz       ampseq_demo
SRR26819541     Mozambique      NA      -25.58  32.35   NA      SRR26819541_1.subsampled.fastq.gz       SRR26819541_2.subsampled.fastq.gz       ampseq_demo
SRR26819508     Mozambique      NA      -25.58  32.35   NA      SRR26819508_1.subsampled.fastq.gz       SRR26819508_2.subsampled.fastq.gz       ampseq_demo
SRR26819595     Mozambique      NA      -25.58  32.35   NA      SRR26819595_1.subsampled.fastq.gz       SRR26819595_2.subsampled.fastq.gz       ampseq_demo
SRR26819527     Mozambique      NA      -25.58  32.35   NA      SRR26819527_1.subsampled.fastq.gz       SRR26819527_2.subsampled.fastq.gz       ampseq_demo
SRR26819151     Mozambique      NA      -25.58  32.35   NA      SRR26819151_1.subsampled.fastq.gz       SRR26819151_2.subsampled.fastq.gz       ampseq_demo
~
~
~
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```

View of the file as plain text

Malaria Plasmodium Illumina | Upload | Malaria_Plasmodium_Illumina

app.terra.bio/#upload?workspace=8c366203-217a-4b27-98c8-9843bd5760d5&collection=MAD4HatTeR_Mozambique

New Chrome available

DATA UPLOADER

WORKSPACE	gates-malaria Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone	Change
COLLECTION	**MAD4HatTeR_Mozambique**	Change
DATA FILES	Includes **100** files	Change

UPLOAD YOUR METADATA FILES

Creating a new Table: **MAD4HatTeR_Mozambique**

Cancel | Create Table

If this table looks right to you, click the button on the right to create the table in your workspace.

entity: MAD4HatTeR_Mozam...	Country	Geo_Level	Latitude	Longitude	Temp_Level
SRR26819303	Mozambique	NA	-25.58	32.35	NA
SRR26819141	Mozambique	NA	-25.58	32.35	NA
SRR26819531	Mozambique	NA	-25.58	32.35	NA
SRR26819135	Mozambique	NA	-25.58	32.35	NA
SRR26819139	Mozambique	NA	-25.58	32.35	NA
SRR26819398	Mozambique	NA	-25.58	32.35	NA
SRR26819246	Mozambique	NA	-25.58	32.35	NA
SRR26819397	Mozambique	NA	-25.58	32.35	NA
SRR26819570	Mozambique	NA	-25.58	32.35	NA
SRR26819214	Mozambique	NA	-25.58	32.35	NA

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina | Malaria_Plasmodium_Illumina

app.terra.bio/#workspaces/gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone/data

New Chrome available

WORKSPACES

Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

Search all tables

MAD4HatTeR_Mo... (50)

REFERENCE DATA

No references been added.
Add reference

OTHER DAT

Workspac

Files

Edit | Open With... | Export | Settings | 0 rows selected | Advanced Search | Search

Rate: $0.00 per hour

MAD4H...	Country	Geo_Level	Latitude	Longitude
SRR26...	Mozambique	NA	-25.58	32.35
SRR26819139	Mozambique	NA	-25.58	32.35
SRR26819141	Mozambique	NA	-25.58	32.35
SRR26819151	Mozambique	NA	-25.58	32.35
SRR26819200	Mozambique	NA	-25.58	32.35
SRR26819202	Mozambique	NA	-25.58	32.35
SRR26819206	Mozambique	NA	-25.58	32.35
SRR26819207	Mozambique	NA	-25.58	32.35
SRR26819208	Mozambique	NA	-25.58	32.35
SRR26819211	Mozambique	NA	-25.58	32.35
SRR26819212	Mozambique	NA	-25.58	32.35
SRR26819213	Mozambique	NA	-25.58	32.35
SRR26819214	Mozambique	NA	-25.58	32.35
SRR26819215	Mozambique	NA	-25.58	32.35

1 - 50 of 50 « ‹ 1 › » Items per page: 100

Sample Table has been created. Now let's create the set.

Malaria Plasmodium Illumina / Malaria_Plasmodium_Illumina

app.terra.bio/#workspaces/gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone/data

New Chrome available

WORKSPACES

Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone ›
Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data

TABLES

Search all tables

MAD4HatTeR_Mo... (50)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Edit | Open With... | Export | Settings | 50 rows selected | Advanced Search | Search

Rate: $0.00 per hour

MAD4H...	Country	Geo_Level	Latitude	Longitude
[illegible]8819135	Mozambique	NA	-25.58	32.35
SRR26819139	Mozambique	NA	-25.58	32.35
SRR26819141	Mozambique	NA	-25.58	32.35
SRR2681915[illegible]	Mozambique	NA	-25.58	32.35
SRR26819[illegible]	Mozambique	[illegible]	-25.58	32.35
SRR26819202	Mozambique	NA	-25.58	32.35
SRR26819206	Mozambique	NA	-25.58	32.35
SRR26819207	Mozambique	NA	-25.58	32.35
SRR2681[illegible]	Mozambique	NA	-25.58	32.35
SRR26819211	Mozambique	NA	-25.58	32.35
SRR26819212	Mozambique	NA	-25.58	32.35
SRR26819213	Mozambique	NA	-25.58	32.35
SRR26819214	Mozambique	NA	-25.58	32.35
SRR26819215	Mozambique	NA	-25.58	32.35

1 - 50 of 50 | « ‹ 1 › » | Items per page: 100

Select the desired samples. All samples can be selected at once by clicking on the top box, or only a subset of them by checking individual boxes.

Malaria Plasmodium Illumina / Malaria_Plasmodium_Illumina

app.terra.bio/#workspaces/gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone/data

New Chrome available

WORKSPACES

Workspaces › gates-malaria/Malaria_Plasmodium_Illumina_Amplicon_Data_Upload_Clone ›

Data

DASHBOARD | DATA | ANALYSES | WORKFLOWS | JOB HISTORY

Import Data | Edit | Open With... | Export | Settings | 50 rows selected | Advanced Search | Search

Rate: $0.00 per hour

Add row

Add column

Edit selected rows

Delete selected rows

Save selection as set

TABLES

Search all tables

MAD4HatTeR_Mo... (50)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

	4H...	Country	Geo_Level	Latitude	Longitude
	26819135	Mozambique	NA	-25.58	32.35
	26819139	Mozambique	NA	-25.58	32.35
	6819141	Mozambique	NA	-25.58	32.35
☑	SRR26819151	Mozambique	NA	-25.58	32.35
☑	SRR26819200	Mozambique	NA	-25.58	32.35
☑	SRR26819202	Mozambique	NA	-25.58	32.35
☑	SRR26819206	Mozambique	NA	-25.58	32.35
☑	SRR26819207	Mozambique	NA	-25.58	32.35
☑	SRR26819208	Mozambique	NA	-25.58	32.35
☑	SRR26819211	Mozambique	NA	-25.58	32.35
☑	SRR26819212	Mozambique	NA	-25.58	32.35
☑	SRR26819213	Mozambique	NA	-25.58	32.35
☑	SRR26819214	Mozambique	NA	-25.58	32.35
☑	SRR26819215	Mozambique	NA	-25.58	32.35

1 - 50 of 50 « ‹ 1 › » Items per page: 100

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina | Malaria_Plasmodium_Illumina

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Data

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Import Data

TABLES

Search all tables

MAD4HatTeR_Mo... (50)

REFERENCE DATA

No references have been added.
Add reference data

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Files

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Create a MAD4HatTeR_Mozambique set

Set name (required)

MAD4HatTeR_Mozambique_set

Cancel | Save

Add a name to the set.

Click save

MAD4H...	Country		ude	ngitude
SRR26819135	Mozambique	NA	-25.58	32.35
SRR26819139	Mozambique	NA	-25.58	32.35
SRR26819141	Mozambique	NA	-25.58	32.35
SRR26819151	Mozambique	NA	-25.58	32.35
SRR26819200	Mozambique	NA	-25.58	32.35
SRR26819202	Mozambique	NA	-25.58	32.35
SRR26819206	Mozambique	NA	-25.58	32.35
SRR26819207	Mozambique	NA	-25.58	32.35
SRR26819208	Mozambique	NA	-25.58	32.35
SRR26819211	Mozambique	NA	-25.58	32.35
SRR26819212	Mozambique	NA	-25.58	32.35
SRR26819213	Mozambique	NA	-25.58	32.35
SRR26819214	Mozambique	NA	-25.58	32.35
SRR26819215	Mozambique	NA	-25.58	32.35

1 - 50 of 50 | « ‹ 1 › » | Items per page: 100

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina | Malaria_Plasmodium_Illumina

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Data

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Import Data

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moz... (1)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DAT

Workspac

Files

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MAD4H...	MAD4HatTeR_Mozambiques
MAD4HatTeR_...	SRR26819135, SRR2... (50 entities)

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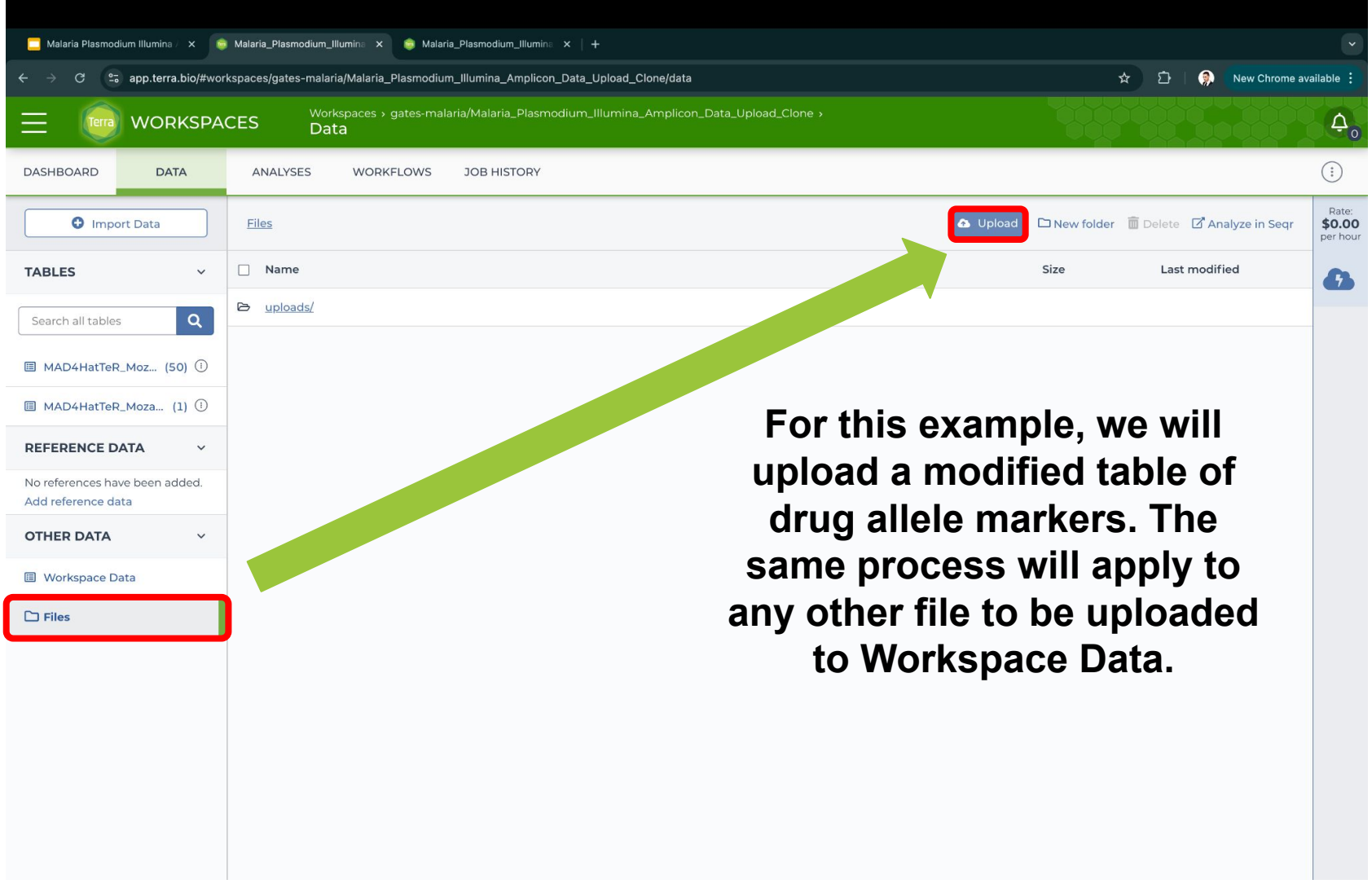
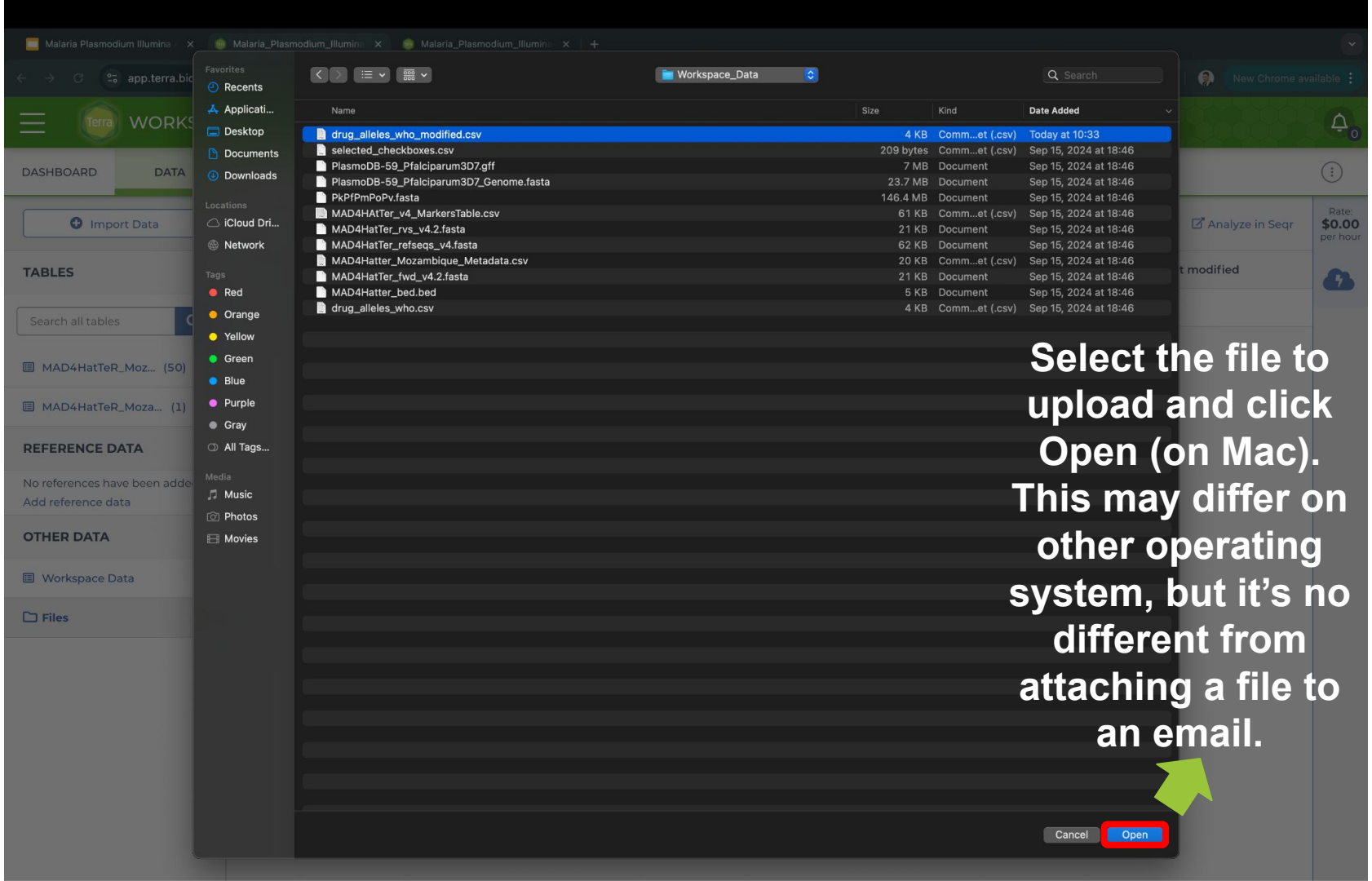
1 - 1 of 1 « ‹ 1 › » Items per page: 100

The set has been created.

Uploading Workspace Data



For this example, we will upload a modified table of drug allele markers. The same process will apply to any other file to be uploaded to Workspace Data.



Select the file to upload and click Open (on Mac). This may differ on other operating system, but it's no different from attaching a file to an email.

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina | Malaria_Plasmodium_Illumina

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Data

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Import Data

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moza... (1)

REFERENCE DATA

No references have been added.
Add reference data

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Workspace Data

Files

Files

Upload | New folder | Delete | Analyze in Seqr

Rate: $0.00 per hour

Name	Size	Last modified
drug_alleles_who_modified.csv	4 KB	Today
uploads/		

Copy URL to clipboard

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina | Malaria_Plasmodium_Illumina

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Import Data

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MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moza... (1)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Key	Value	Description
BackUp_ASVs	M4H_Mozambique_DS_TestSet6_n32_1-32.xlsx	MAD4HAtter BackUp ASVs
ForwardPrimersMAD4Hatter	MAD4HatTer_fwd_v4.2.fasta	Forward primers for MAD4Hatter Amplicon panel
MAD4Hatter_BED	MAD4Hatter_bed.bed	MAD4Hatter BED file
MAD4Hatter_Mozambique_Metadata	MAD4Hatter_Mozambique_Metadata.csv	Metadata for MAD4Hatter Mozambique
Markers	MAD4HAtTer_v4_MarkersTable.csv	Markers of resistance for Genotyping Analysis
PlasmoDB-59_Pfalciparum3D7Genome	PlasmoDB-59_Pfalciparum3D7_Genome.fasta	Genome of Pfalciparum3D7 in fasta format
PlasmoDB-59_Pfalciparum3D7Gff	PlasmoDB-59_Pfalciparum3D7.gff	Gff file of Pfalciparum3D7
reference_genomes	PkPfPmPoPv.fasta	Reference genomes file
ReferenceSeq_MAD4Hatter	MAD4HatTer_refseqs_v4.fasta	Reference sequences for MAD4HAtter amplicon panel
ReversePrimersMAD4Hatter	MAD4HatTer_rvs_v4.2.fasta	Reverse primers for MAD4Hatter Amplicon panel
Selected_Checkboxes	selected_checkboxes.csv	Selected data points
WHO_Drug_Resistance_Markers	drug_alleles_who.csv	WHO Markers of resistance for Genotyping Analysis

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina | Malaria_Plasmodium_Illumina

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Upload TSV
Delete selected variables

TABLES

Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moza... (1)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

		Value	Description
	p_ASVs	M4H_Mozambique_DS_TestSet6_n32_1-32.xlsx	MAD4HAtter BackUp ASVs
☐	ForwardPrimersMAD4Hatter	MAD4HatTer_fwd_v4.2.fasta	Forward primers for MAD4Hatter Amplicon panel
☐	MAD4Hatter_BED	MAD4Hatter_bed.bed	MAD4Hatter BED file
☐	MAD4Hatter_Mozambique_Metadata	MAD4Hatter_Mozambique_Metadata.csv	Metadata for MAD4Hatter Mozambique
☐	Markers	MAD4HAtTer_v4_MarkersTable.csv	Markers of resistance for Genotyping Analysis
☐	PlasmoDB-59_Pfalciparum3D7Genome	PlasmoDB-59_Pfalciparum3D7_Genome.fasta	Genome of Pfalciparum3D7 in fasta format
☐	PlasmoDB-59_Pfalciparum3D7Gff	PlasmoDB-59_Pfalciparum3D7.gff	Gff file of Pfalciparum3D7
☐	reference_genomes	PkPfPmPoPv.fasta	Reference genomes file
☐	ReferenceSeq_MAD4Hatter	MAD4HatTer_refseqs_v4.fasta	Reference sequences for MAD4HAtter amplicon panel
☐	ReversePrimersMAD4Hatter	MAD4HatTer_rvs_v4.2.fasta	Reverse primers for MAD4Hatter Amplicon panel
☐	Selected_Checkboxes	selected_checkboxes.csv	Selected data points
☐	WHO_Drug_Resistance_Markers	drug_alleles_who.csv	WHO Markers of resistance for Genotyping Analysis

Malaria Plasmodium Illumina | Malaria_Plasmodium_Illumina | Malaria_Plasmodium_Illumina

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MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moza... (1)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

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Rate: $0.00 per hour

Key	Value	Description
BackUp_ASVs	M4H_Mozambique_DS_TestSet6_n32_1-32.xlsx	MAD4HAtter BackUp ASVs
ForwardPrimersMAD4Hatter	MAD4HatTer_fwd_v4.2.fasta	Forward primers for MAD4Hatter Amplicon panel
MAD4Hatter_BED	MAD4Hatter_bed.bed	MAD4Hatter BED file
MAD4Hatter_Mozambique_Metadata	MAD4Hatter_Mozambique_Metadata.csv	Metadata for MAD4Hatter Mozambique
Markers	MAD4HAtTer_v4_MarkersTable.csv	Markers of resistance for Genotyping Analysis
PlasmoDB-59_Pfalciparum3D7Genome	PlasmoDB-59_Pfalciparum3D7_Genome.fasta	Genome of Pfalciparum3D7 in fasta format
PlasmoDB-59_Pfalciparum3D7Gff	PlasmoDB-59_Pfalciparum3D7.gff	Gff file of Pfalciparum3D7
reference_genomes	PkPfPmPoPv.fasta	Reference genomes file
ReferenceSeq_MAD4Hatter	MAD4HatTer_refseqs_v4.fasta	Reference sequences for MAD4HAtter amplicon panel
ReversePrimersMAD4Hatter	MAD4HatTer_rvs_v4.2.fasta	Reverse primers for MAD4Hatter Amplicon panel
Selected_Checkboxes	selected_checkboxes.csv	Selected data points
WHO_Drug_Resistance_Markers	drug_alleles_who.csv	WHO Markers of resistance for Genotyping Analysis
WHO_Drug_Resistance_Markers_Modified	gs://fc-8c366203-217a-4b27-9 String	1arkers of resistance for Genotyping Analysis

Type a key; paste the link in value; and add a Descriptor.

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Import Data

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Search all tables

MAD4HatTeR_Moz... (50)

MAD4HatTeR_Moza... (1)

REFERENCE DATA

No references have been added.
Add reference data

OTHER DATA

Workspace Data

Files

Edit | Download TSV | 0 rows selected

Search

Rate: $0.00 per hour

Key	Value	Description
BackUp_ASVs	M4H_Mozambique_DS_TestSet6_n32_1-32.xlsx	MAD4HAtter BackUp ASVs
ForwardPrimersMAD4Hatter	MAD4HatTer_fwd_v4.2.fasta	Forward primers for MAD4Hatter Amplicon panel
MAD4Hatter_BED	MAD4Hatter_bed.bed	MAD4Hatter BED file
MAD4Hatter_Mozambique_Metadata	MAD4Hatter_Mozambique_Metadata.csv	Metadata for MAD4Hatter Mozambique
Markers	MAD4HAtTer_v4_MarkersTable.csv	Markers of resistance for Genotyping Analysis
PlasmoDB-59_Pfalciparum3D7Genome	PlasmoDB-59_Pfalciparum3D7_Genome.fasta	Genome of Pfalciparum3D7 in fasta format
PlasmoDB-59_Pfalciparum3D7Gff	PlasmoDB-59_Pfalciparum3D7.gff	Gff file of Pfalciparum3D7
reference_genomes	PkPfPmPoPv.fasta	Reference genomes file
ReferenceSeq_MAD4Hatter	MAD4HatTer_refseqs_v4.fasta	Reference sequences for MAD4HAtter amplicon panel
ReversePrimersMAD4Hatter	MAD4HatTer_rvs_v4.2.fasta	Reverse primers for MAD4Hatter Amplicon panel
Selected_Checkboxes	selected_checkboxes.csv	Selected data points
WHO_Drug_Resistance_Markers	drug_alleles_who.csv	WHO Markers of resistance for Genotyping Analysis
WHO_Drug_Resistance_Markers_Modified	drug_alleles_who_modified.csv	Modified WHO Markers of resistance for Genotyping Analy...

The new variable has been created.