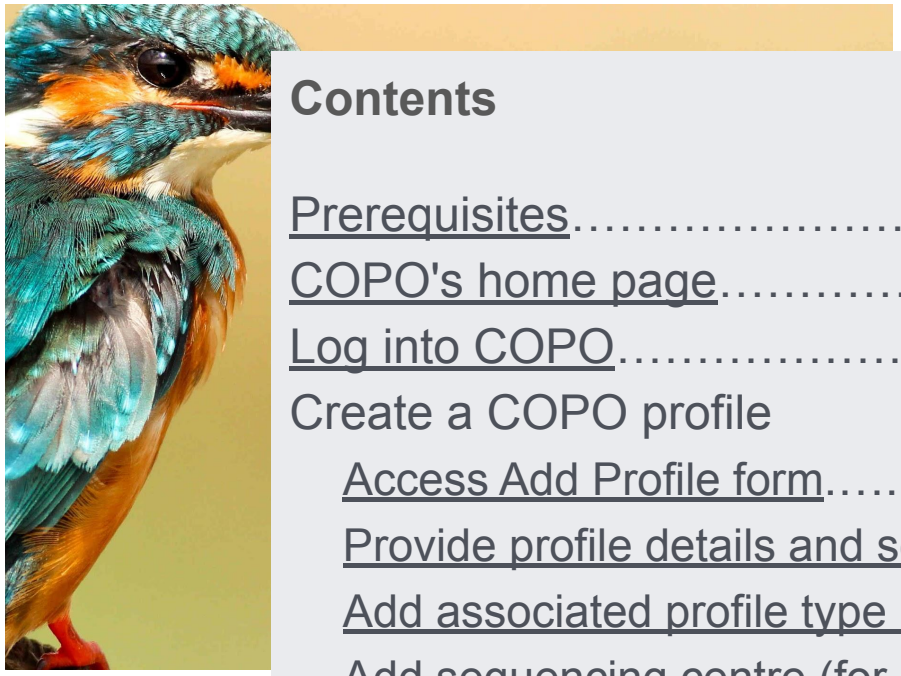
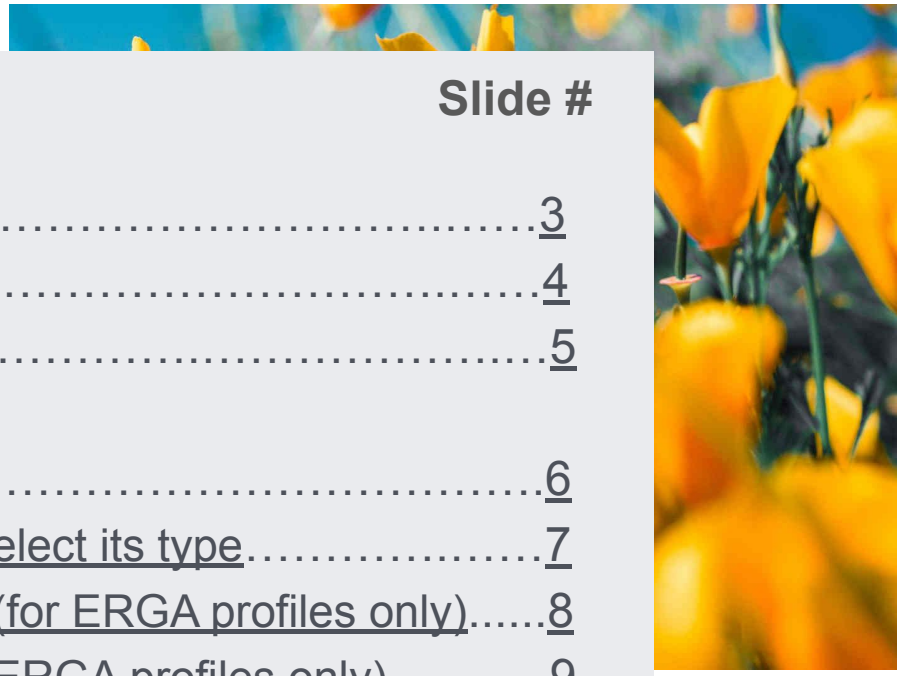
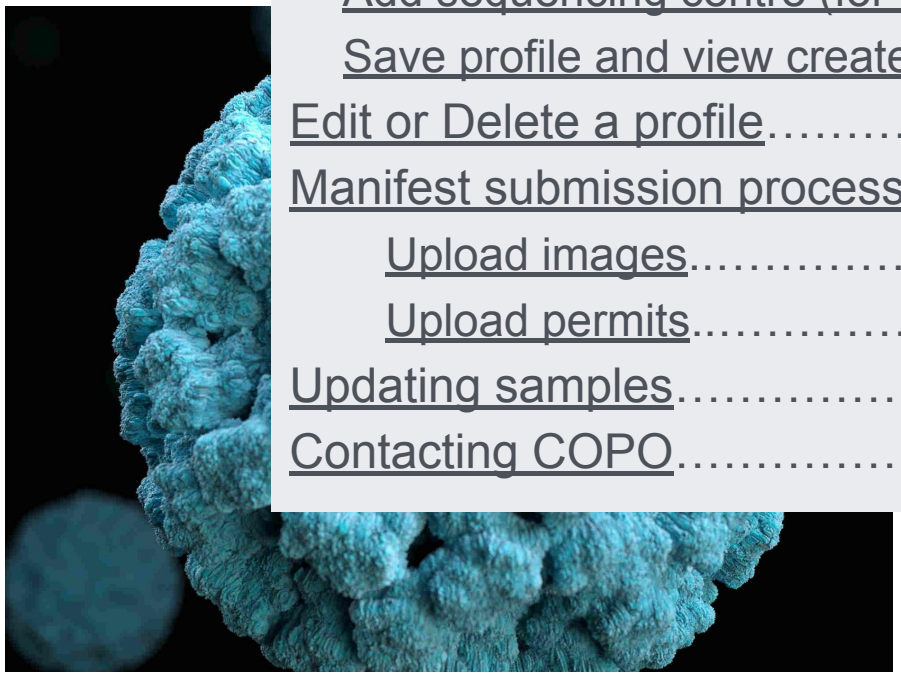
COPO
VISUAL DOCUMENTATION FOR MANIFEST SUBMISSION
Collaborative OPen Omics
ei.copo@earlham.ac.uk, @copo-project
Earlham Institute
Decoding Living Systems

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Prerequisites:

- An ORCid account
- Contact ei.copo@earlham.ac.uk to be added to a project manifest group
- Ensure that you have the latest version of the manifest if you are submitting samples as part of -

  ➔ Aquatic Symbiosis Genomics (ASG) project, please refer to the latest metadata manifest

  ➔ Darwin Tree of Life (DToL) project, please refer to the latest metadata manifest here

  ➔ European Reference Genome Atlas (ERGA) project, please refer to the latest metadata manifest here

ℹ The latest manifest templates can also be found in our documentation.

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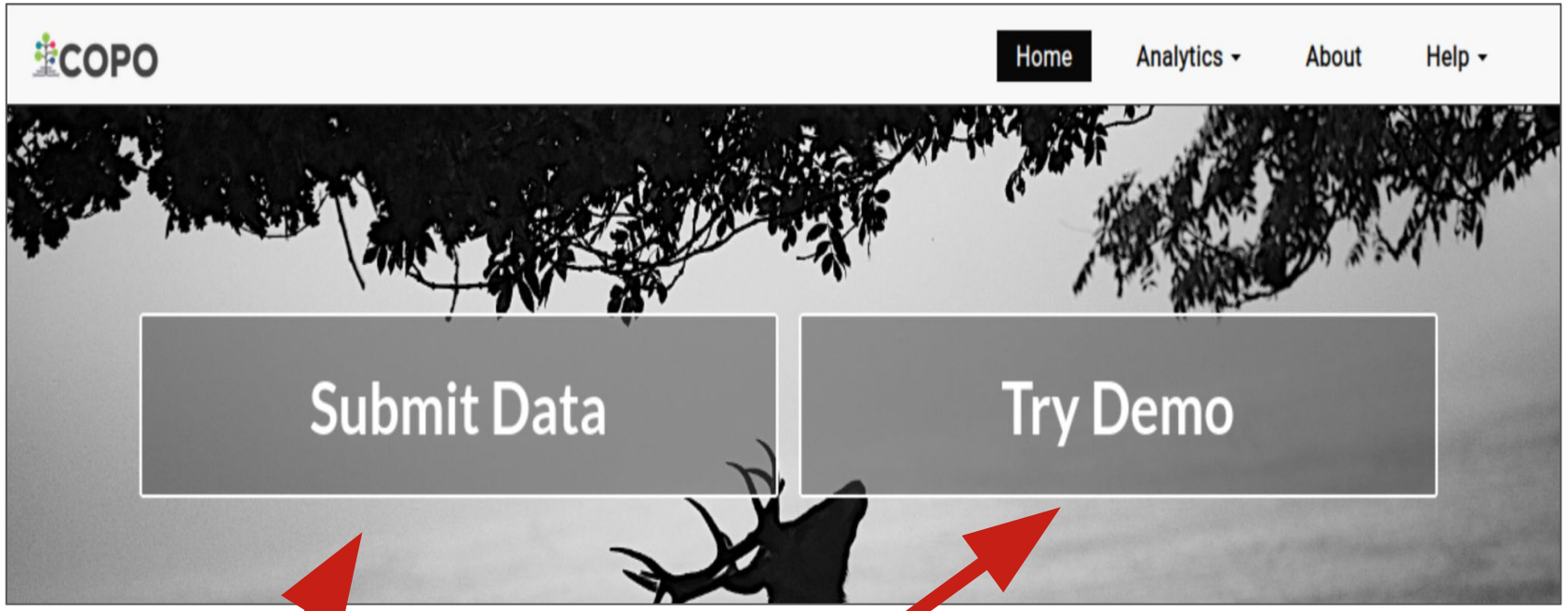
COPO's home page:



To familiarise with the platform

Once you are confident

IMPORTANT - Submissions to European Nucleotide Archive (ENA) through the demo server will not persist, accessions created will be deleted after 24 hours.

The demo server is frequently updated so it may occasionally be unreachable and you may find that we have deleted your past uploads.

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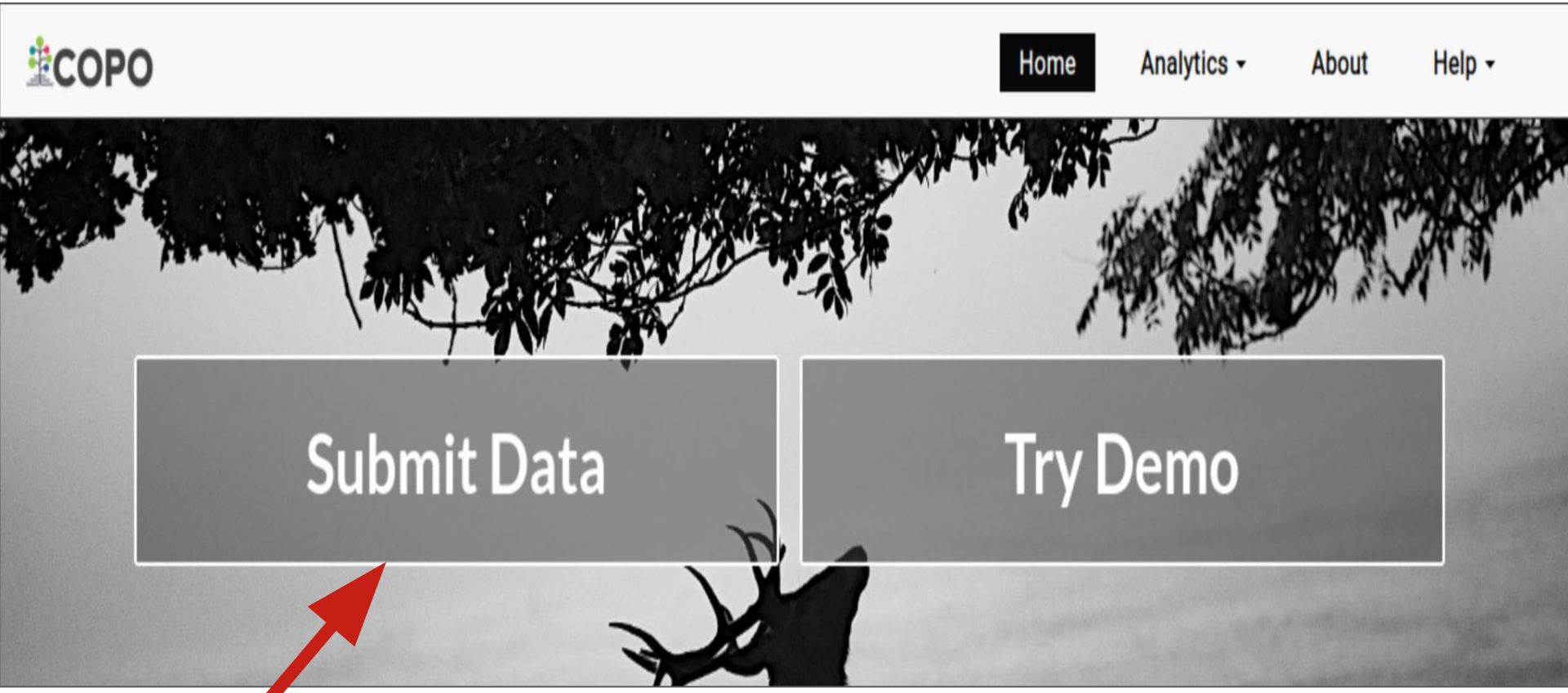
Click “Submit Data” button to log in with your ORCiD credentials:



An ORCiD sign-in form will be displayed after you click the **Submit Data** button.

Enter your ORCiD credentials to proceed to the COPO **Work Profiles** web page.

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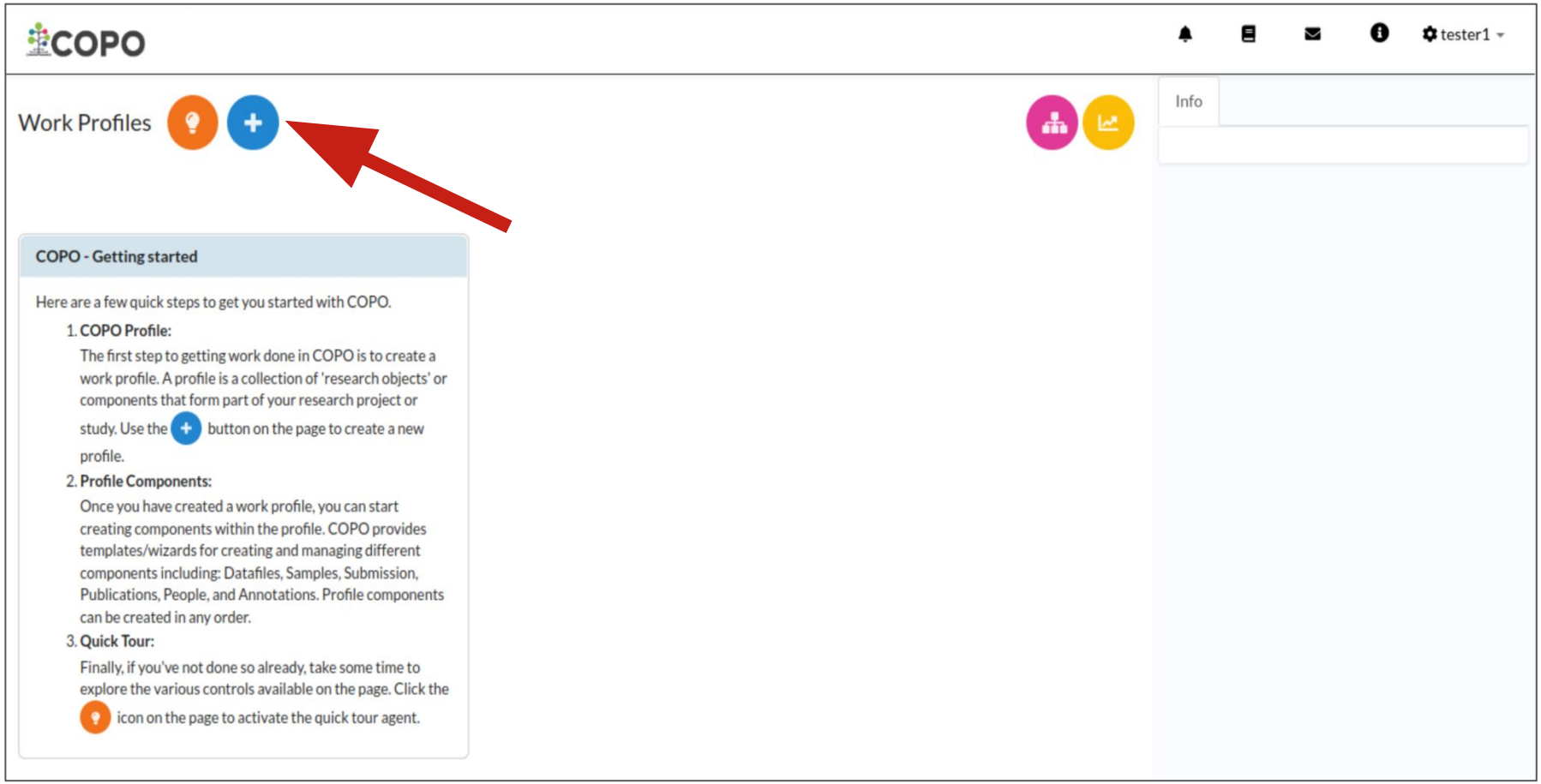
Create a profile:



An **Add Profile** form will be displayed after you click the blue button that has a white plus sign in its centre.

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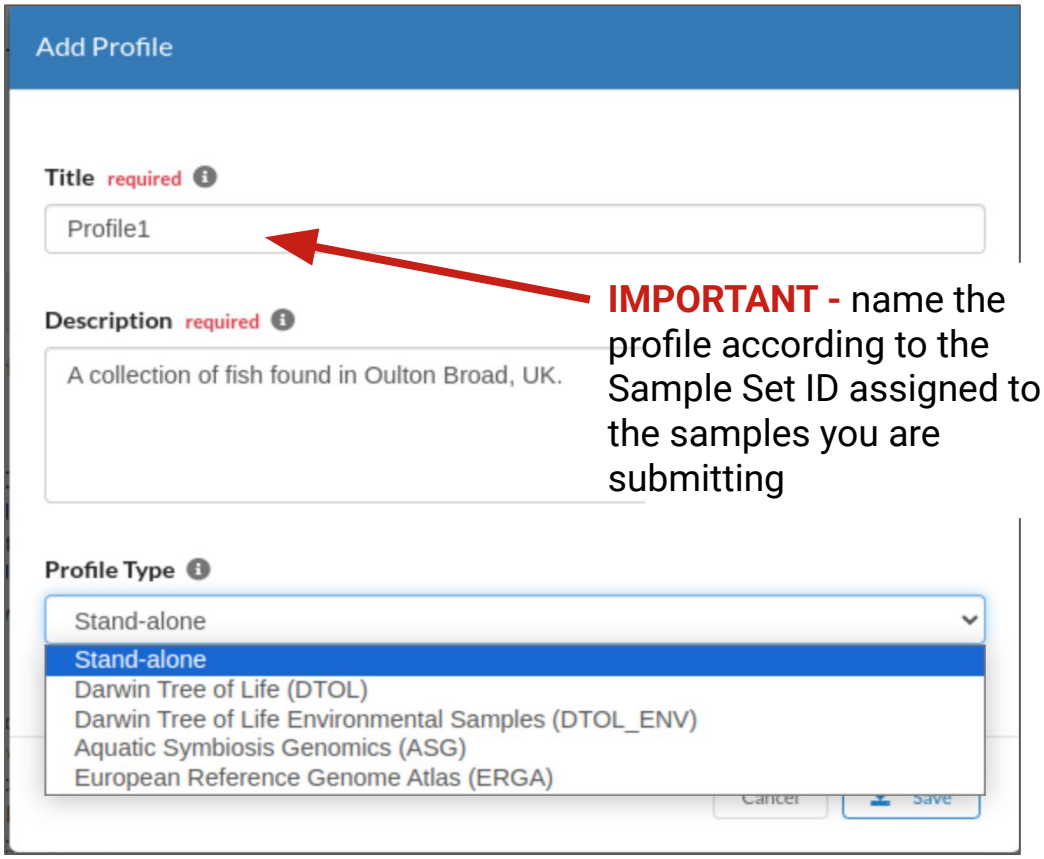
Create a profile:



IMPORTANT - name the profile according to the Sample Set ID assigned to the samples you are submitting

IMPORTANT - If you cannot see the project that you are associated with in the **Profile Type** dropdown menu of the **Add Profile** form, you need to be added to the relevant group.

Please stop here and get in touch with ei.copo@earlham.ac.uk.

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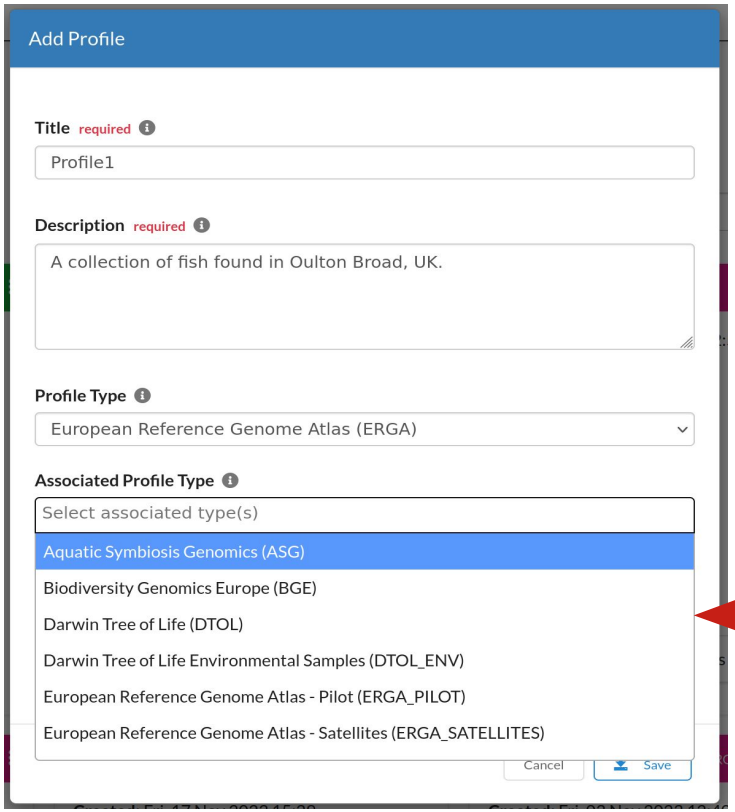
Add associated profile type:



NOTE - for ERGA profile types only

- If your desired profile type is a part of a larger project, select the associated type from the **Associated Profile Type** dropdown menu.

- More than one associated type can be selected from the dropdown menu for the profile type.

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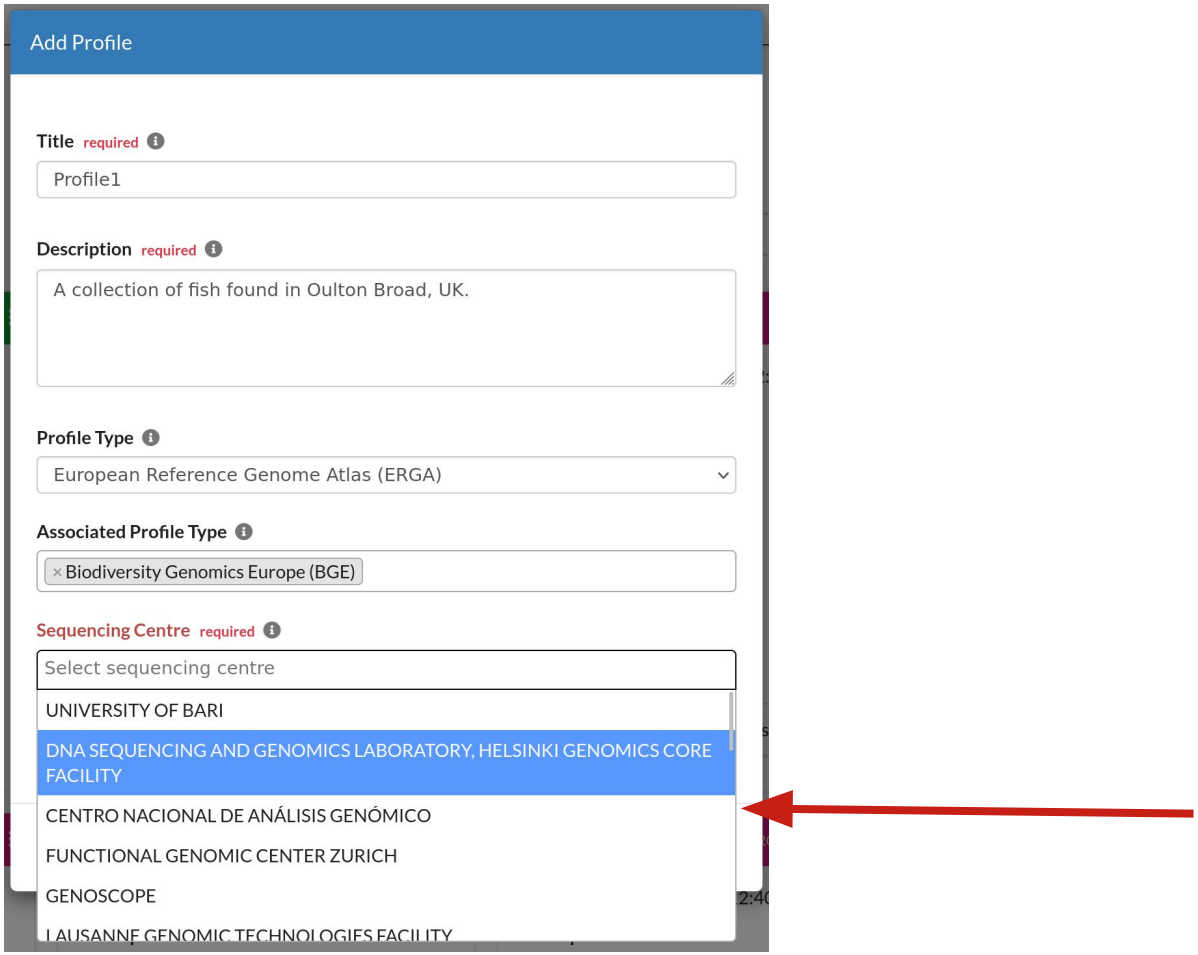
Add sequencing centre:



NOTE - for ERGA profile types only

- Select the the centre where your samples will be sequenced at from the **Sequencing Centre** dropdown menu.

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New profile created:

After having provided the details in the **Add Profile** form and clicked the **Save** button, your new profile will be displayed on the COPO **Work Profiles** web page

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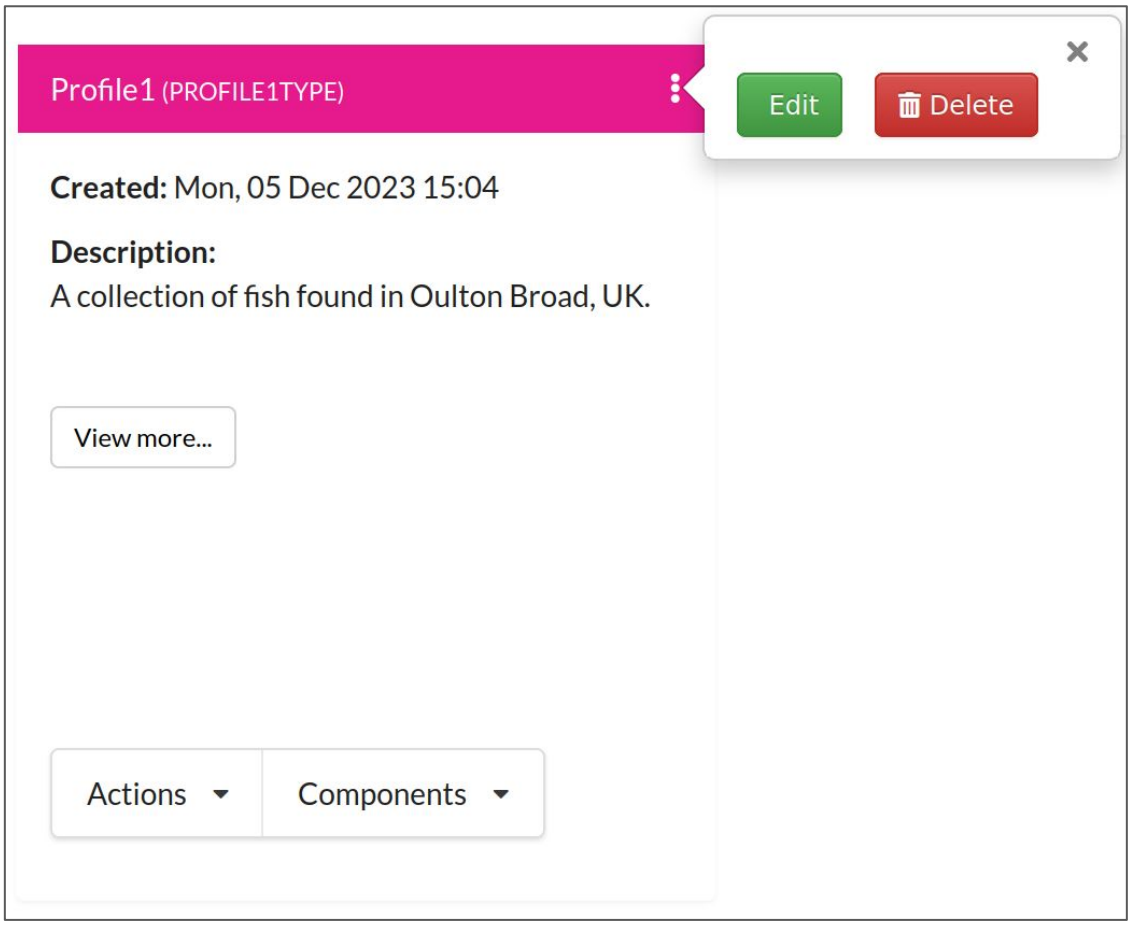
Edit or Delete profile:



If you would like to edit or delete a profile that you have created, click the white vertical ellipsis (⋮) located at the top right of the desired profile panel to view the profile options to do so

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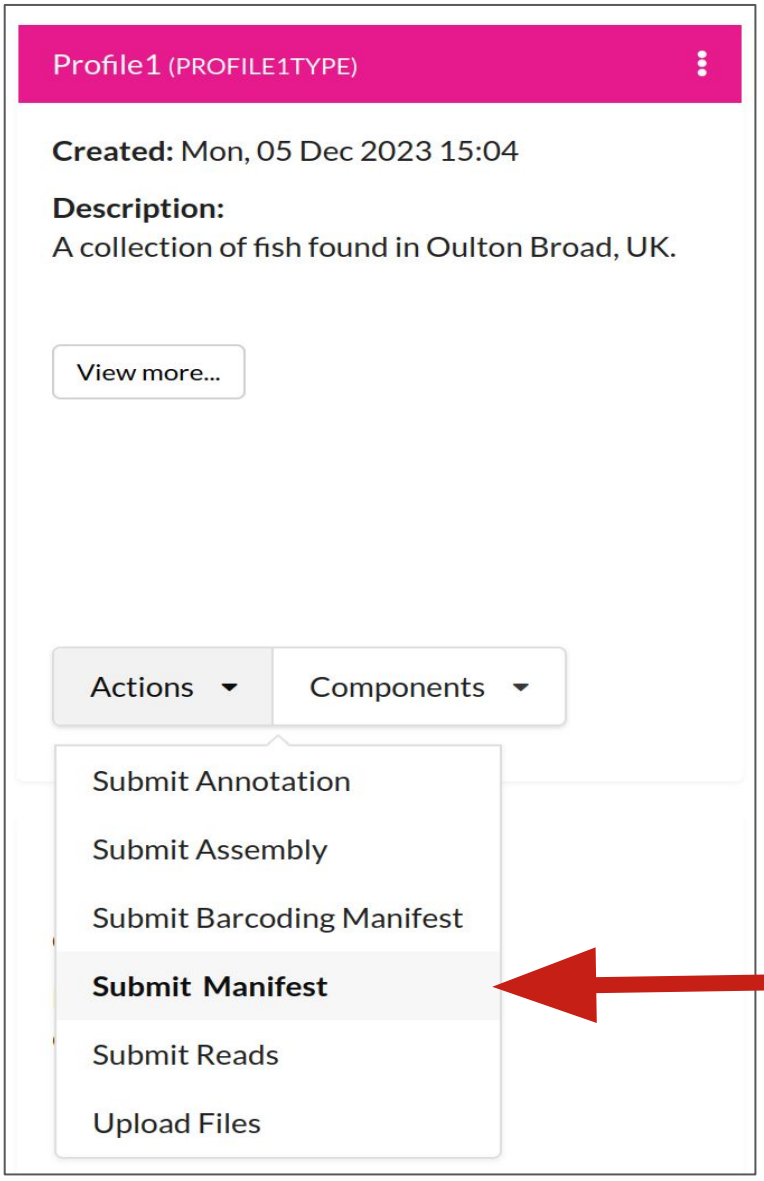
Upload a manifest:



The colour and wording of this profile panel will differ depending on which project you are submitting a manifest for.

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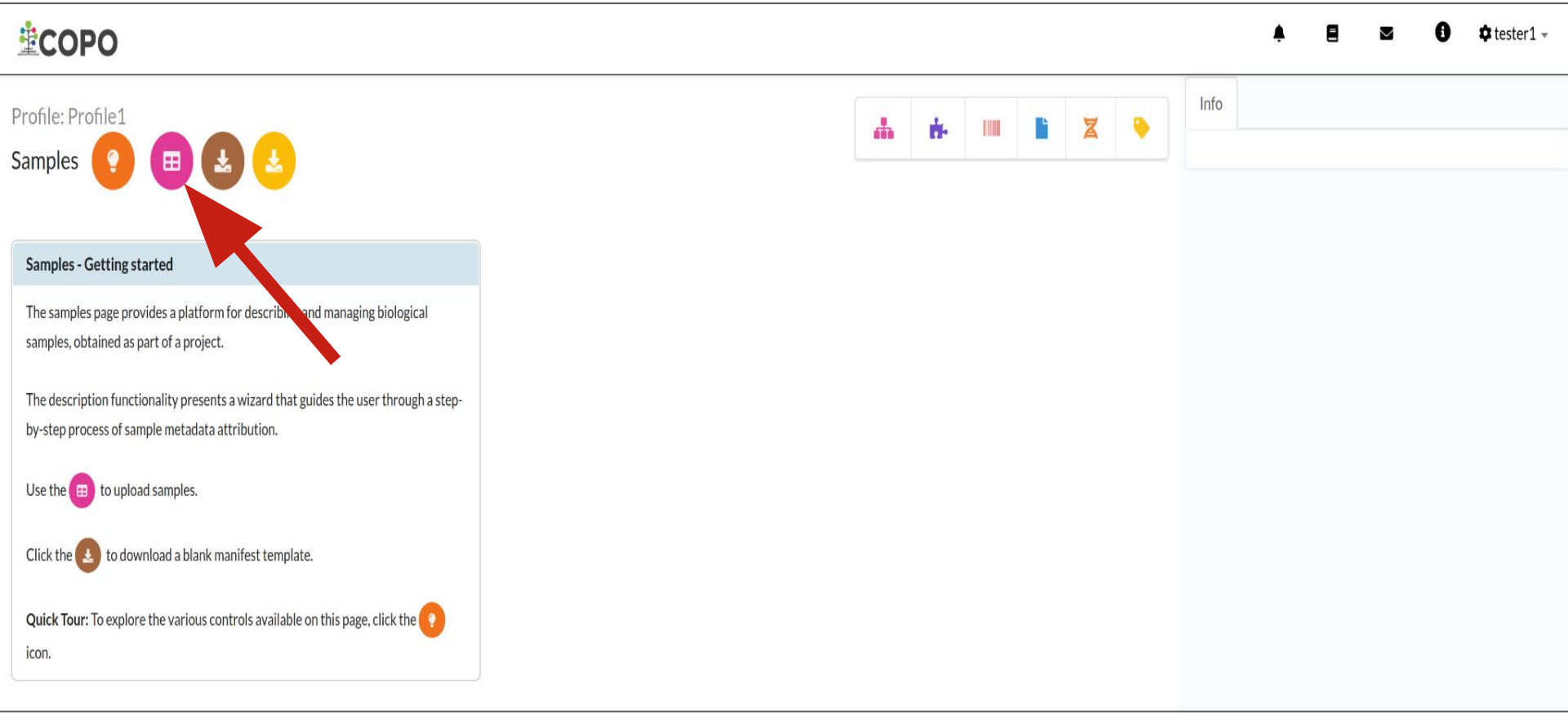
Upload a manifest:



The colour and wording of the **Samples** web page will differ depending on which project you are submitting a manifest for.

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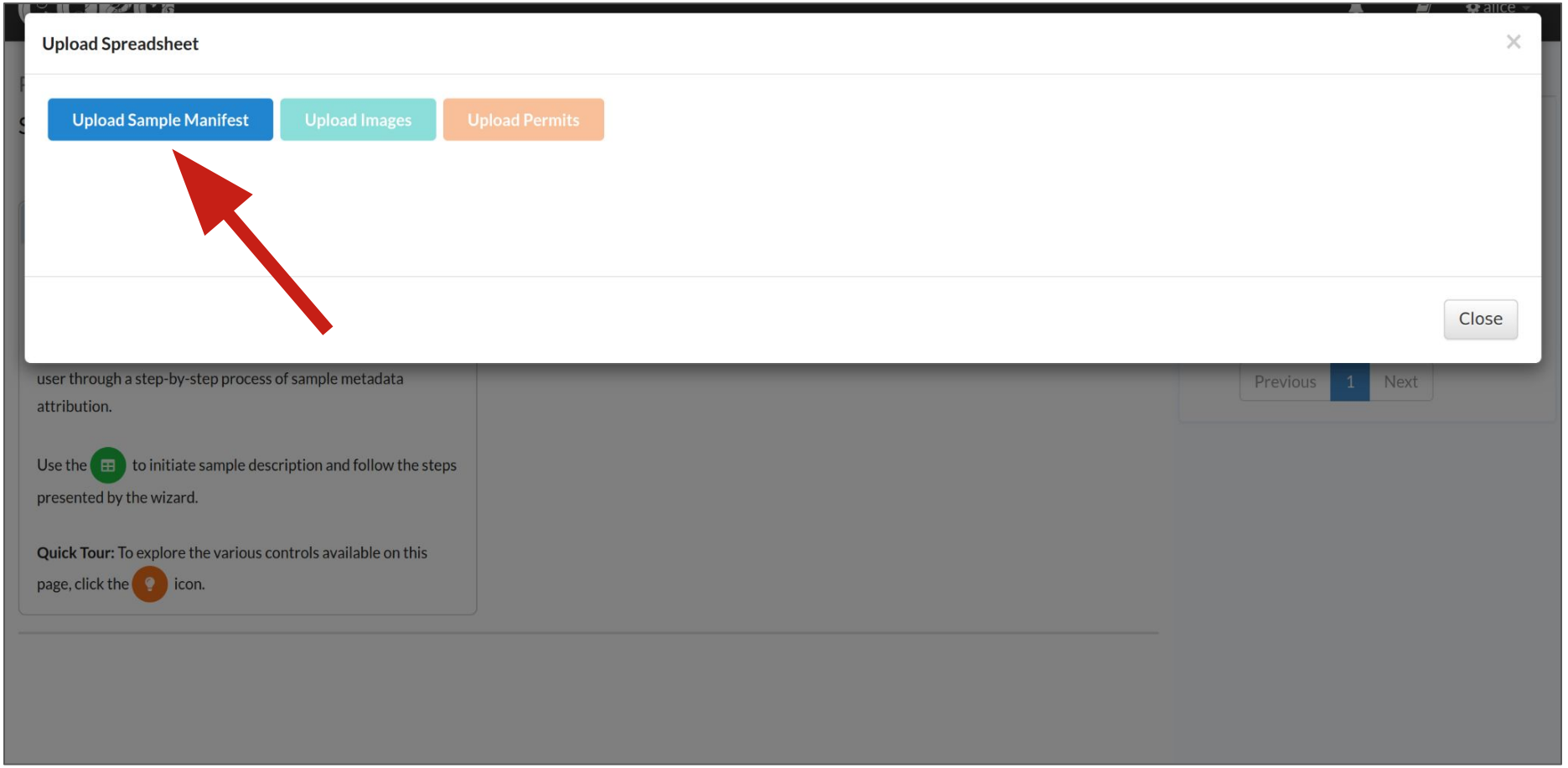
Upload a manifest:



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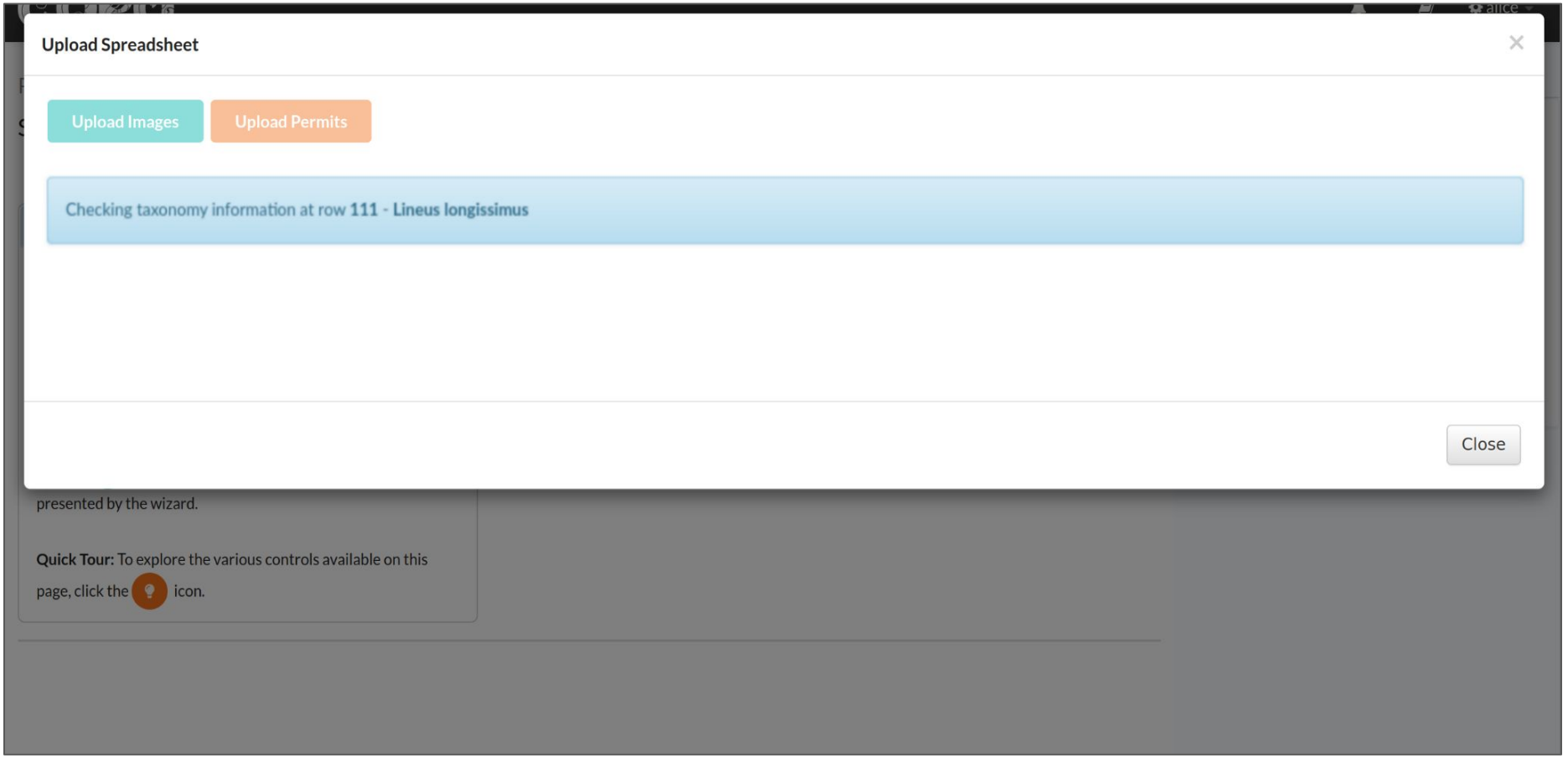
COPO will validate taxonomy information and manifest format:



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What's happening (part 1):

- COPO is retrieving information from National Centre for Biotechnology Information (NCBI) to check that the taxonomy information provided is correct. We also check that the TAXON_ID is submittable to ENA.
- If some of the taxonomy fields are missing (excluding SCIENTIFIC_NAME), COPO will make an educated guess about what these fields should be and will display warnings about what is going to be filled in.

  The taxonomy checks will be much quicker if you fill in TAXON_ID.
- COPO will substitute scientific name synonyms with the official scientific name. It will display a warning and also record the change in OTHER_INFORMATION.
- If any taxonomy field is incorrect, COPO will display an error and reject the manifest. You can download the error list with the red "Export Errors" button on the top right.
- **If you are unhappy with any of the warnings or errors, DO NOT click the finish button instead, contact NCBI to discuss the taxonomy.**

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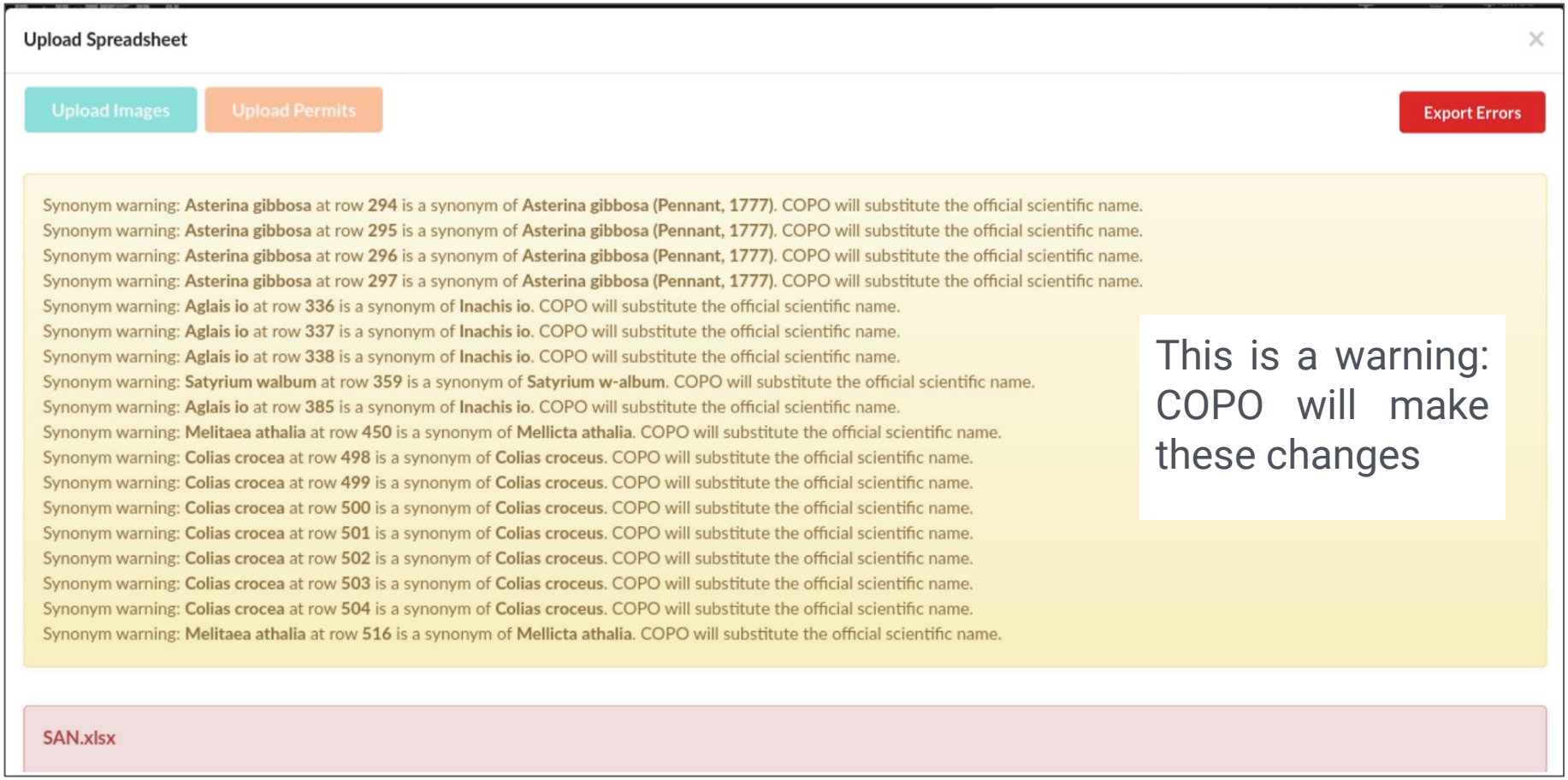
Manifest uploaded -taxonomy warnings-:



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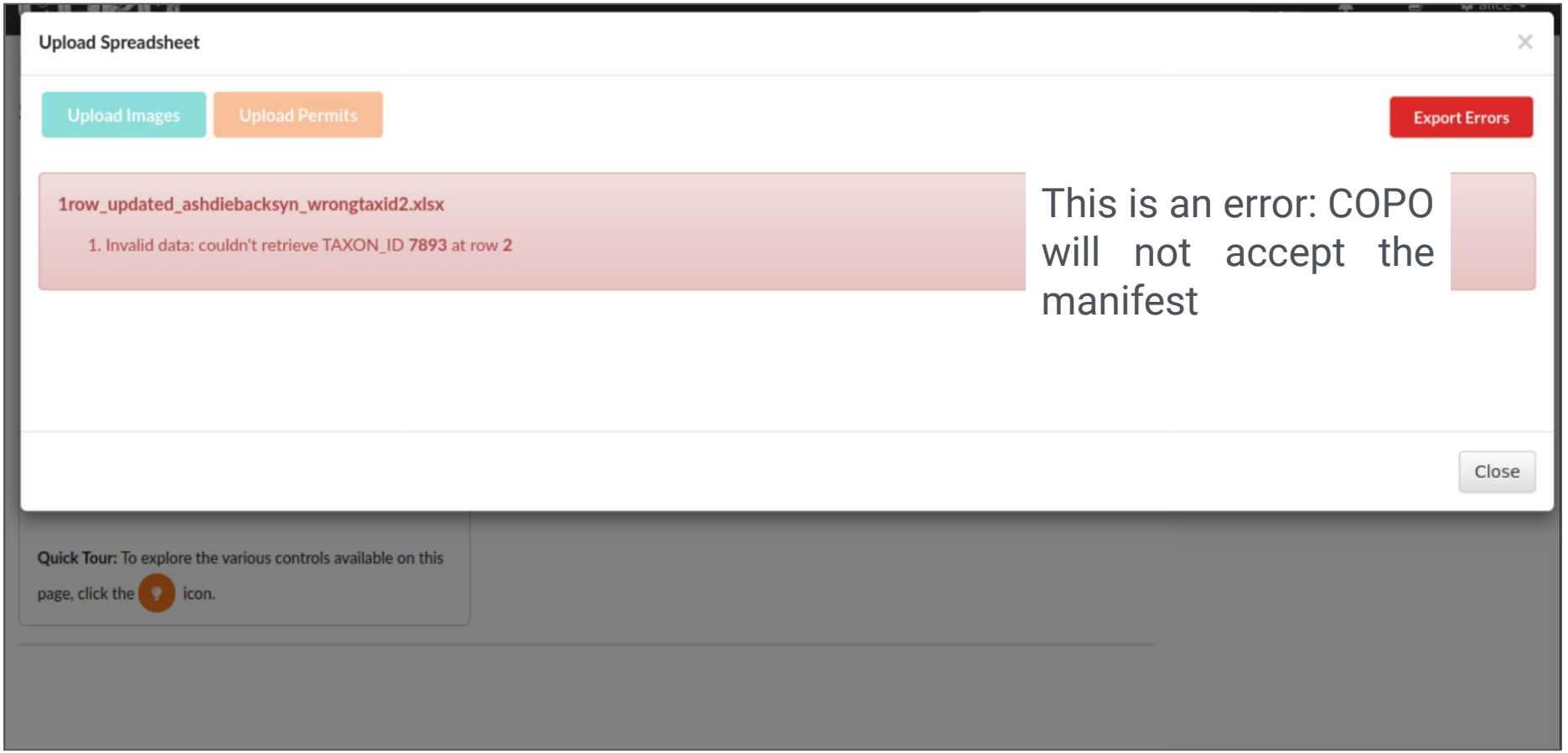
Manifest uploaded -taxonomy errors-:



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What's happening (part 2):

- **ONLY IF** the taxonomy validation was successful and produced no errors, will COPO check the manifest against SOP specifications. This includes checks for general format, missing data, cells that have restricted values, etc..

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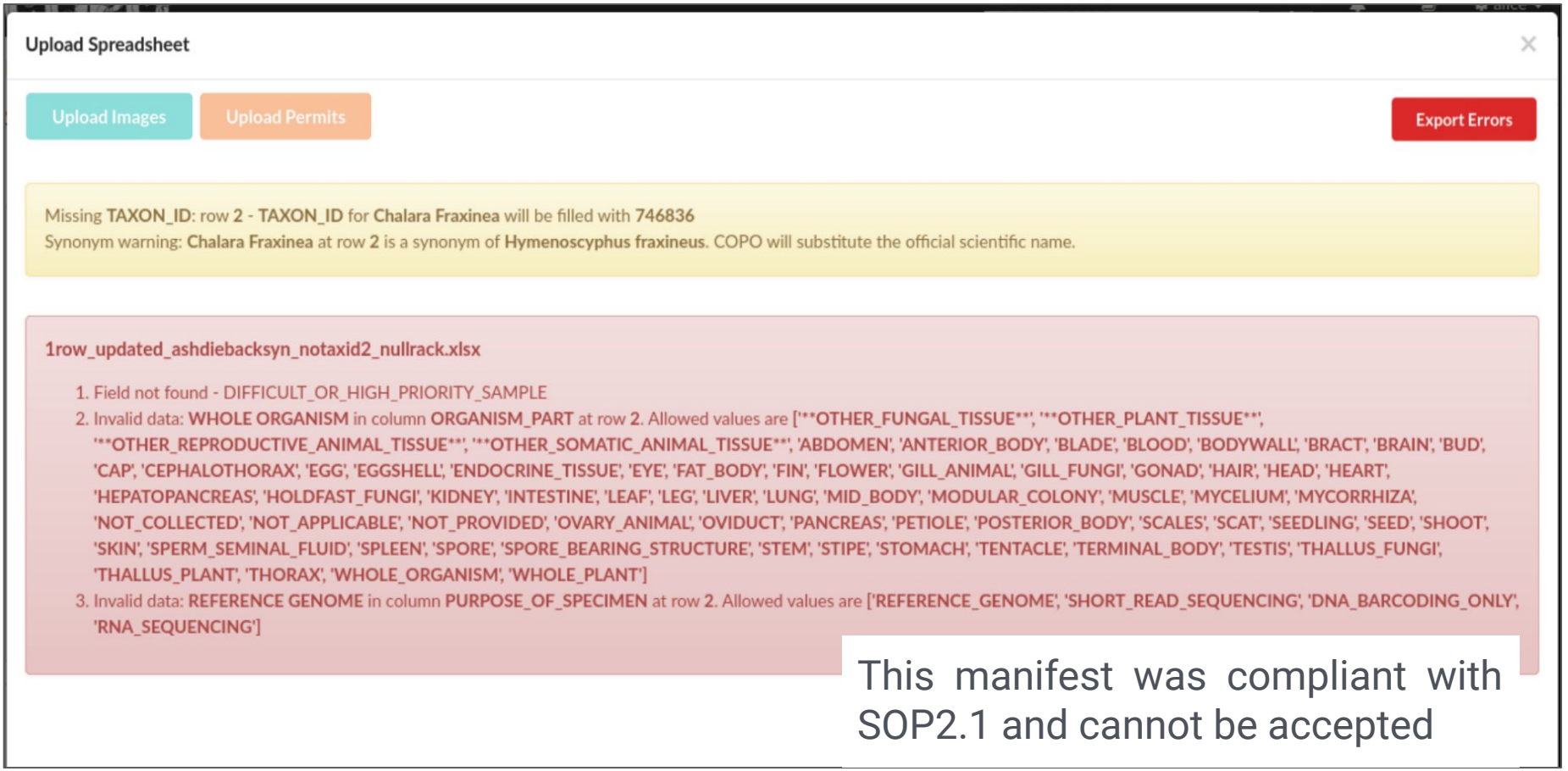
Manifest uploaded - with compliance errors-:



This manifest was compliant with SOP2.1 and cannot be accepted

The errors should guide you to correct the manifest. You will have to correct and re-upload the updated spreadsheet

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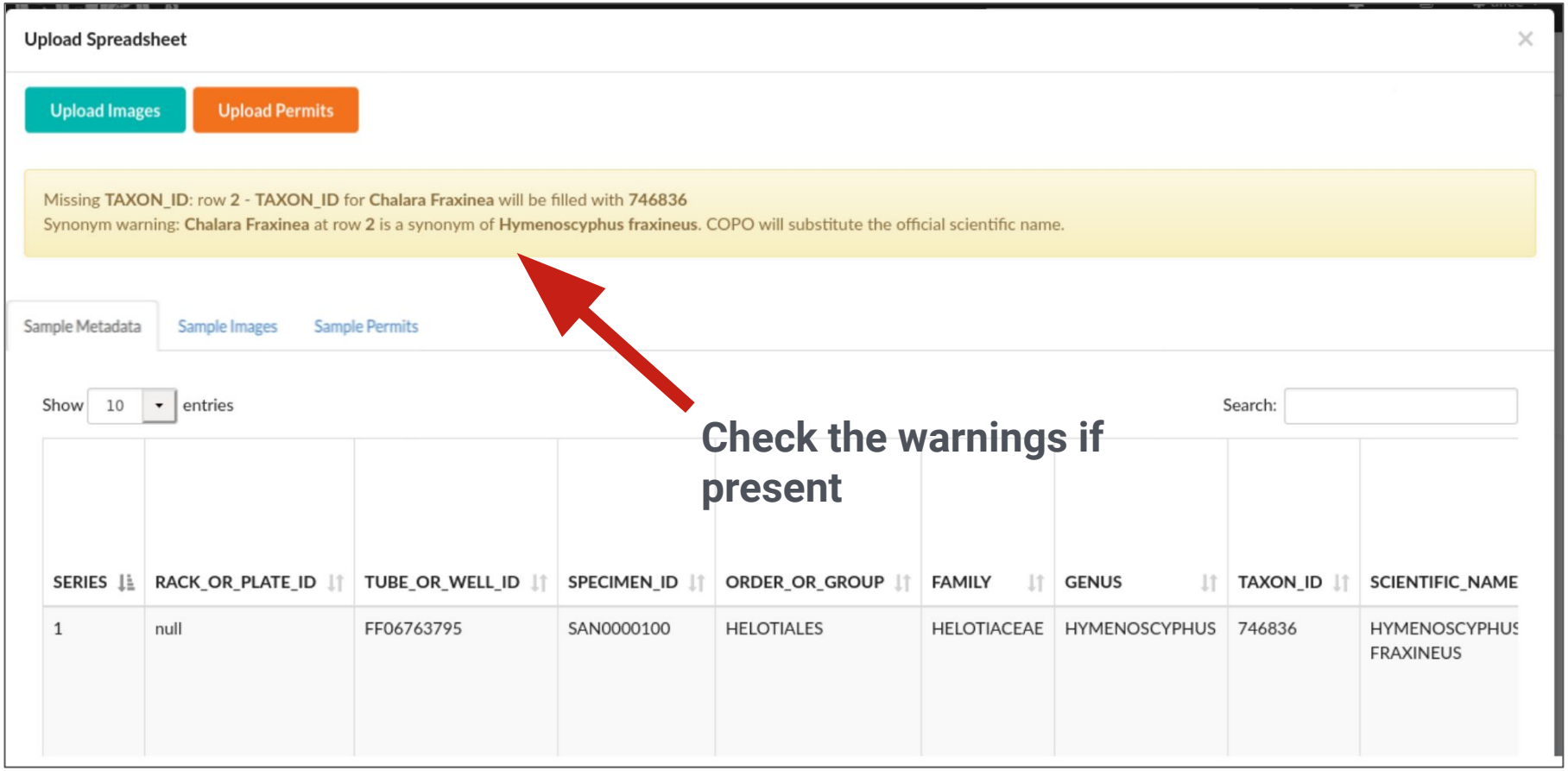
Manifest uploaded -correct manifest-:



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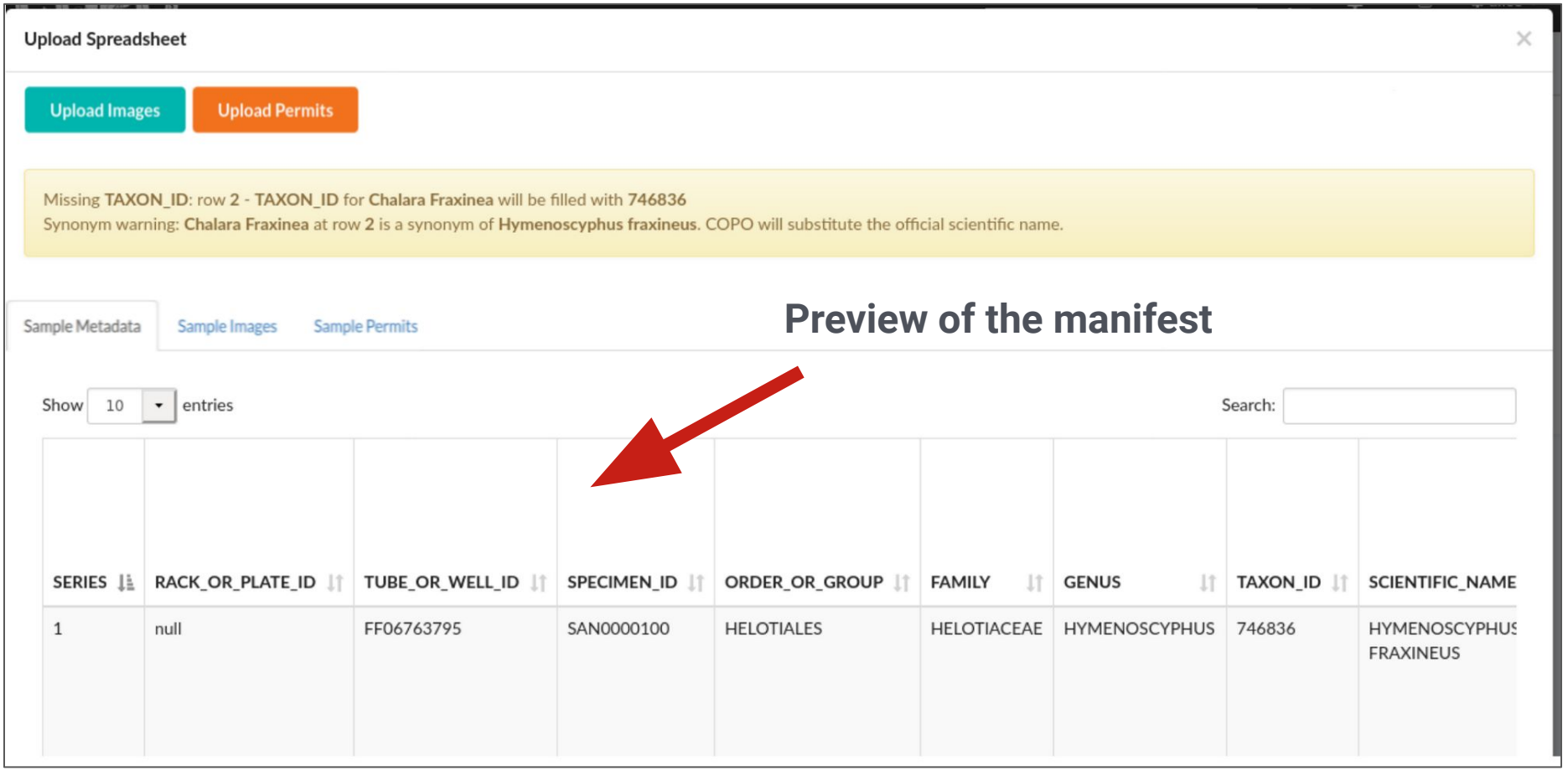
Manifest uploaded -correct manifest-:



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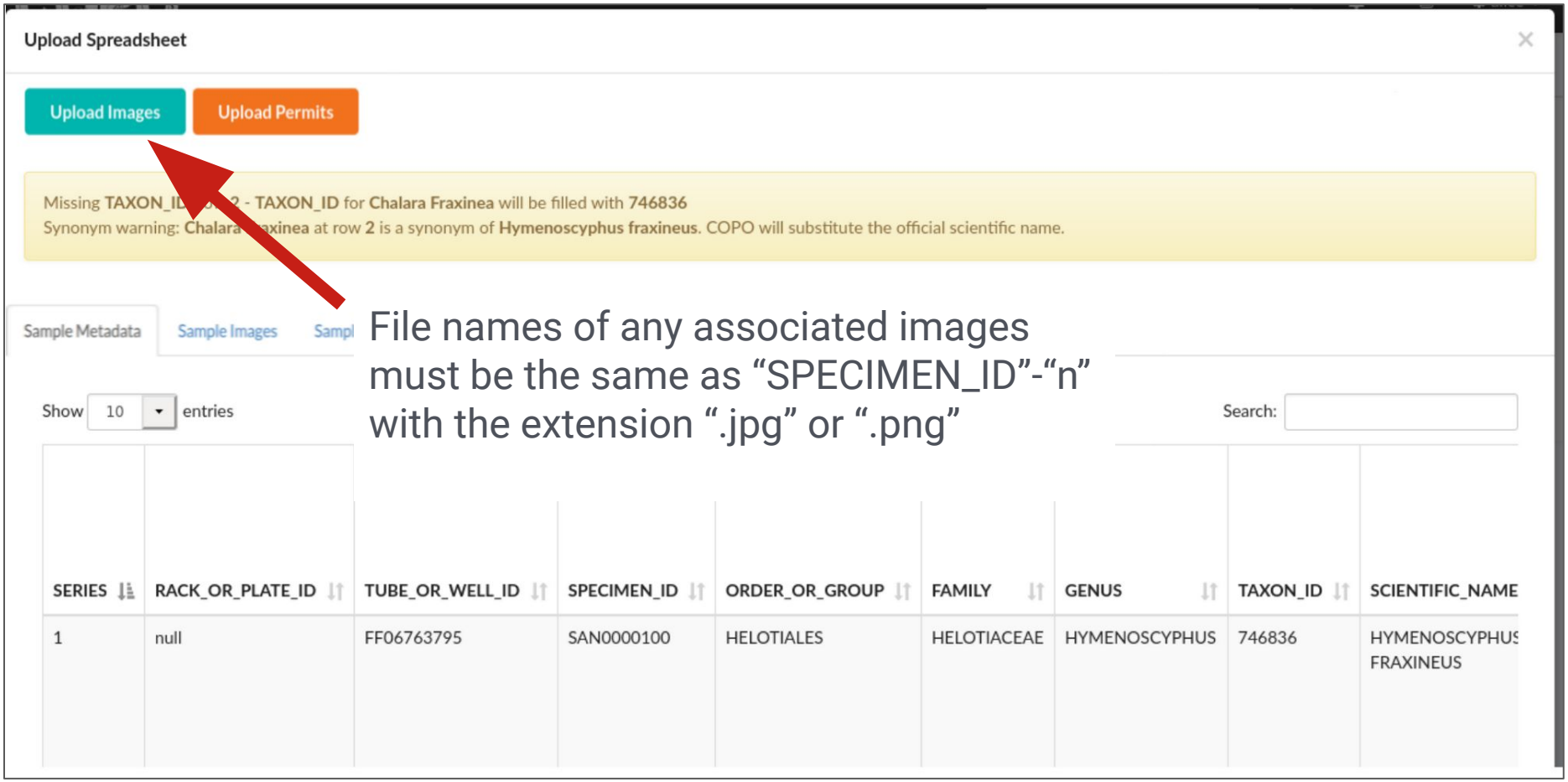
Upload images:



File names of any associated images must be the same as “SPECIMEN_ID”-“n” with the extension “.jpg” or “.png”

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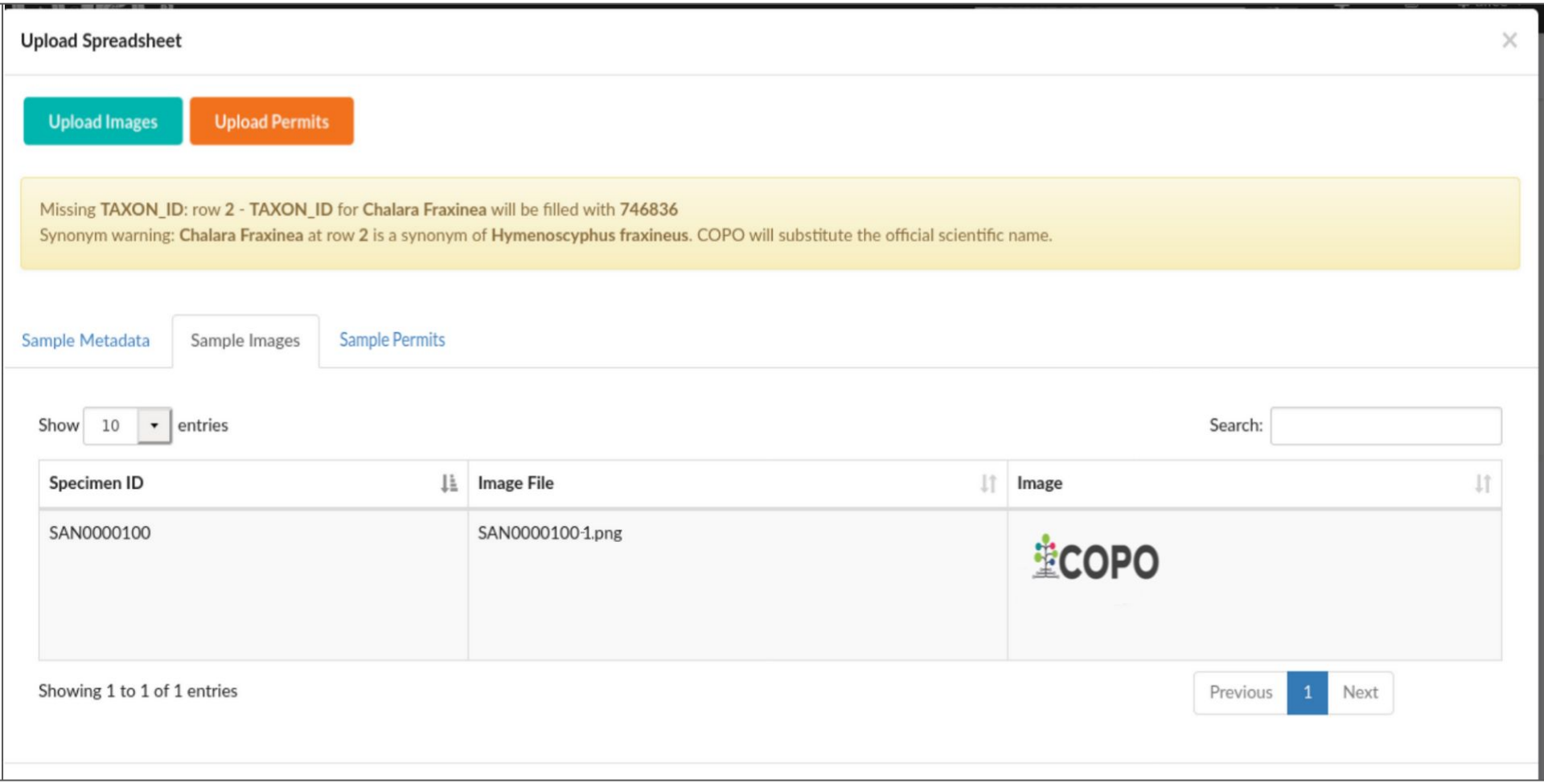
Uploaded images:



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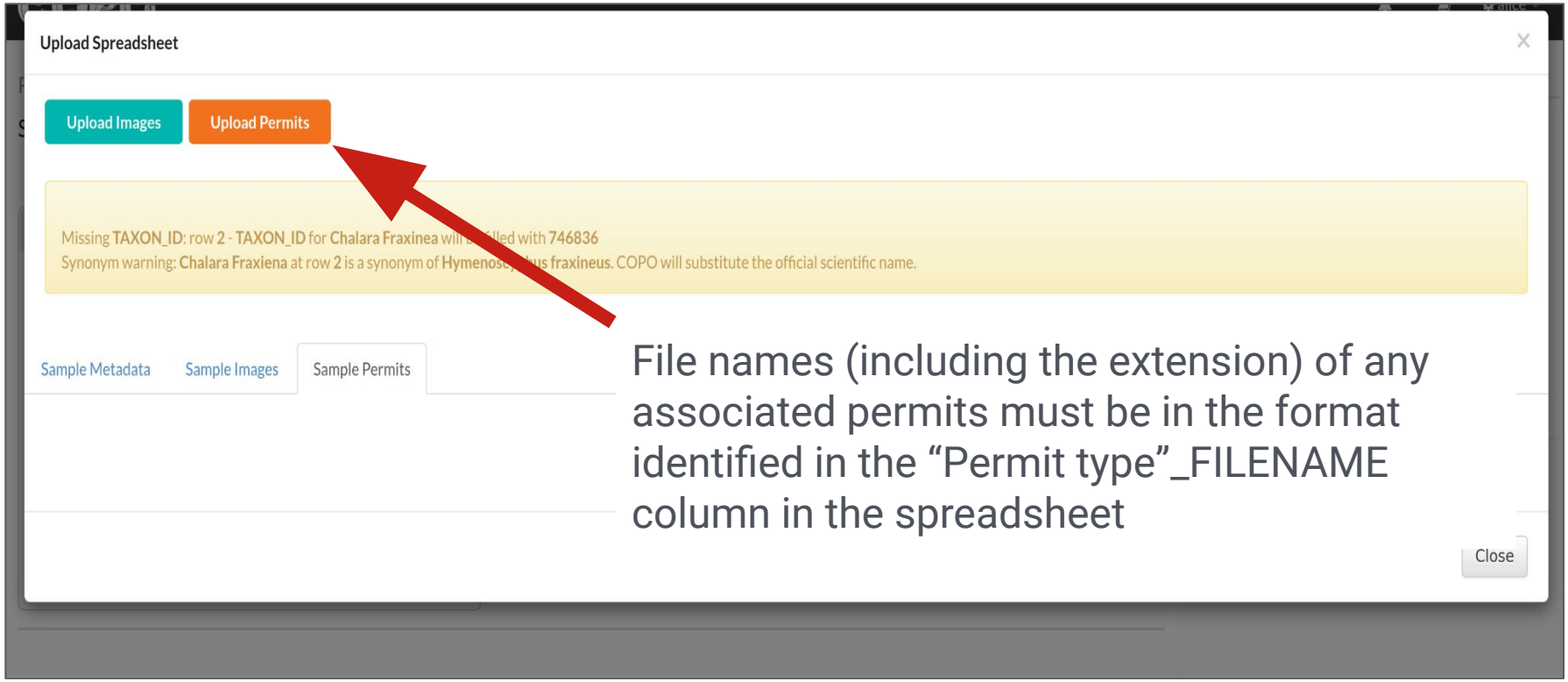
Upload permits:



IMPORTANT - If you have more than one permit file to upload, they must be uploaded at the same time i.e. after you have clicked the "Upload Permits" button, navigate to the directory where the permits are stored and **CTRL + click** all of the permits so that all the permits are highlighted and uploaded at the same time.

All permit files have to be selected/opened from the directory and uploaded together not one after the other.

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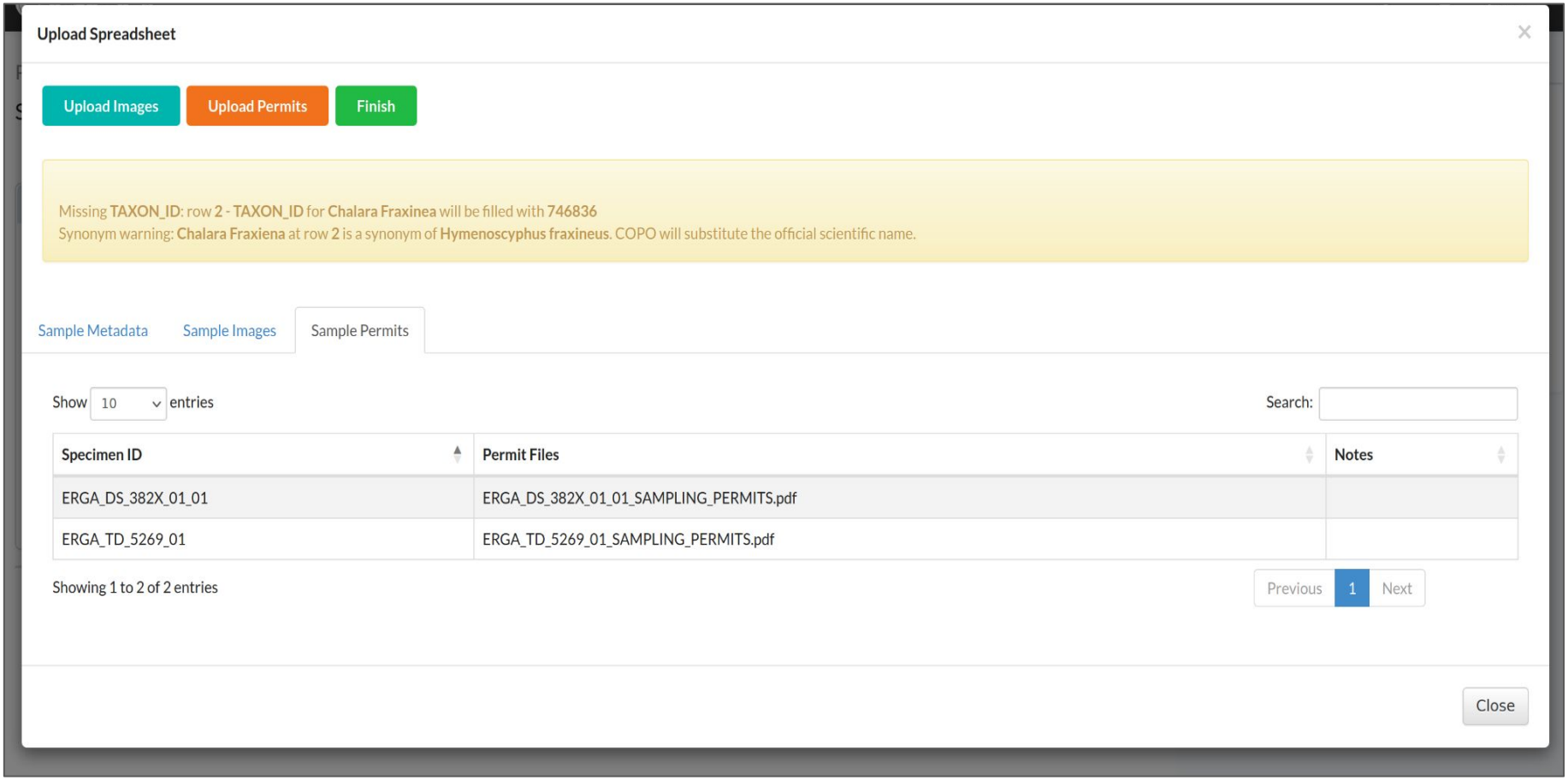
Uploaded permits:



If there are any errors with the permit upload process, they will be displayed in the **Notes** table column of the **Sample Permits** tab

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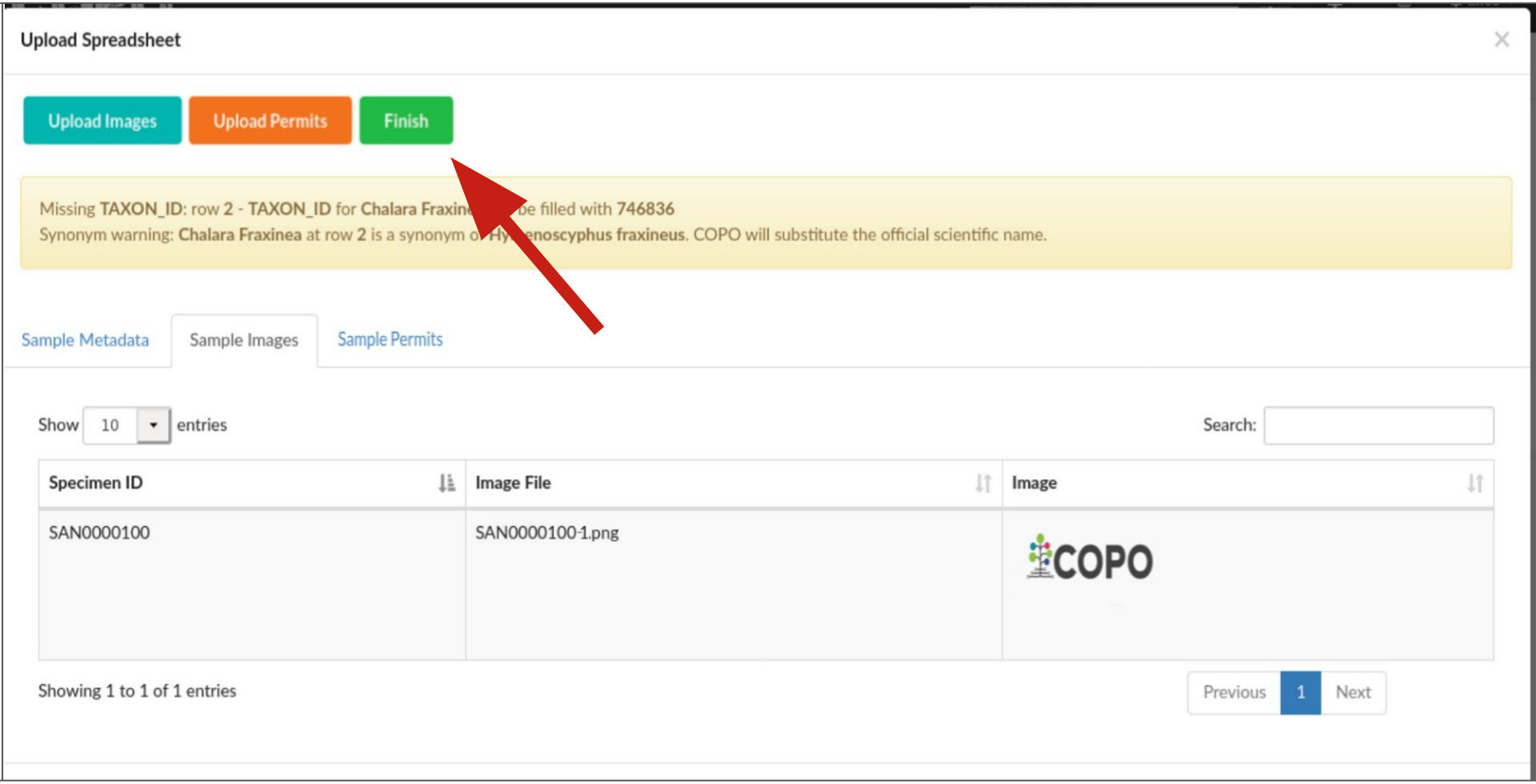
Create the samples in COPO by clicking “Finish”:



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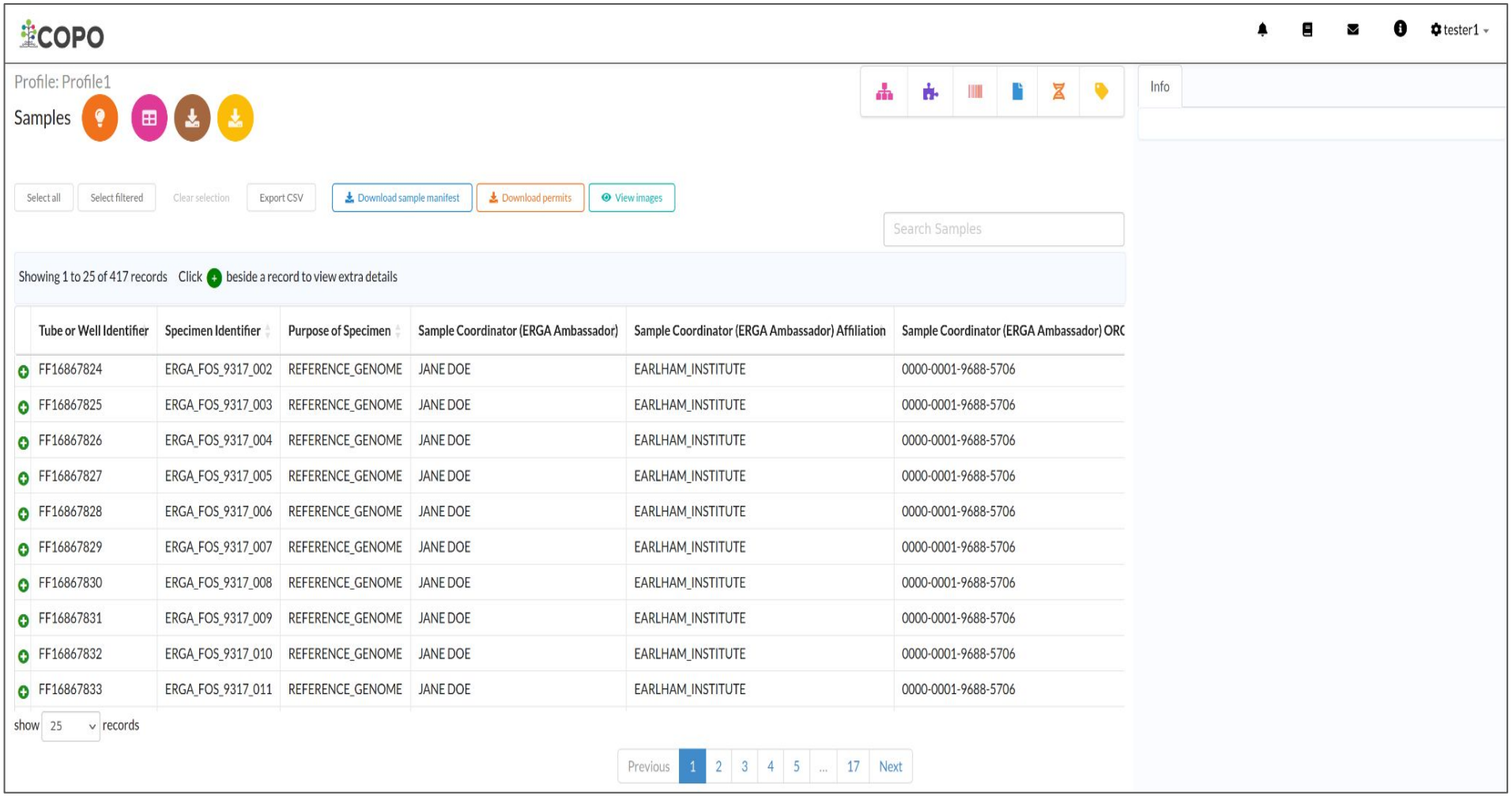
Uploaded samples:



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Sample Managers:

- At this point, the sample managers will be emailed that a new manifest has been uploaded. They will be able to accept or reject each sample after inspection.

  After samples are accepted by a sample manager, they will be submitted to European Nucleotide Archive (ENA).

  Accessions can be inspected by:

  - Scrolling right in the previous view
  - Clicking the button on the **Samples** web page to access the **Accessions** web page for the desired profile
  - Clicking the

component button associated with the desired profile on the **Work Profiles** web page to access the **Accessions** web page

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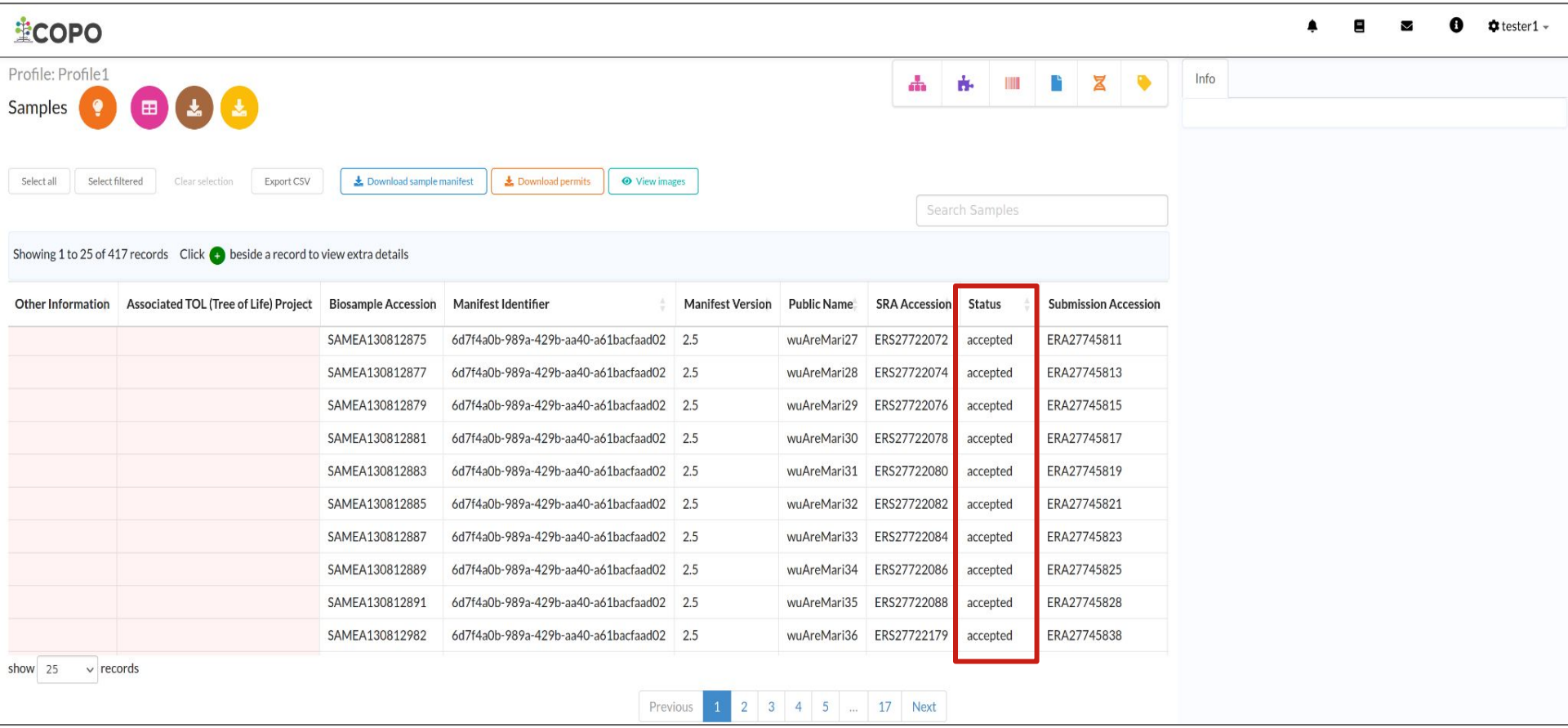
Accepted samples:



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Updating samples:

- To update samples, reupload a manifest with the amended changes. The new value will be detected and updated automatically once the resubmission is successfully completed.

  More information regarding sample updates can be found here.

ℹ Not all field values of existing samples can be updated by resubmitting a manifest with the amendments.

The fields that can be updated are listed here.

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If you encounter any errors or unexpected behaviour, please email ei.copo@earlham.ac.uk or open a GitHub issue in the COPO repository.

If you have a feature request for future releases, please open an issue in the GitHub repository.

For detailed information regarding manifest submission and COPO, please see our documentation.

collaborative-open-plant-omics/COPO-production

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