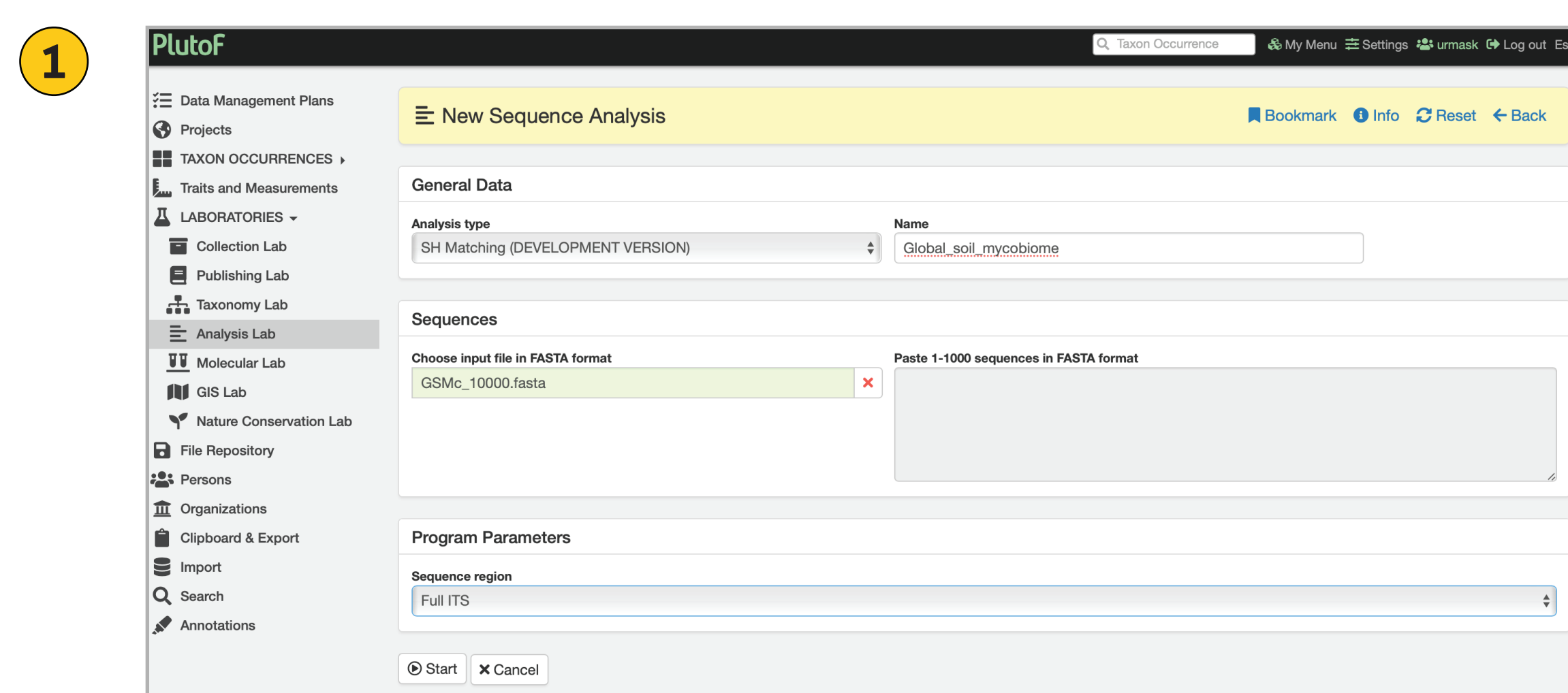


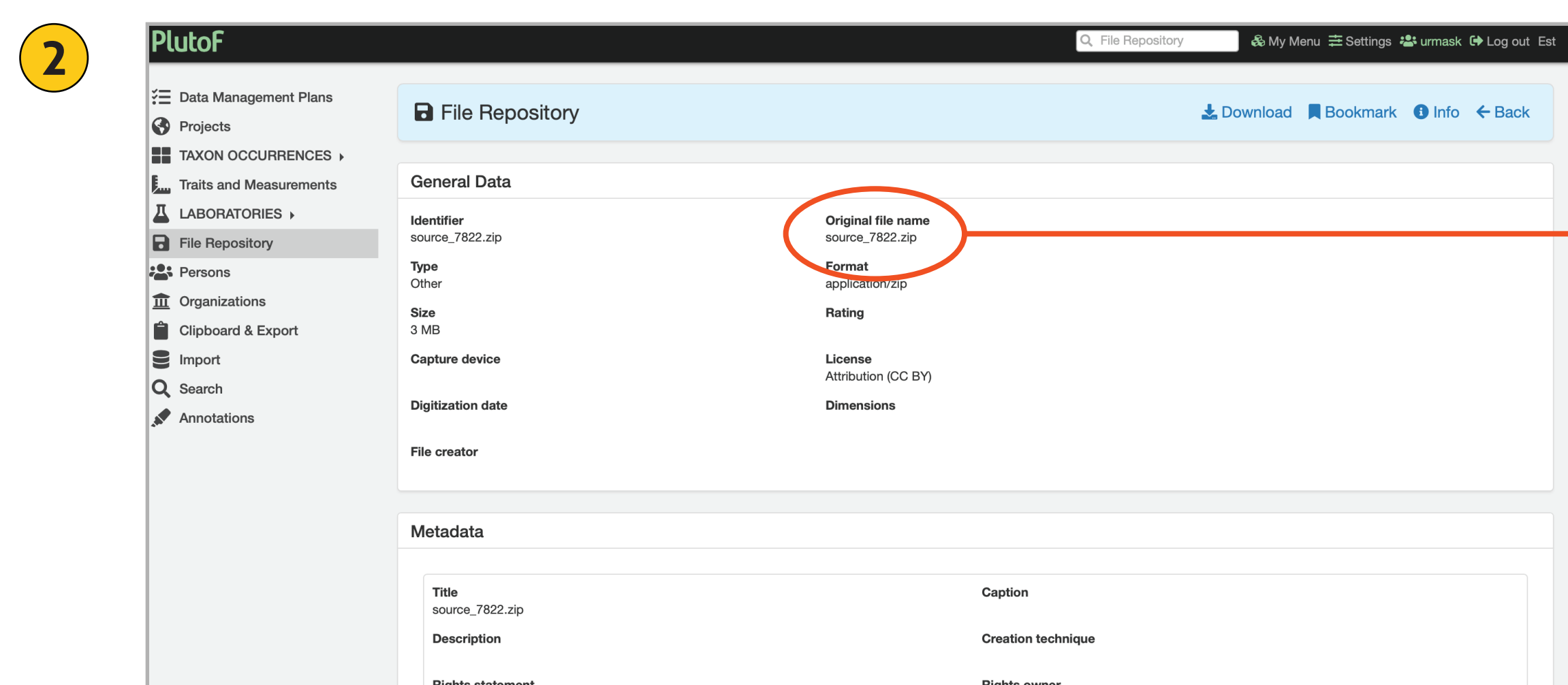
Species hypothesis matching analysis

The new UNITE species hypotheses (SH) matching analysis is a digital service for species discovery from environmental DNA. The service is based on UNITE datasets (<https://unite.ut.ee>) hosted in PlutoF (<https://plutof.ut.ee>). Its output includes information on what SHs are present in eDNA samples, whether they represent potentially undescribed species, whether these SHs have been found in other studies, and more. The output provides DOI (digital object identifier)-based stable identifiers for unambiguous communication of species found in eDNA. DOIs are connected to the taxonomic backbone of PlutoF and GBIF (<https://www.gbif.org>). In this way, every DOI is accompanied by a taxon name that is used simultaneously for the communication of species. In the case of potentially undescribed species or species that are not present in the UNITE SH system, preliminary DOIs are issued by the PlutoF system. UNITE services are focused on fungi but cover all Eukarya by using publicly available rDNA ITS marker sequences and accompanying sample metadata. Analysis results can be published in GBIF as DNA-derived occurrence data. The source code of the UNITE SH matching analysis tool is freely available in GitHub (https://github.com/TU-NHM/sh_matching_pub) with an implementation accessible online on PlutoF platform for registered users. Further information about the UNITE resources is provided in the references below.

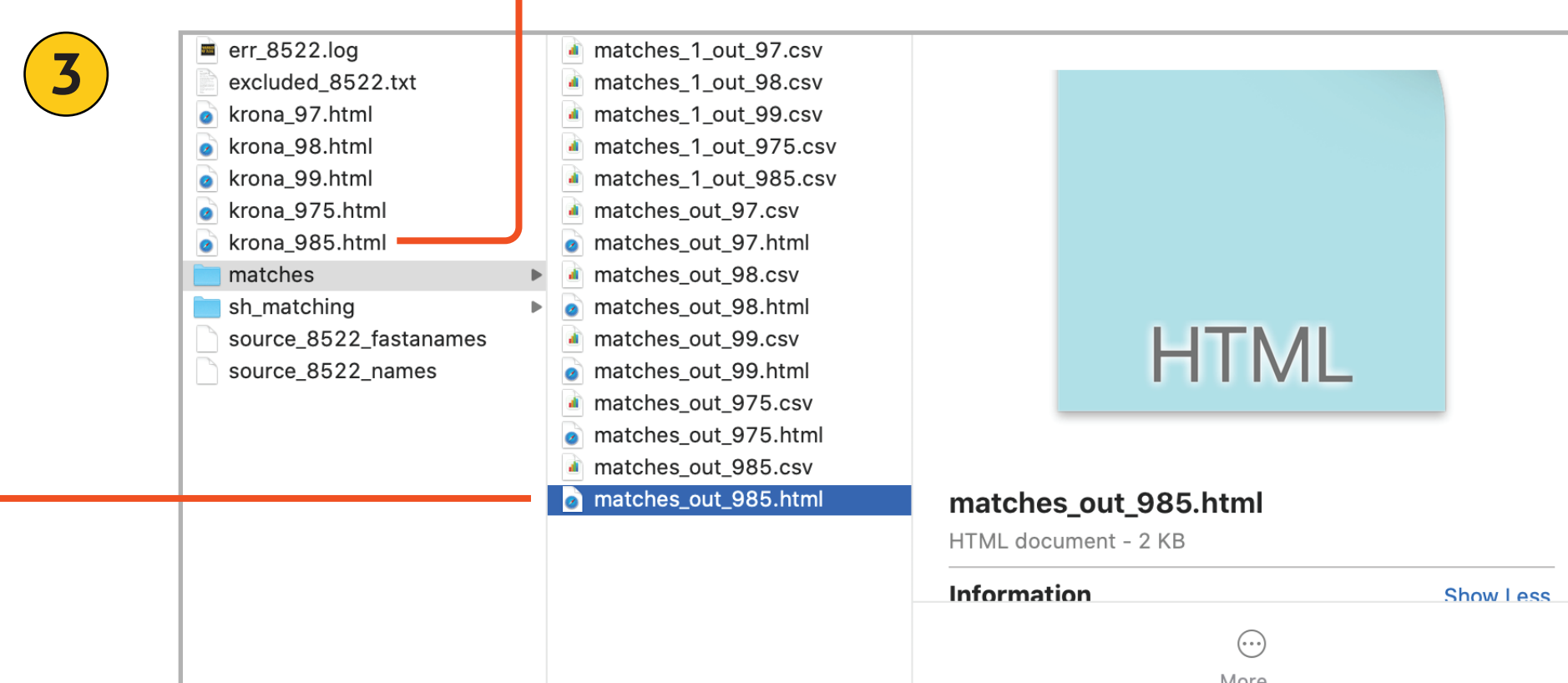
Screenshots of the SH analysis and its results



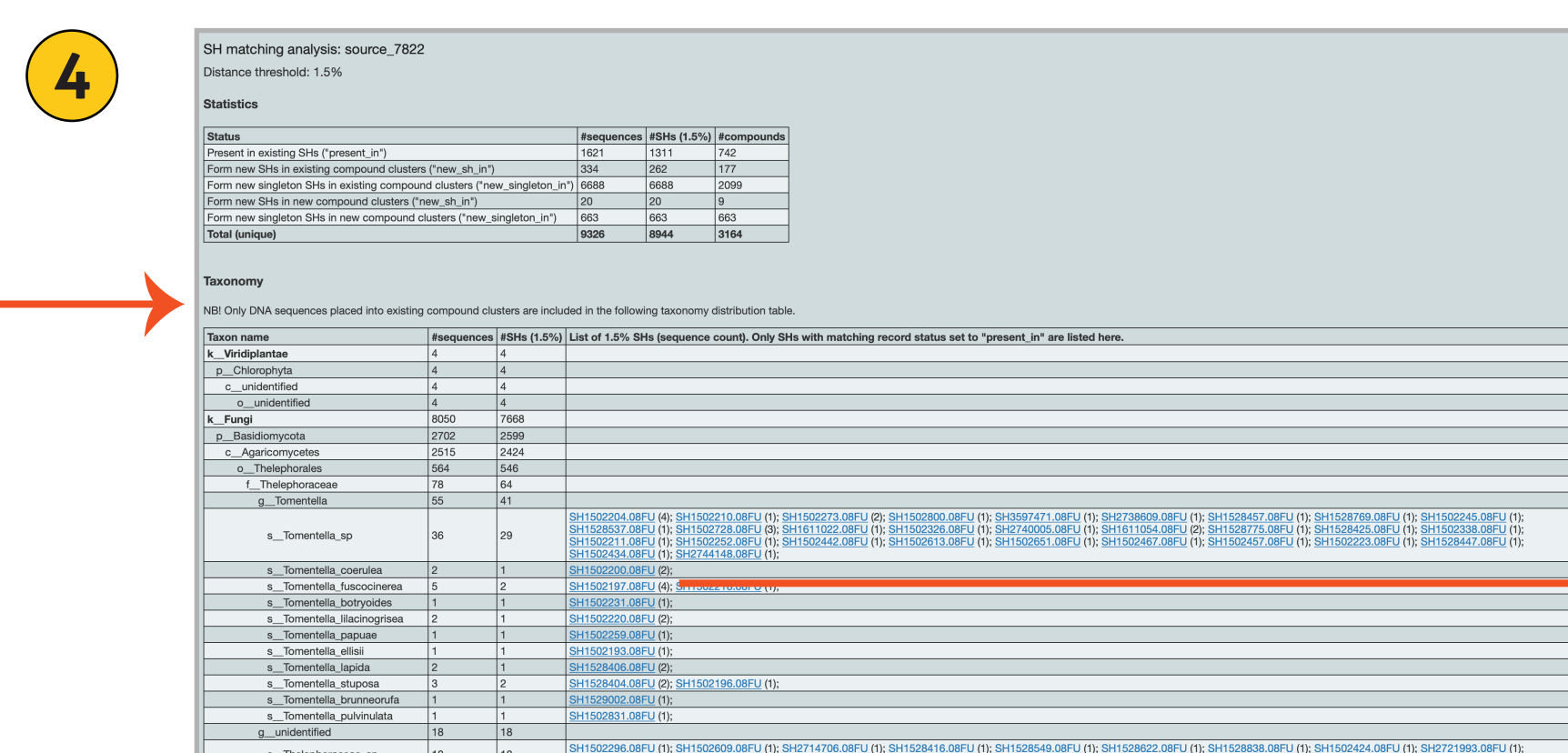
1. New SH matching analysis can be started in PlutoF Analysis lab.



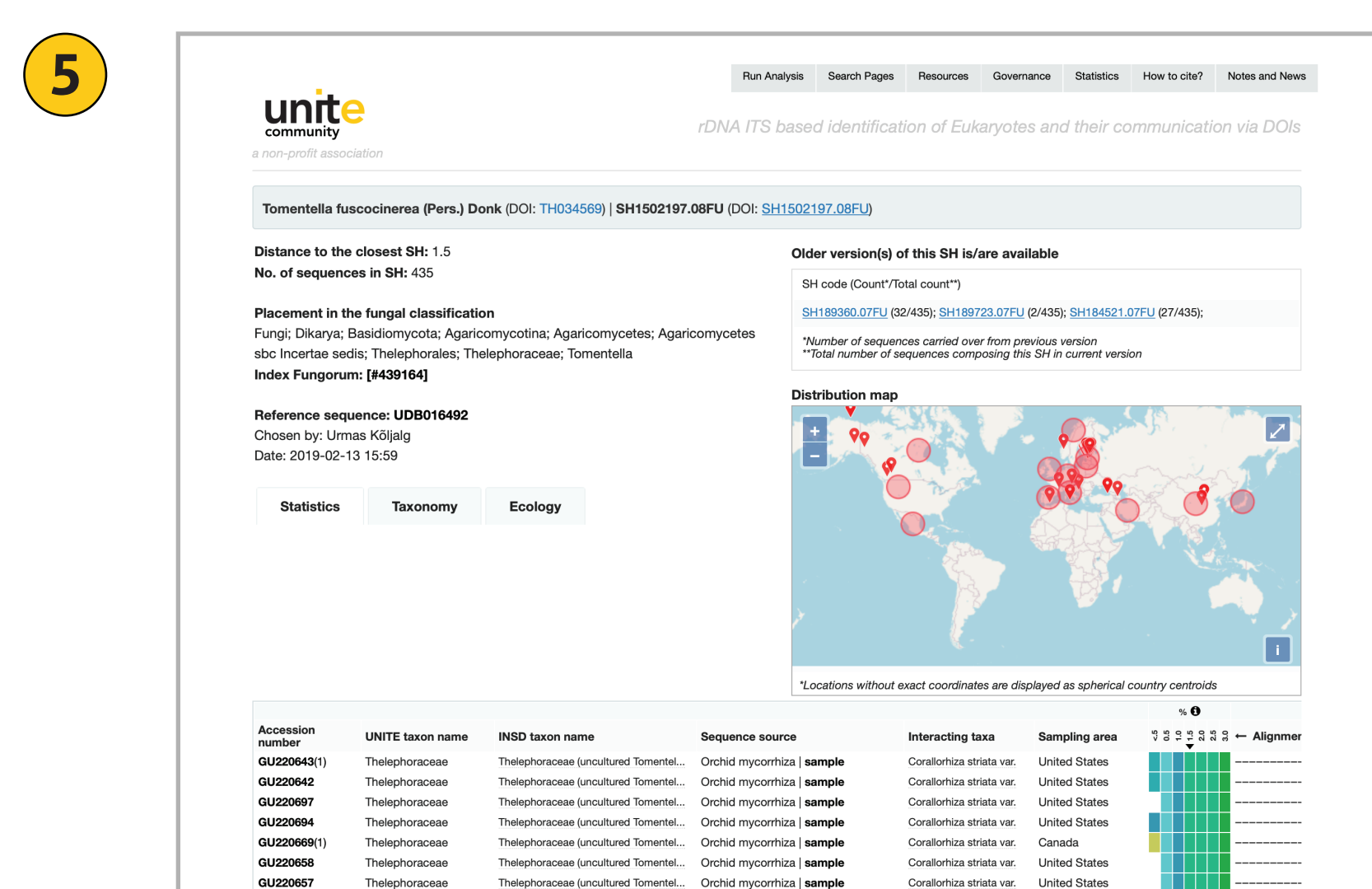
2. Analysis results in compressed format are stored in PlutoF File Repository for private use.



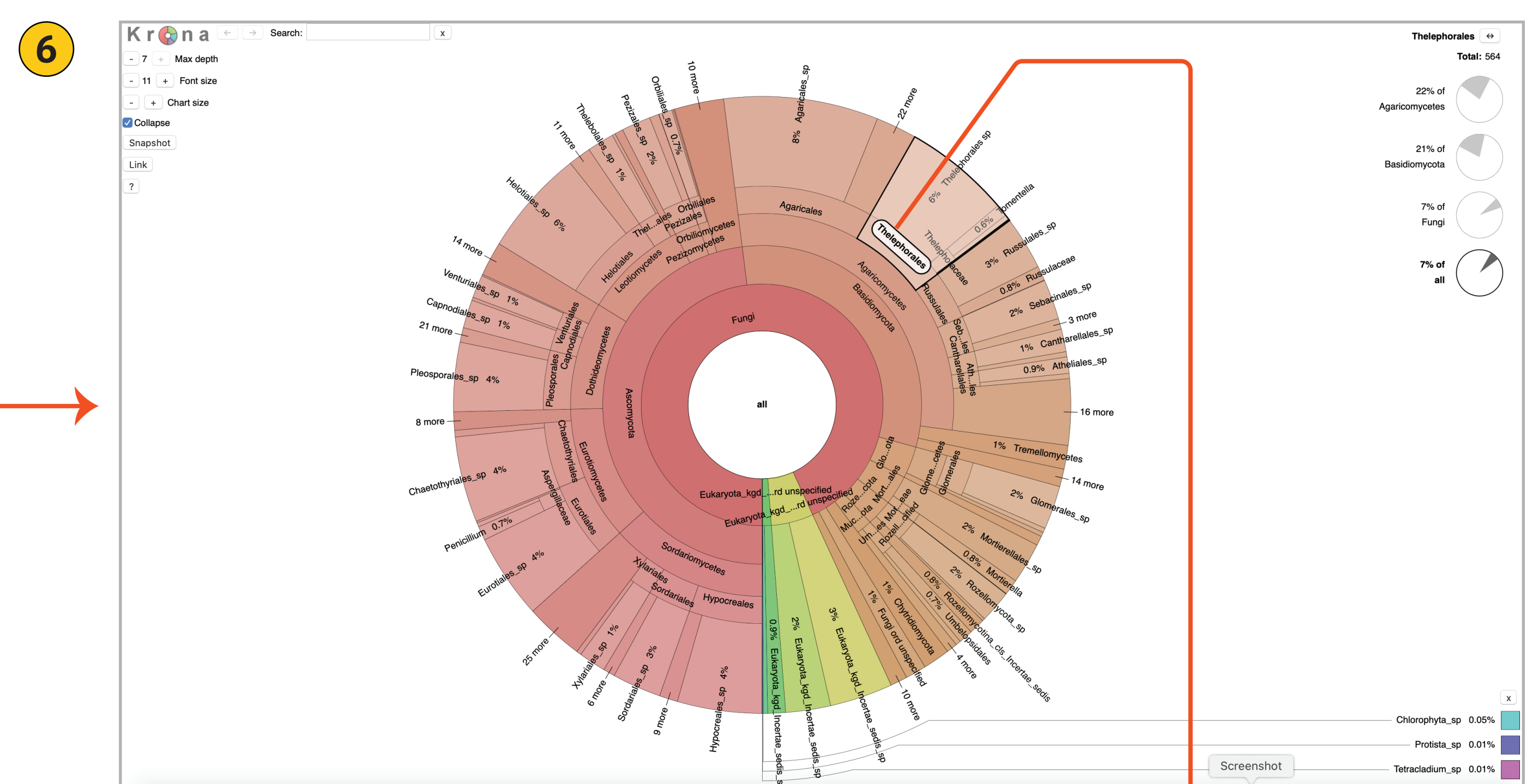
3. List of output files extracted from the downloaded zip file.



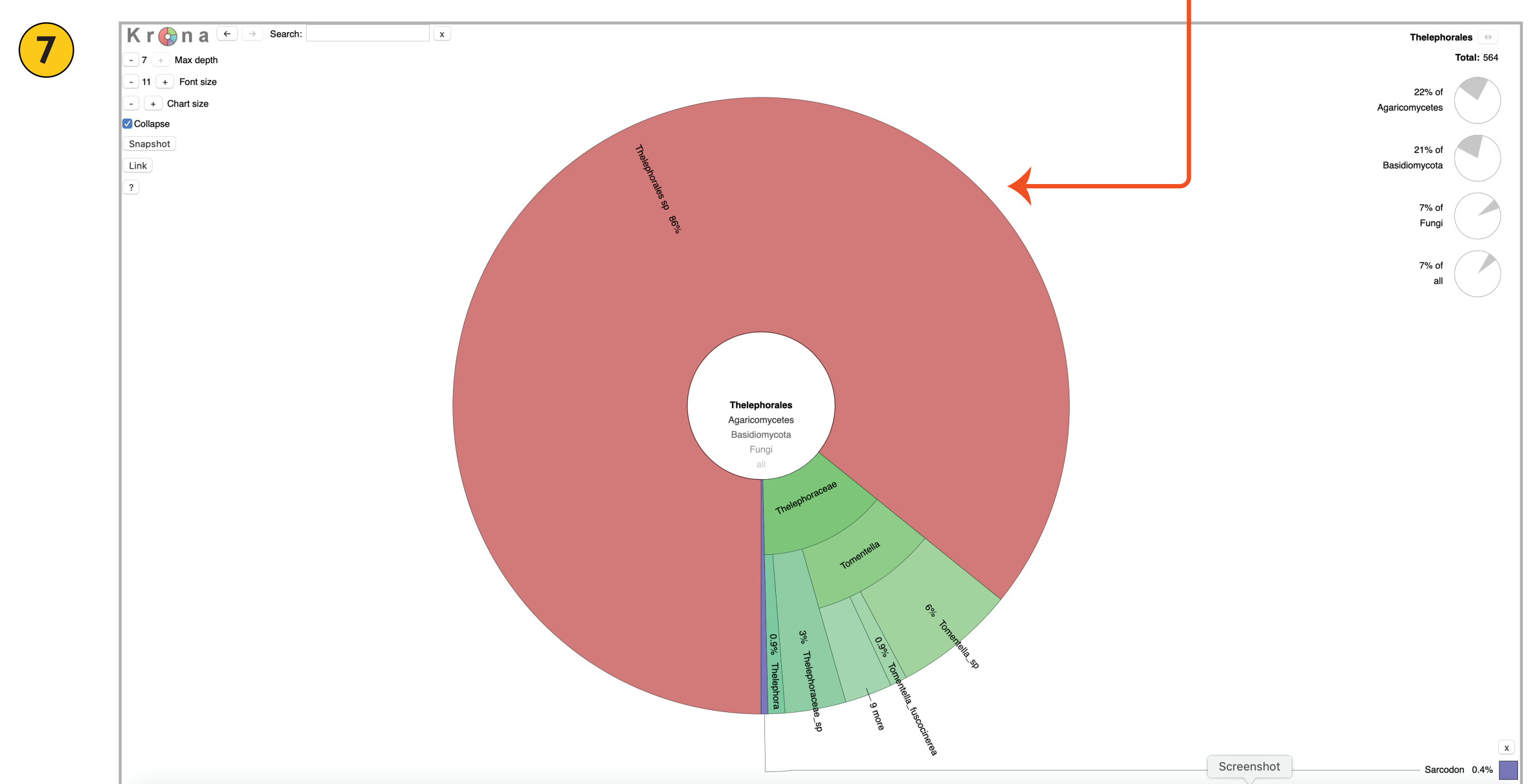
4. Screenshot of the HTML output summarizing the analysis results present in the accompanying CSV files.



5. Screenshot of the SH1502197.08FU.



6. Krona chart showing the identification results across classification.



7. Krona chart showing the identification results across Thelephorales (Fungi).

Organisation updates

The UNITE Community became a non-profit association in January 2022. It is governed by a general meeting of the members of the association, which in turn elects a management board. UNITE's advisory board will be formed in the fall of 2022. UNITE Community will also invite new members to join the association.

References

- Abarenkov K, Nilsson RH, Larsson K-H, *et al.* (2010). The UNITE database for molecular identification of fungi - recent updates and future perspectives. *New Phytologist* **186**: 281-285.
- Kõljalg U, Nilsson RH, Abarenkov K, *et al.* (2013). Towards a unified paradigm for sequence-based identification of Fungi. *Molecular Ecology* **22**: 5281-5277.
- Kõljalg U, Nilsson HR, Schigel D, *et al.* (2020). The taxon hypothesis paradigm—On the unambiguous detection and communication of taxa. *Microorganisms* **8**: 1910.
- Nilsson RH, Larsson K-H, Taylor AFS, *et al.* (2019). The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. *Nucleic Acid Research* **47**: D259-D264.