



Exercise: Attaching Track Hubs

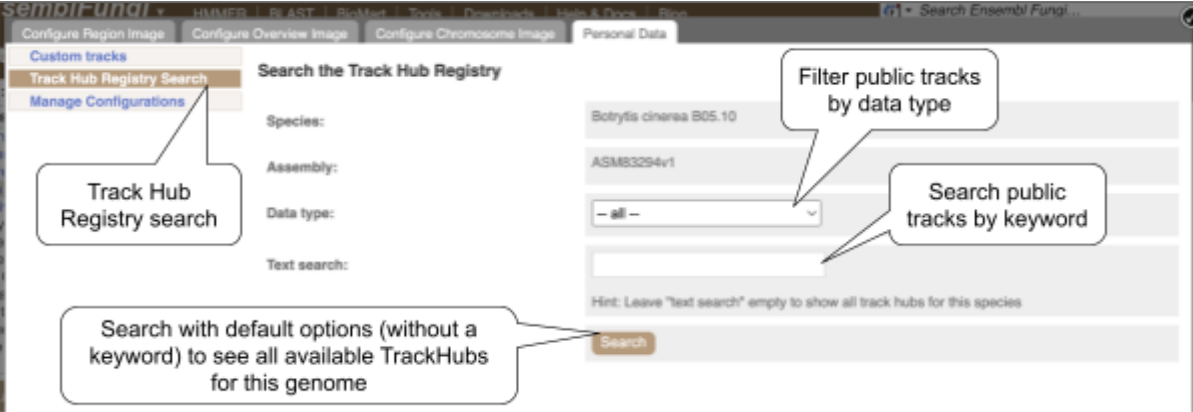
There are a number of publicly available datasets that are available to add onto views in Ensembl. You can find full lists of these at www.trackhubregistry.org. We're going to search and add these files from within Ensembl.

Go to fungi.ensembl.org and search for the region **6:1854110-1894000** in the species *Botrytis cinerea* B05.10.



Search: Botrytis cinerea B05.10 for
6:1854110-1894000 **Go**
e.g. **NAT2** or **alcohol***

This will take you directly to the Region in Detail page in the location tab. Click on the  Custom tracks button, found just below the Configure this page button on the left. A pop-up will appear, click on [Track Hub Registry Search](#) on the left-hand navigation panel.



Custom tracks
Track Hub Registry Search
Manage Configurations

Search the Track Hub Registry

Species: Botrytis cinerea B05.10
Assembly: ASM83294v1
Data type: **- all -**
Text search:
Hint: Leave "text search" empty to show all track hubs for this species
Search

Filter public tracks by data type
Search public tracks by keyword
Track Hub Registry search
Search with default options (without a keyword) to see all available TrackHubs for this genome

Just click [Search](#) with no options selected.

semblFungi | CHM1P | BLAST | BioMart | Tools | Downloads | Help & Contact | Blog

Configure Region Image | Configure Overview Image | Configure Chromosome Image | Personal Data

Custom tracks | Track Hub Registry Search | Manage Configurations

Search Results

Searched *Botrytis cinerea* B05.10 ASM83294v1

Found 4 track hubs - [Search again](#)

Can't see the track hub you're interested in?

We only search for hubs compatible with assemblies used on this website - please [search the registry directly](#) for data on other assemblies.

Alternatively, you can [manually attach any hub](#) for which you know the URL.

RNA-Seq alignment hub SRP062592

Description: Next Generation Sequencing Facilitates Quantitative Analysis of Cucumber and *Botrytis cinerea* Transcriptome Changes During Infection ; [SRP062592](#)

Data type: transcriptomics

Number of tracks: 2

[Attach this hub](#)

RNA-Seq alignment hub SRP080917

Description: Molecular analysis of interaction between the grapevine flower and *Botrytis cinerea* ; [SRP080917](#)

Data type: transcriptomics

Number of tracks: 6

[Attach this hub](#)

RepetDB *Botrytis cinerea* B05.10 (ASM83294v1)

Description: Repeat region consensus copies annotations created by TEannot (from the REPET package). Go to [RepetDB](#) for more info.

Data type: genomics

Number of tracks: 5

[Attach this hub](#)

RNA-Seq alignment hub SRP093589

There are four available TrackHubs for this assembly.

Choose the **RNA-Seq alignment hub SRP062592** by clicking on the ‘[Attach this hub](#)’ button. It is a next generation sequencing quantitative analysis of cucumber and *Botrytis cinerea* transcriptome changes during Infection. Close the pop-up window.

The TrackHub should now load and appear on the most-detailed image at the bottom of the Region in Detail page.



If you zoom in further you can see a more detailed representation of the data.



(a) Go to www.trackhubregistry.org and search for **SRP062592**. Can you jump to Ensembl directly from the Track Hub Registry page?

The Track Hub Registry

A global centralised collection of publicly accessible track hubs

The goal of the Track Hub Registry is to allow third parties to advertise [track hubs](#), and to make it easier for researchers around the world to discover and use track hubs containing different types of genomic research data.

SRP062592

The Track Hub Registry Submit data Documentation About Help

Search by keywords: hg Register Login

Home / SRP062592 - GCA_000832945.1

SRP062592 Botrytis cinerea B05.10 GCA_000832945.1

General Info

Remote data tracks: 1

Data Type: transcriptomics

File type(s):

cram: 1

Source URL: [View](#)

Mon Dec 12 2022 17:52:41 GMT+0000

All is Well

View in Genome Browser

ENSEMBL UCSC VECTORBASE NCBI GDV

Hub

Name: SRP062592

Short Label: RNA-Seq alignment hub SRP062592

Long Label: Next Generation Sequencing Facilitates Quantitative Analysis of Cucumber and Botrytis cinerea Transcriptome Changes During Infection ; SRP062592

Assembly Hub: X

Public URL: [View](#)

Species

Taxonomy 332648

Scientific name: Botrytis cinerea B05.10

Common name:

Assembly Information

Accession	Name	Long Name	UCSC Synonym
GCA_000832945.1	ASM83294v1		ASM83294v1

If you have your own files, or know a file you want to attach that is not present on the TrackHub registry, you can also attach these. There are two ways to do this, either by URL or by file upload.

Larger files, such as BAM files generated by NGS, need to be attached as remote files by URL. There are some BAM files for *Schizosaccharomyces pombe* available at: ftp://ftp.ensemblgenomes.org/pub/misc_data/bam/fungi/Spom/

Let's take a look at that URL.

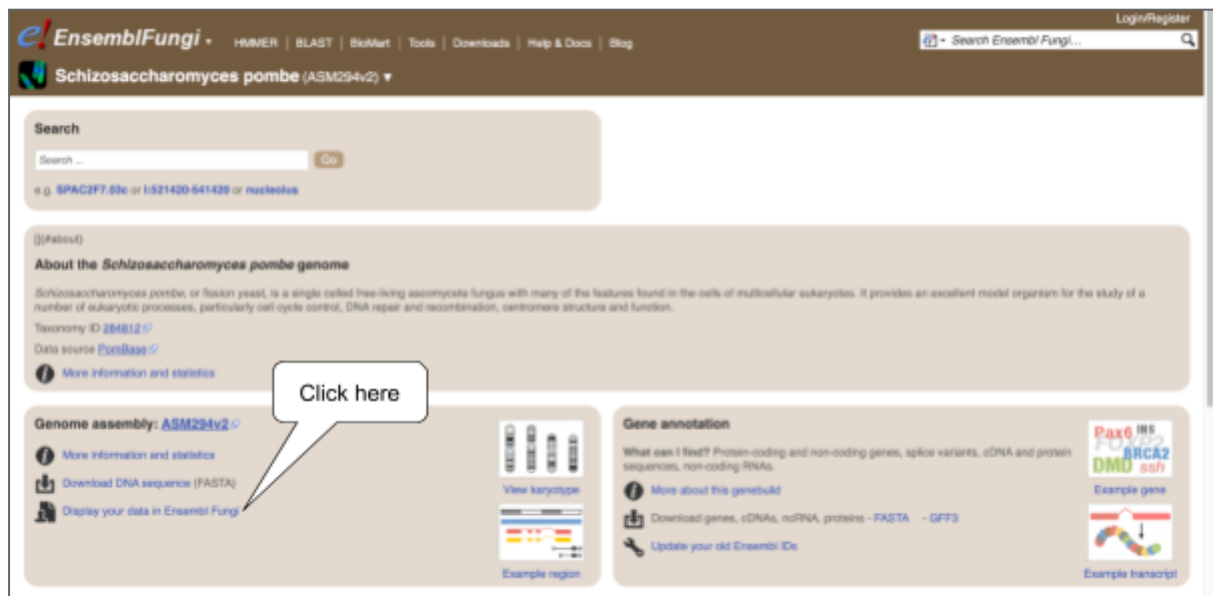
NOTE: Many internet browsers have recently dropped support for FTP, including the latest Firefox and Google Chrome versions. Firefox v87.0 still contains built-in FTP implementation. If you struggle to open the FTP site, try the HTTP version: https://ftp.ebi.ac.uk/ensemblgenomes/pub/misc_data/bam/fungi/Spom/

Index of /ensemblgenomes/pub/misc_data/bam/fungi/Spom

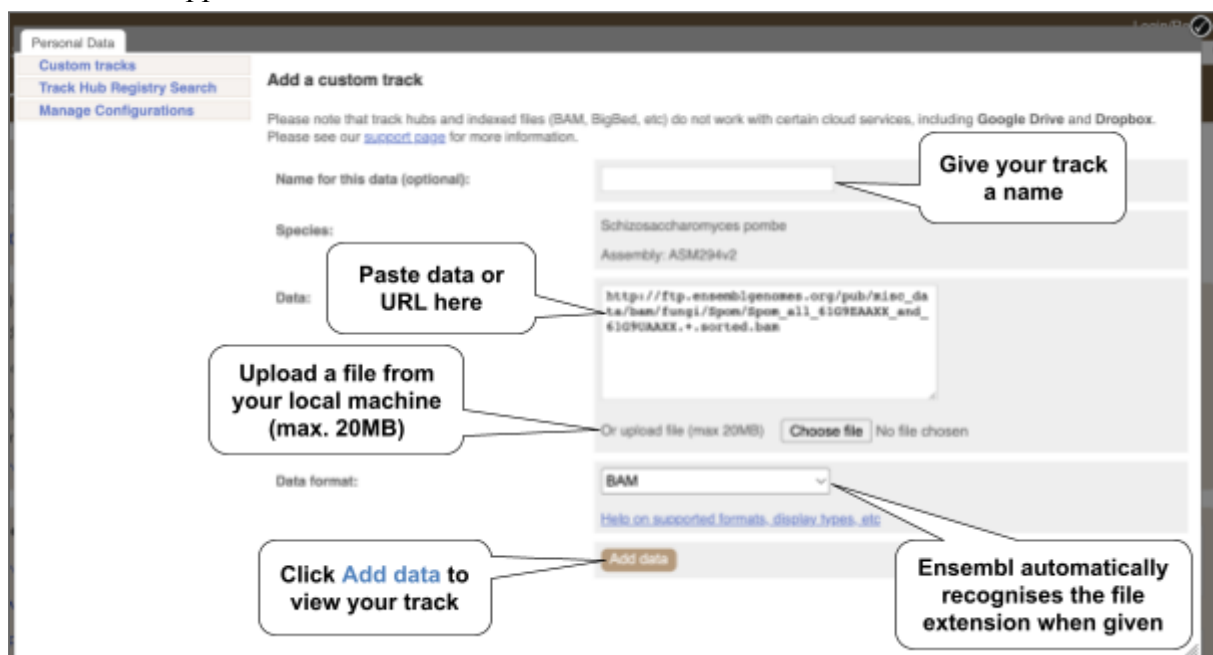
Name	Last modified	Size	Description
Parent Directory		-	
Spom_all_61G9EAAXX_and_61G9UAAXX+.sorted.bam	2014-11-26 15:06	3.3G	
Spom_all_61G9EAAXX_and_61G9UAAXX+.sorted.bam.bai	2014-11-26 15:06	36K	
Spom_all_61G9EAAXX_and_61G9UAAXX-.sorted.bam	2014-11-26 15:04	3.8G	
Spom_all_61G9EAAXX_and_61G9UAAXX-.sorted.bam.bai	2014-11-26 15:04	37K	

Here you can see two BAM files (.bam) with corresponding index files (.bam.bai). We're interested in the files [Spom_all_61G9EAAXX_and_61G9UAAXX+.sorted.bam](#) and [Spom_all_61G9EAAXX_and_61G9UAAXX+.sorted.bam.bai](#). These files are the BAM file and the index file respectively. When attaching a BAM file to Ensembl Genomes, there must be an index file in the same folder.

From the Ensembl Fungi homepage, click on *Schizosaccharomyces pombe*, then on [Display your data in Ensembl Fungi](#).



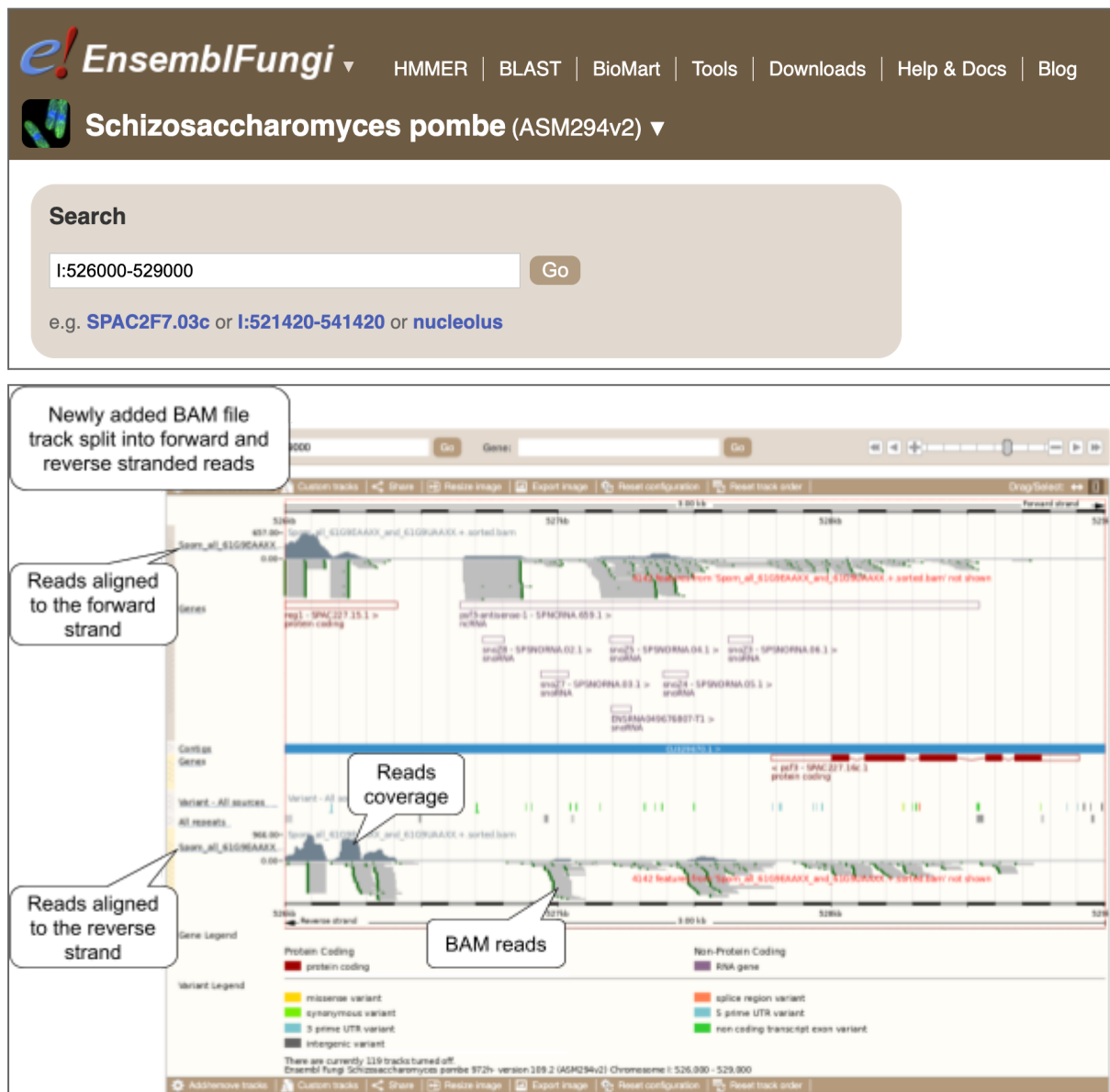
A menu will appear:



The interface detects file extensions if you upload or attach a file. If you want to upload a file just click on [Choose file](#), choose the file and it should automatically detect the file type you have submitted.

If you have a URL, like the one we located earlier, paste in the URL of the BAM file itself (ftp://ftp.ensemblgenomes.org/pub/misc_data/bam/fungi/Spom/Spom_all_61G9EAAXX_and_61G9UAAXX.+.sorted.bam).

Since this is a file, the interface is able to detect the “.BAM” file extension and automatically labels the format as **BAM**. Click on [Add data](#) and close the menu. It may take a while to load as there is a lot of data (Firefox tends to be fast). Once the data has been uploaded, you’ll get a thank you message. Close the window and jump to a Location Tab to see this data. Let’s go to [I:526000-529000](#).



You can zoom in to see the sequence itself. Drag out boxes in the view to zoom in, until you see a sequence of individual reads, or jump to a 110 bp region: [I:526085-526195](#).

(b) Change the track style of the newly added track to **Unlimited** (showing all reads). Can you spot a site called differently from the reference in our sample? What is its genomic position? What is the read coverage at this position on the forward strand? Would you consider it a real variant or an artefact?

