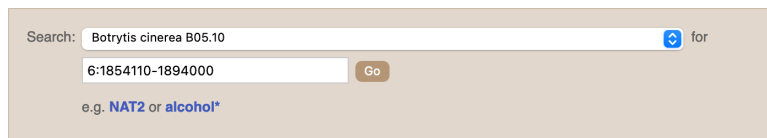


Exercise: Attaching Track Hubs

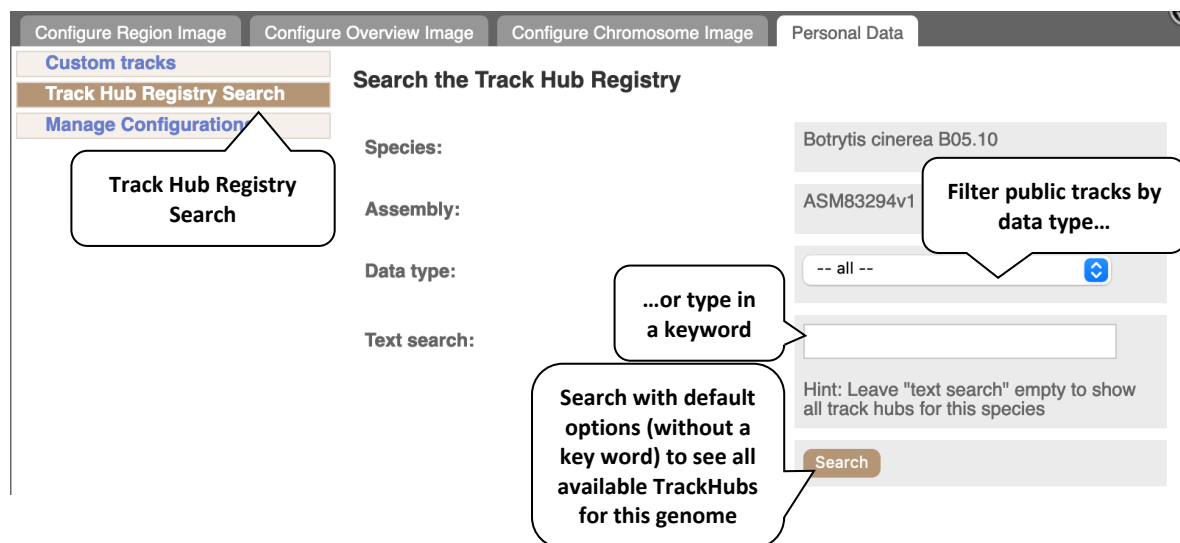
There are a number of publicly available datasets that are available to add onto views in Ensembl. You can find full lists of these at www.trackhubregistry.org. We're going to search and add these files from within Ensembl.

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.



The screenshot shows the 'Search the Track Hub Registry' interface. On the left, a navigation panel has three items: 'Custom tracks', 'Track Hub Registry Search' (highlighted), and 'Manage Configuration'. A callout points to 'Track Hub Registry Search'. The main area has a title 'Search the Track Hub Registry' and several input fields: 'Species:' (filled with 'Botrytis cinerea B05.10'), 'Assembly:' (filled with 'ASM83294v1'), 'Data type:' (a dropdown menu with '-- all --' selected), and 'Text search:' (an empty text box). A callout points to the 'Data type:' dropdown with the text 'Filter public tracks by data type...'. Another callout points to the 'Text search:' field with the text '...or type in a keyword'. A third callout points to the 'Search' button with the text 'Search with default options (without a key word) to see all available TrackHubs for this genome'. Below the 'Text search:' field, there is a hint: 'Hint: Leave "text search" empty to show all track hubs for this species'.

Just click **Search** with no options selected.

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 3 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

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

RNA-Seq alignment hub SRP093589

Description: *Botrytis cinerea* strain:SAS405 X SAS56 Transcriptome or Gene expression ; [SRP093589](#)

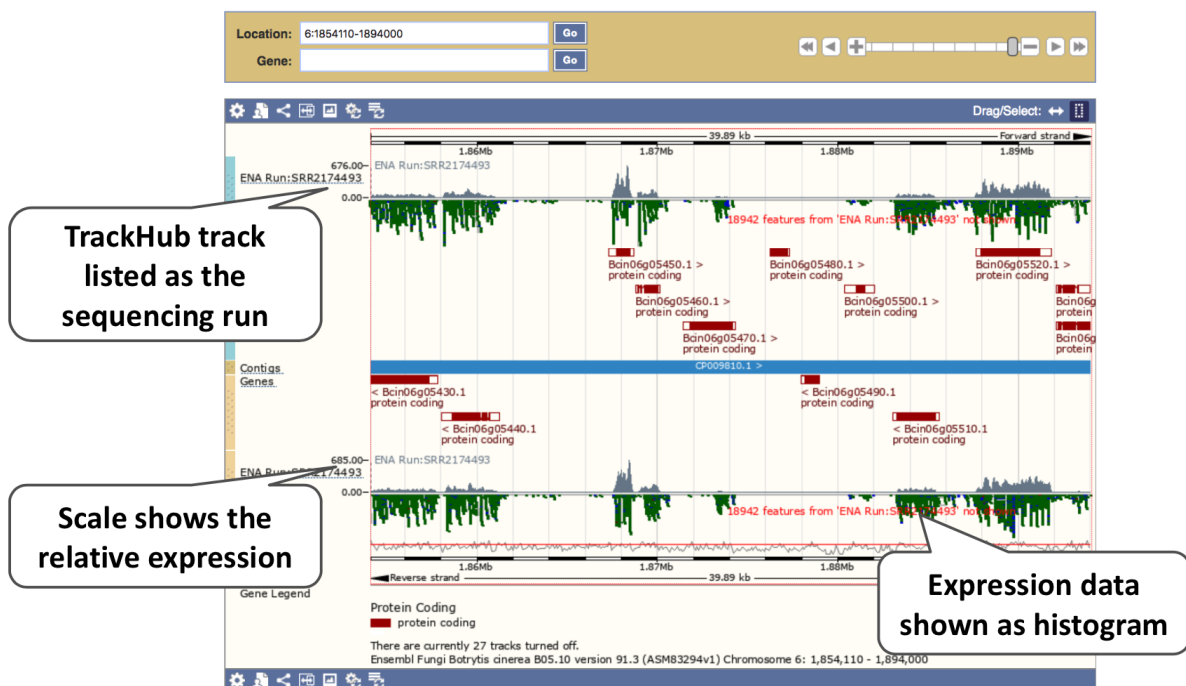
Data type: transcriptomics

Number of tracks: 19

There are three 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 Enter the search terms... Sign up Login

HOME / SEARCH

Current Filters

SRP062592

Species

Assembly

Hub

Data Type

Search Results

Track Collections 1 to 2 of 2

RNASeq-er alignment hub for ENA runs in SRP062592

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

Species: 3659 - *Cucumis sativus*

Assembly: GCA_000004075.2 - ASM407v2

View in Genome Browser View Info

Unchecked

RNA-Seq alignment hub SRP062592

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

Species: 332648 - *Botrytis cinerea* B05.10

Assembly: GCA_000832945.1 - ASM83294v1

View in Genome Browser View Info

Ensembl

NCBI GDV

1

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:

http://ftp.ebi.ac.uk/ensemblgenomes/pub/misc_data/bam/fungi/Spom/

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

 [\[parent directory\]](#)

Name	Size	Date Modified
 Spom_all_61G9EAAXX_and_61G9UAAXX+.sorted.bam	3.3 GB	26/11/2014, 00:00:00
 Spom_all_61G9EAAXX_and_61G9UAAXX+.sorted.bam.bai	36.3 kB	26/11/2014, 00:00:00
 Spom_all_61G9EAAXX_and_61G9UAAXX-.sorted.bam	3.8 GB	26/11/2014, 00:00:00
 Spom_all_61G9EAAXX_and_61G9UAAXX-.sorted.bam.bai	36.8 kB	26/11/2014, 00:00:00

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](#).

Genome assembly: [ASM294v2](#)

-  [More information and statistics](#)
-  [Download DNA sequence \(FASTA\)](#)
-  [Display your data in Ensembl Fungi](#)



[View karyotype](#)



[Example region](#)

A menu will appear:

Personal Data

Custom tracks

[Track Hub Registry Search](#)

[Manage Configurations](#)

Add a custom track

Please note that track hubs and indexed files (BAM, BigBed, etc) do not work with certain cloud services, including **Google Drive** and **Dropbox**. Please see our [support page](#) for more information.

Name for this data (optional):

Species: Schizosaccharomyces pombe
Assembly: ASM294v2

Data:

Or upload file (max 20MB)
 no file selected

Data format: BAM

[Help on supported formats, display type](#)

Give your track a name

Paste data or file URL

You can upload your own data from your computer here (max 20MB)

Ensembl automatically recognises the file extension

Click Add data once ready

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).

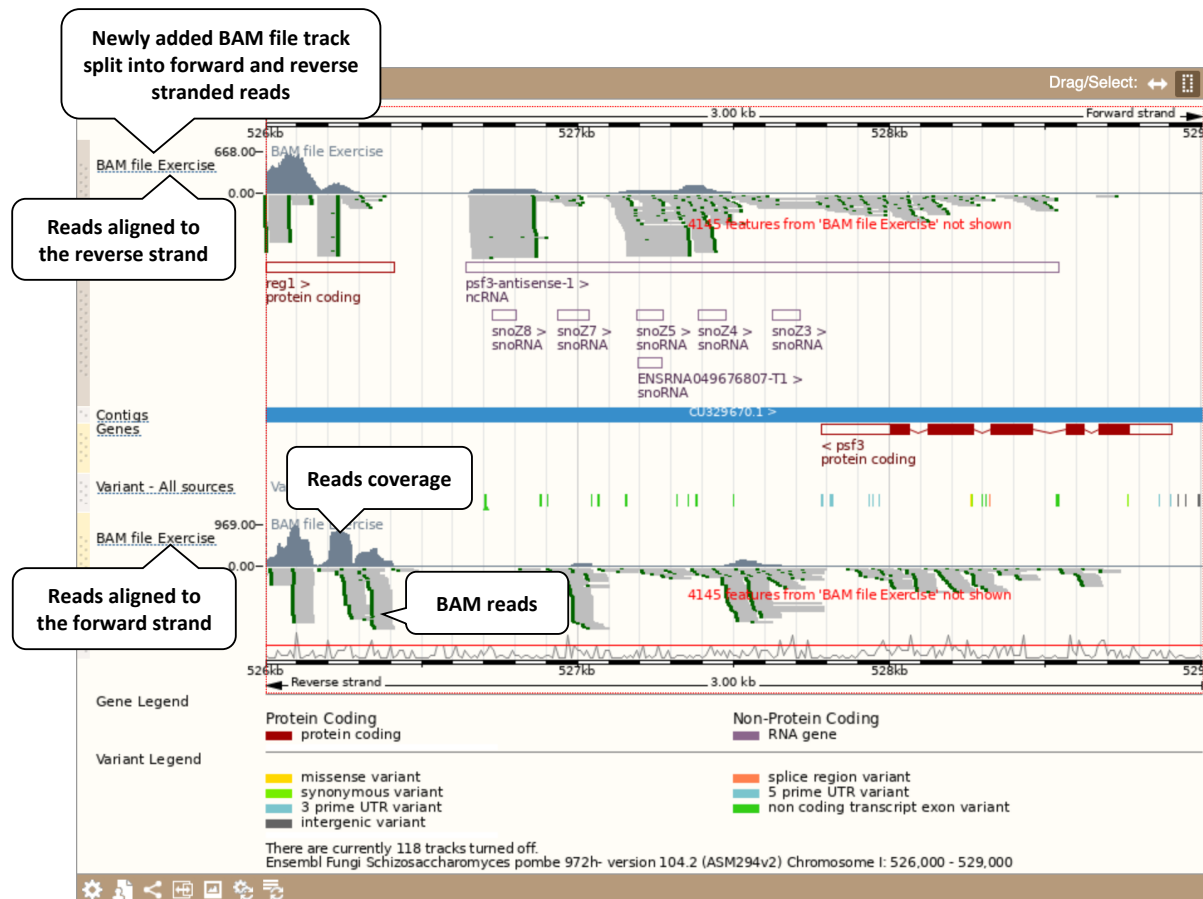
Since this is a file, the interface is able to detect the “.BAM” file extension and automatically labels the format as [BAM](#). Click on [Add data](#) and close the menu. It may take a while to load as there is a lot of data (Firefox tends to be fast). Once the data has been uploaded, you’ll get a thank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

EnsemblFungi ▾ [HMMER](#) | [BLAST](#) | [BioMart](#) | [Tools](#) | [Downloads](#) | [Help & Docs](#) | [Blog](#)

Schizosaccharomyces pombe (ASM294v2) ▾

Search

e.g. [SPAC2F7.03c](#) or [I:521420-541420](#) or [nucleolus](#)



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?

