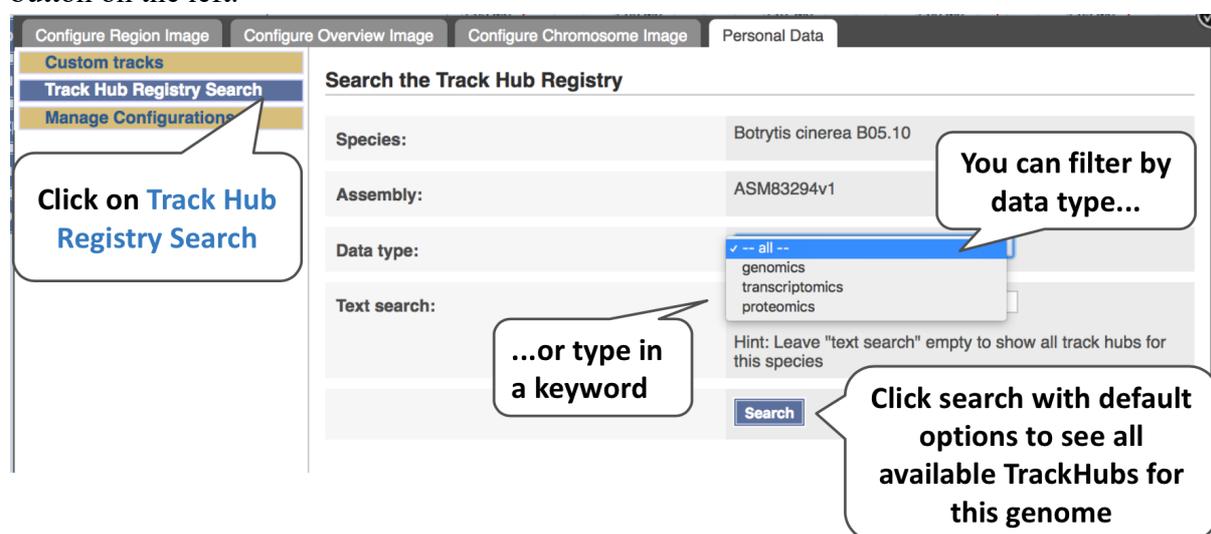


Demo: Attaching TrackHubs

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 see how to search and add these files from within Ensembl.

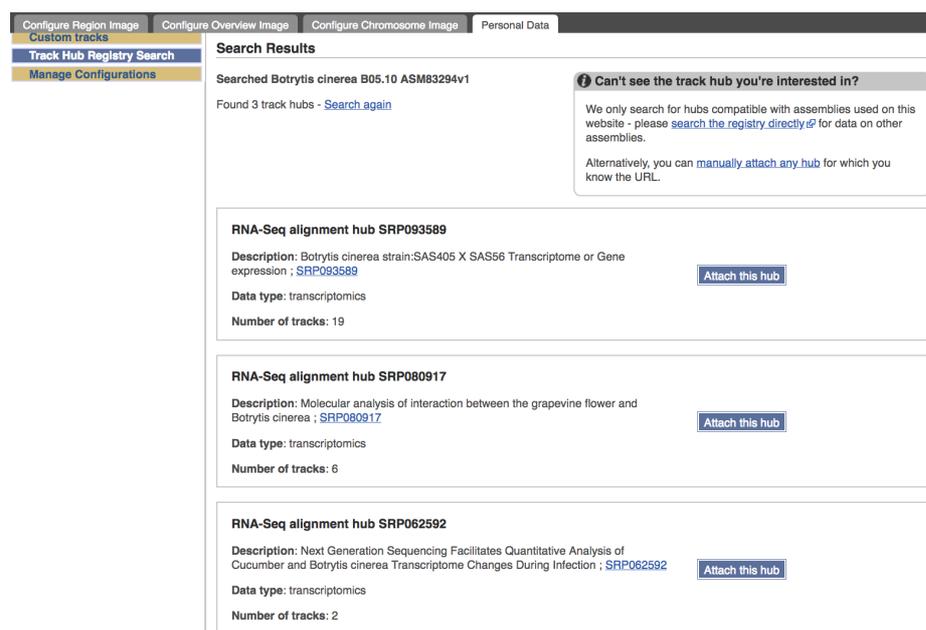
Go to fungi.ensembl.org and search for the region **6:1854110-1894000** in the species **Botrytis cinerea B05.10**. This will take you directly to the Region in Detail page in the location tab.

Click on the  button, found just below the Configure this page button on the left.



The screenshot shows the 'Search the Track Hub Registry' form. The left sidebar has a 'Custom tracks' menu with 'Track Hub Registry Search' selected. A callout points to this menu item: 'Click on Track Hub Registry Search'. The search form has fields for 'Species' (Botrytis cinerea B05.10), 'Assembly' (ASM83294v1), 'Data type' (a dropdown menu with options: -- all --, genomics, transcriptomics, proteomics), and 'Text search'. A callout points to the dropdown: 'You can filter by data type...'. Another callout points to the 'Text search' field: '...or type in a keyword'. A 'Search' button is at the bottom right, with a callout: 'Click search with default options to see all available TrackHubs for this genome'. The top navigation bar includes 'Configure Region Image', 'Configure Overview Image', 'Configure Chromosome Image', and 'Personal Data'.

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

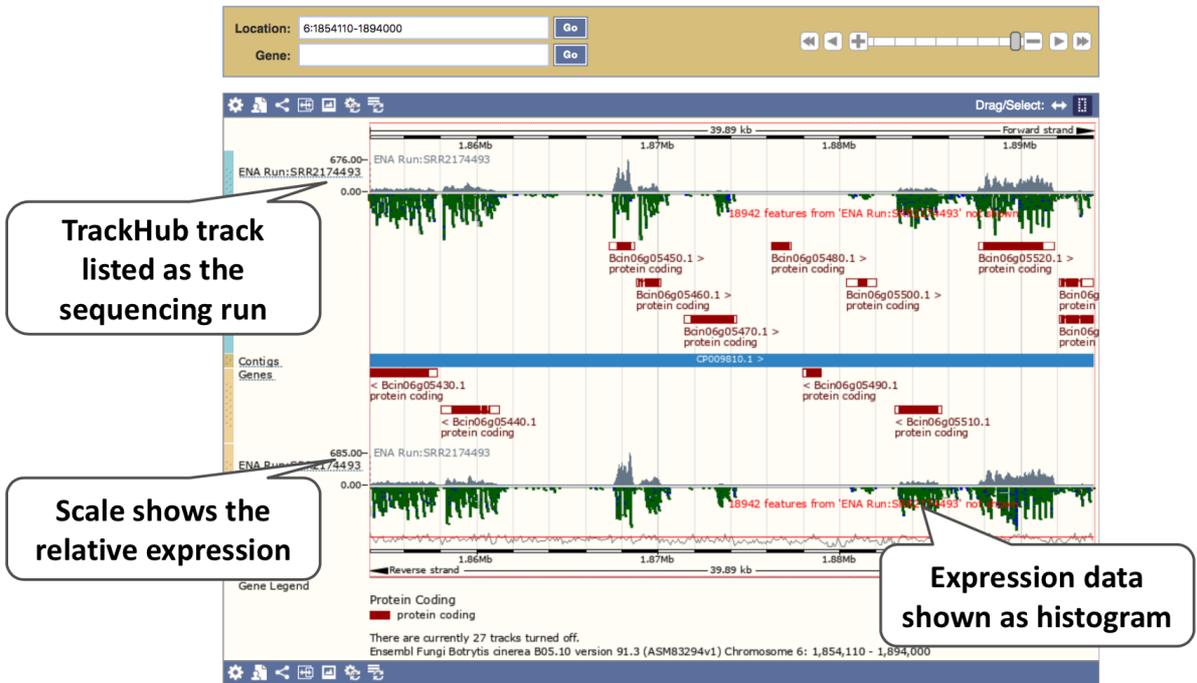


The screenshot shows the 'Search Results' page. The top navigation bar is the same as in the previous screenshot. The left sidebar has 'Track Hub Registry Search' selected. The main content area shows 'Searched Botrytis cinerea B05.10 ASM83294v1' and 'Found 3 track hubs - [Search again](#)'. A warning box says: '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.' Below are three results, each with an 'Attach this hub' button:

- RNA-Seq alignment hub SRP093589**
Description: Botrytis cinerea strain:SAS405 X SAS56 Transcriptome or Gene expression ; [SRP093589](#)
Data type: transcriptomics
Number of tracks: 19
- 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
- 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

There are three available TrackHubs for this assembly. Choose the last one RNA-Seq alignment hub SRP062592 by clicking on the 'Attach this hub' button. 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.



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 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.

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.

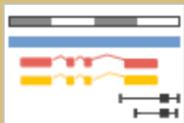
From the Ensembl Fungi homepage, click on [Schizosaccharomyces pombe](#), then on [Display your data in Ensembl Fungi](#).

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:

The screenshot shows the 'Add a custom track' form. On the left, a navigation menu includes 'Personal Data', 'Custom tracks', 'Track Registry Search', and 'Manage'. The form title is 'Add a custom track'. A note at the top states: '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.'

The form fields are:

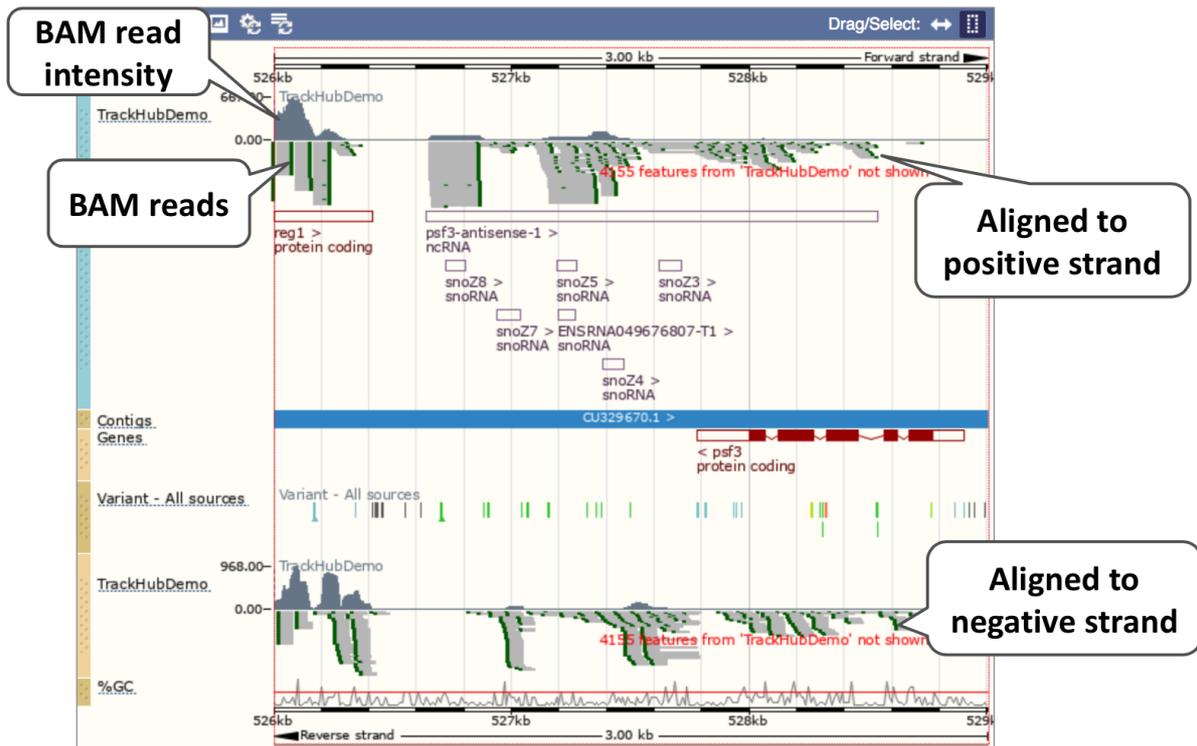
- Name for this data (optional):** A text input field containing 'TrackHubDemo'. A callout box says 'Give your track a name'.
- Species:** A dropdown menu showing 'Schizosaccharomyces pombe' and 'Assembly: ASM294v2'.
- Data:** A large text area with the placeholder 'Paste in data or provide a file URL'. A callout box says 'Paste data or upload URL'.
- Or upload file (max 20MB):** A file selection button labeled 'Choose file' with the text 'No file chosen' next to it. A callout box says 'If you have your own data you can upload the file here'.
- Data format:** A dropdown menu with a link 'Help on supported formats, display types, etc'.
- Add data:** A blue button at the bottom of the form.

The interface detects file types 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, so automatically labels the format as [BAM](#). Click on [Add data](#) and close the menu.

To see this data, jump to a region. Let’s go to I:526000-529000.



We can zoom in to see the sequence itself. Drag out boxes in the view to zoom in, until you see a view like this.

