

Exercise: Ensembl Fungi whole-genome alignments

Let's look at some of the comparative genomics views in the Location tab.

(a) Find the region **14:1128520-1142558** in *Fusarium solani* and go to the [Region in detail](#) page. This region includes four genes we identified from our first BioMart query: *PEP5*, *PDA1*, *ESP3* and *PEP5*.



Search: for

e.g. [NAT2](#) or [alcohol*](#)

We can look at individual species comparative genomics tracks in this view by clicking on [Configure this page](#). In the Comparative genomics section turn on all of the available species' alignments in the normal style.



Location: 14:1128520-1142558

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

Find a track

- Active tracks
- Favourite tracks
- Track order
- Search results
- Sequence and assembly (2/4)
- Genes and transcripts (2/2)
- mRNA and protein alignments (0/4)
- EST alignments (0/1)
- RNA alignments (0/3)
- Comparative genomics (1/1)**
- Repeat regions (0/9)
- Information and decorations (8/10)
- Display options

Search for track hubs

Custom tracks

Manage configurations

Reset configuration

Reset track order

Select from available configurations: [Save current configuration](#)

Comparative genomics

☒ *Fusarium verticillioides* - LASTz net

Looking for more data? Search the [Trackhub Registry](#) for external sources of annotation

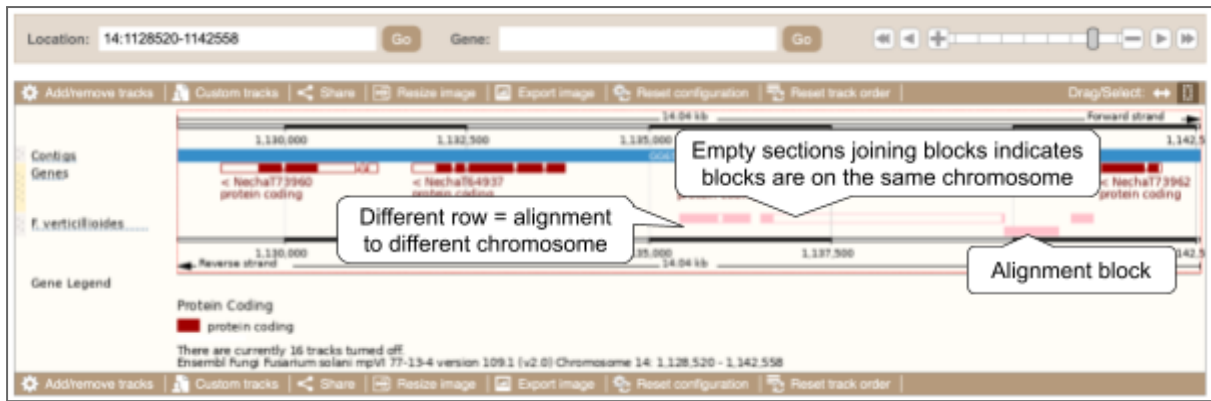
Key

- ☒ Track style
- ☒ Forward strand
- ☒ Reverse strand
- ☒ Favourite track
- ☒ Track information
- ☒ External data
- ☒ User-added track

Please note that the content of external tracks is not the responsibility of the Ensembl project.

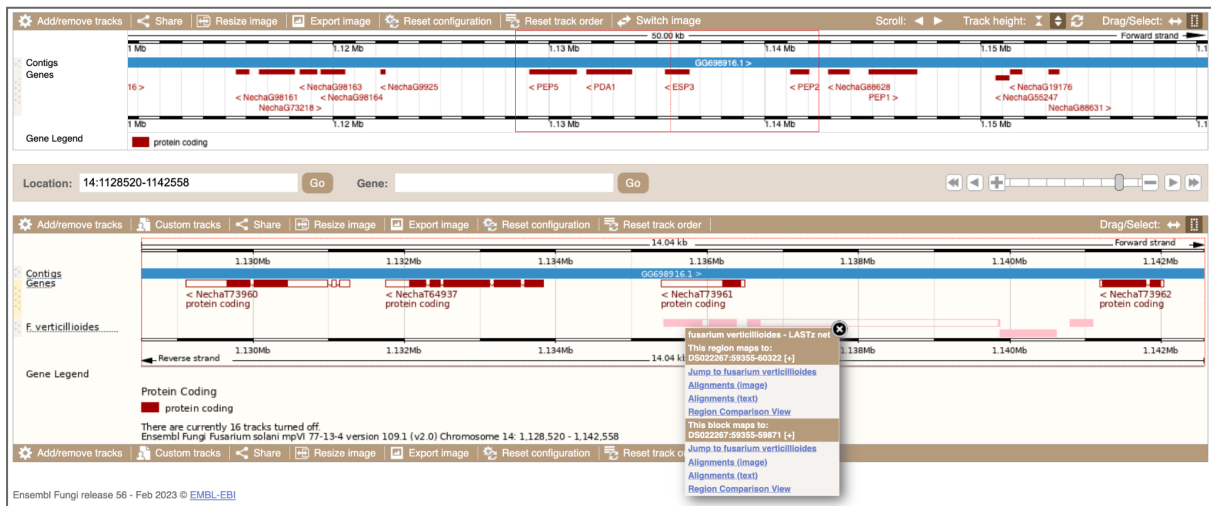
URL-based tracks may either slow down your ensembl browsing experience OR may be unavailable as these are served and stored from other servers elsewhere on the Internet.

We can now see some pink alignments shown on the display. Alignments to the same chromosome are presented in a single row, and gaps in the alignment are shown by linking blocks. If there are alignments to multiple chromosomes in the aligned species these are represented on different rows.



(b) Looking at the pink alignment blocks, does this region in *F. verticillioides* align to multiple different chromosomes in the other species?

(c) Which chromosome(s) does the *F. solani* *ESP3* gene align to in *F. verticillioides*?



We can see that alignments in this region are quite poor for these species, with alignments spanning different chromosomes. This supports the lack of orthologues between these species.

We can view more detailed alignments in the alignment's text / image and region comparison views. Let's first view a text alignment in this region. Click on [Alignments \(text\)](#) on the left and choose *Fusarium verticillioides* from the drop-down menu.

Because this single chromosome region in *F. solani* aligns to regions that are far spread in other genomes, you need to select a specific block for the alignment, as we cannot display a single sequence alignment from more than one region.

A total of 4 alignment blocks have been found. Please select an alignment to view by selecting a Block from the Alignment column.

Alignment (click to view)	Length (bp)	Location on <i>Fusarium solani</i>	Location on <i>Fusarium verticillioides</i>
Block 1	3335	14:1136537-1139871	DS022270:2542-2734
Block 2	961	14:1135422-1136382	DS022267:59355-60322
Block 3	746	14:1139872-1140617	5:2630678-2631429
Block 4	305	14:1140792-1141096	1:1367865-1368184

Blocks ordered by size, not location

F. solani regions all on chromosome 14

F. verticillioides regions across the genome

Let's click on [Block 2](#). This takes you to a new page with a sample of the aligned sequence. Then click the button to [Display full alignment](#). You will see a list of the regions aligned, followed by the sequence alignment. Exons are shown in red. Click on [Configure this page](#), you can turn on the options to view [Show conservation regions](#) and [Mark alignment start/end](#). This will add highlights where the sequence matches.

Display options

Strand: Forward

Number of base pairs per row: 120 bps

Additional exons to display: Core exons

Orientation of additional exons: Display exons in both orientations

Line numbering: None

Codons: Do not show codons

Show conservation regions: ☒

Mark alignment start/end: ☒

Fusarium_solani	ACACAATCATTAGCCTCGGTCGGTACTCGCCATCCCAACAGGTTTCAGCCTGGAACCTGCCCGACGGCGTCAAGCAGCGAAACCATTCCTTGGCAGACCCATCCCTACCGCCGGCC
Fusarium_verticillioides	ACGCAATCACAAGCATCTGGTCGCTCGTACCTTCGAAGCAACTCGCATCACTTGAGATCAGTCCCGCGGGTTCGAGCGGGCGAGTTCACCGTGGACGATGTTGATTGCCAGGGCAA
Fusarium_solani	CTCTGCGACTTCTTCAGAGCTCGGG-----AACTGTAGCGGCACTCGASTTCTTATCTTGAAGAGCGATTTCGAGCCGAGATCAGAGAAGAGCAAGAGACATGCGAGATTCT
Fusarium_verticillioides	CTTTGGGACATCTCGATGGGCTACAGGATATTAAAGATAGCG-CATTGGGG--ATTATCTCAC---GCGATTTCGAGGAGGAATCACCAACTTGC AAAACCGATCGTCAATTTCTCT
Fusarium_solani	CGCGTCTTTATGGATCAGATGTTTGTCTCTGTGTAGATTGCGCATCACTGGAACCAACTCCCGACCCACGAGGCAACCGGT--CTTGTTTA--GGAGGCCGAGGATGCTAAGTATGGA
Fusarium_verticillioides	CGGGTCCGAA---GCCACATGTTTTCGGGACTTAAGCGTTTCGGGATAAATTCGGCCCTACACCTT--CTCCGAGGACGCCCGGAGCTTGGCTACGCGACGAGCGATTGCCACGTTACAG
Fusarium_solani	GGCAGAGCAAGTCAGGATAGAACATGATGGACCACTACCATCTCTTGTACTGGGCAATCTACGGCTAC--GCGAAGCAATCAACTGTTAGTTTCGCGCCATGCACAGCAAGCAACATCA
Fusarium_verticillioides	TGC AAAACGAGCTGGATGGAACATGATGTACACTATCTCTTGTCTCTTGGCGTTTATGGCTCCCGAGCTCAAAAACAGCTCGTTGGATCGCGCTTGCACAACTGCCAAGATCA
Fusarium_solani	CTCAGGAGCATCTTCCCAACATCGCAAGCAAGATAGTGGATTTTTCGTGTACTTAAATCCCGCCGCCGATCAGGTTGCTTCTGATGCCATTTAGACGCTTCTGCTCTCTGCA
Fusarium_verticillioides	TCCAGGAGTATCTACAATCGCAACACAAGCAAGATGATTGACTTT.....
Fusarium_solani	GTGACAGGTGATCAACTATAGTGAACCTCAACCTTGTGCAAGCAACCCATCGCCATCAGCATCCAAACCGGAGCCG--GGCCAGAGCCAGTCGGAGAAAGTGTAGTACAGTATAGGAC
Fusarium_verticillioidesCAATCACTGACTTTTATTCGTTGCGCAATCTGCCATCGCTTGAGCATTGAGCAAGGCGCGAGTAGTACGCCAGCAGGTTCTGCTGAGTTGCAGATAGGAC
Fusarium_solani	ATGGCACTCGGCATAGTGGCGATTTCTGAGCATCTTGTCAACTGCTGTGCTGGG-----TGCCCTTTCTACCAAGCGCTGTCATTCAAGGACGAC--TGGGSCCTCGGTAC
Fusarium_verticillioides	ATGGCACTCAGCGAGTGGCGGTTTCTGGAAGACTGGTTTCACGCAATGCTGGTTCTATGGATGGGCTGCCGTTTTTACCTGCTATCATCGTCCAGGACATCAGTGGAGTTTTCGTCG
Fusarium_solani	TGCAACGAGAGAGGAACACAAGACGGTTCTATGGCTTGAAGCCATTTTGGGTCTTCTCTGTTATCGGCCCGGTATAAGGCTGTATAGTCTAATAGCGCTCTCGGGTGGGCTG
Fusarium_verticillioides	CACCAAGAGAGGGGCGCAAGACGGTCTTCTGCG--TACCATTCCAGTTTGGTTGCAAGATGATGATAGGTGTTTATAAGACTGCTCTGGGACTTCAGCAACTATGCTGCTGGGTTG
Fusarium_solani	GCGAGGCGTACTGGCCCTGGT--TGCGAGAAA
Fusarium_verticillioides	ATGGTGTCTTCTGGCCATGGTATAAGAGAAA

To view an image of the alignments, click on [Region comparison](#) in the left-hand navigation panel. This view is like the Region in Detail page as it shows three images of the genome at different scales. You can add multiple species to this view.

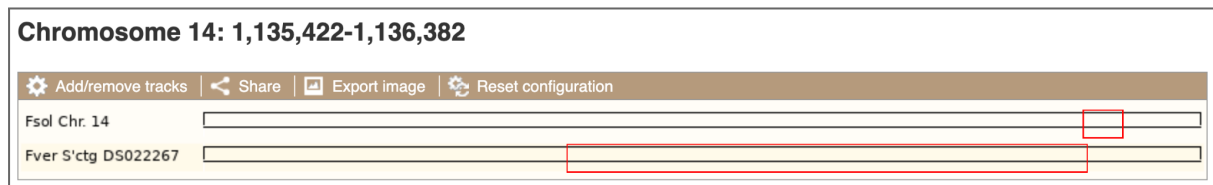
Click on the brown [Select species or regions](#) button. Choose *Fusarium verticillioides* species by clicking on the name. Close the window.

Unselected species ⁰

Selected species ¹

☒ Fusarium verticillioides - lastz

This page, similar to the region in detail page, shows the chromosome positions first. We can see the location of this alignment on the scaffold in *F. verticillioides*.



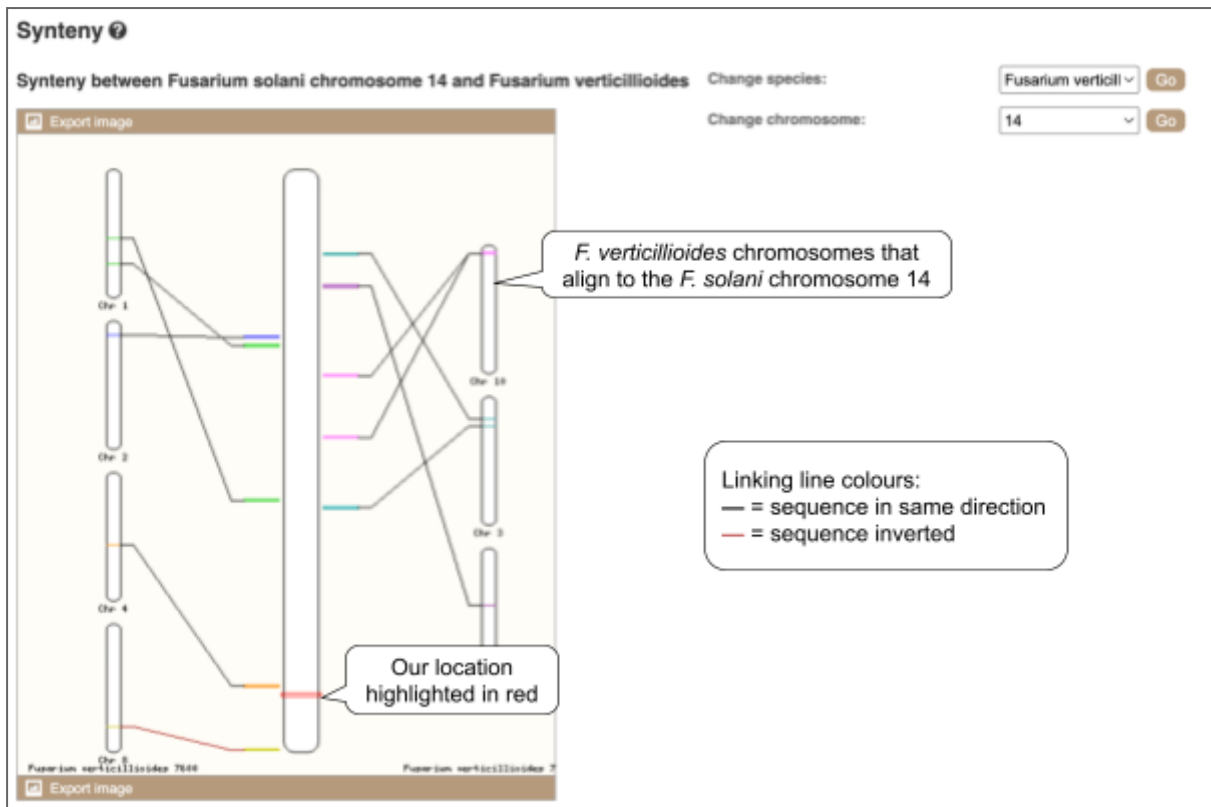
Scroll down to the most detailed image.



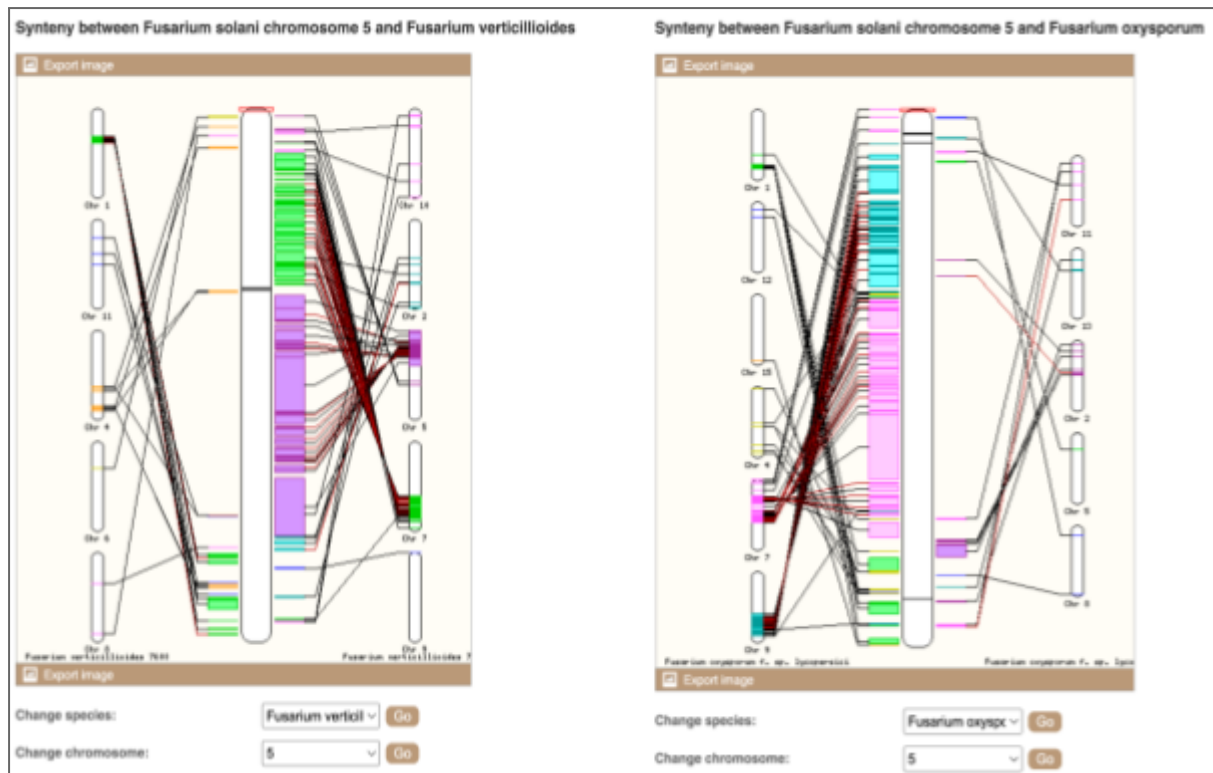
You can add data to both of these views with the same options you had in the Region in Detail page. Click on [Configure this page](#) and look at the top of the menu.

Species to configure:	<div> <div>✓ Fusarium solani</div> <div>Fusarium verticillioides</div> </div>
Select from available configurations:	<div> <div>Default</div> </div>

We can view chromosomal rearrangements in the Synteny view. Click on [Synteny](#) in the left-hand navigation panel.



(d) Which chromosome in *F. verticillioides* is most similar to *F. solani* chromosome 5? Change the display to show *F. oxysporum*. Does this give you the same answer as for *F. verticillioides*?



Additional Exercise - Rearrangements in *Magnaporthe* species

A recent paper Bao et al (2017) ‘PacBio sequencing reveals transposable elements as a key contributor to genomic plasticity and virulence variation in *Magnaporthe oryzae*’ identified a region on chromosome 1 that is shown to be a region of inter-chromosomal rearrangement and inversion. We’re going to take a look at this region and see how it looks in *Magnaporthe oryzae* and *Magnaporthe poae*.

(a) Search for the region 1:5603535-5611402 in *Magnaporthe oryzae*.

Search:

Magnaporthe oryzae

for

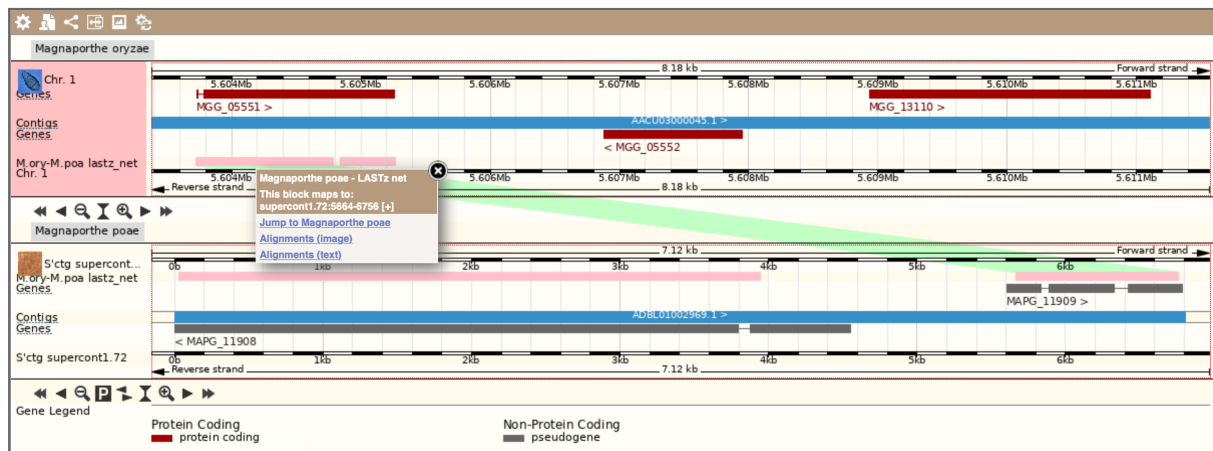
1:5603535-5611402

Go

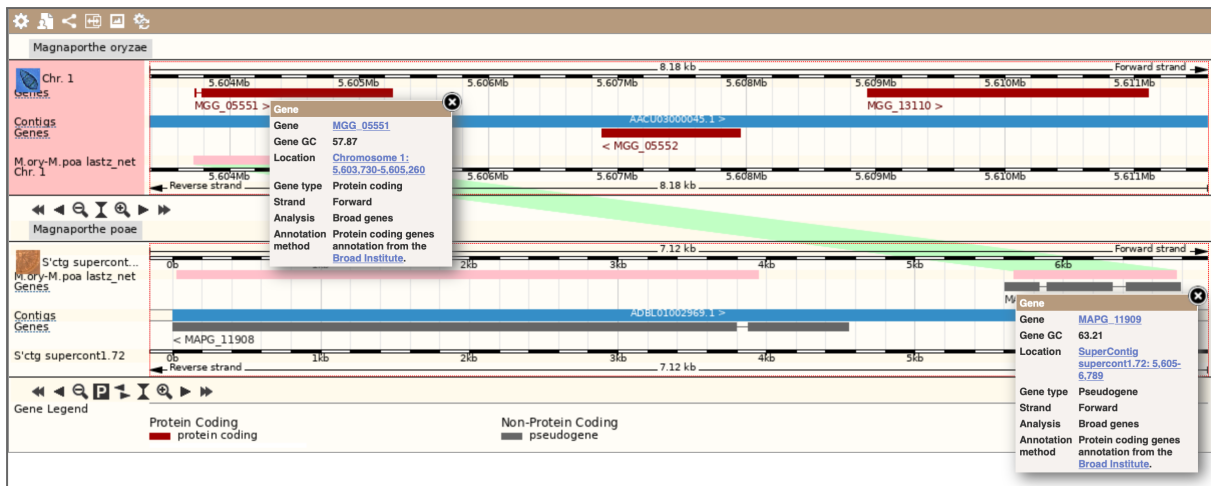
e.g. **NAT2** or **alcohol***

(b) Click on [Region comparison](#) and choose *Magnaporthe poae* from the [Select species or regions](#) pop-up to display an alignment.

(c) Scroll down to the most detailed image. To what region (chromosome/scaffold/contig) does this region align to on the *M. poae* assembly?



(d) Which genes are present in the aligned region for *M. oryzae* and *M. poae*? What are their biotypes?



(e) There is another alignment block in the *M. poae* display. Where does this region map to in *M. oryzae*?

