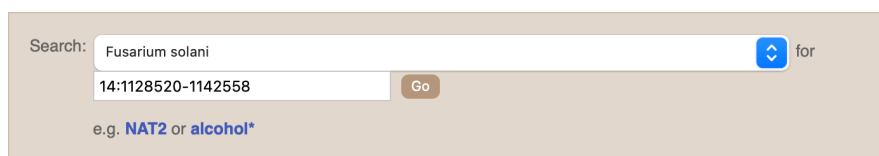


## Exercise: Ensembl Fungi whole genome alignments

We searched for genes that were associated with reduced virulence in *Fusarium solani* that are not present in *Fusarium oxysporum* in the BioMart exercise on Monday. All three genes were found close together in a region on Chromosome 14 that we're going to explore further. 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 the three genes we identified from the BioMart query (*PEP2*, *PEP5* and *PDA1*) and another called *ESP3*.

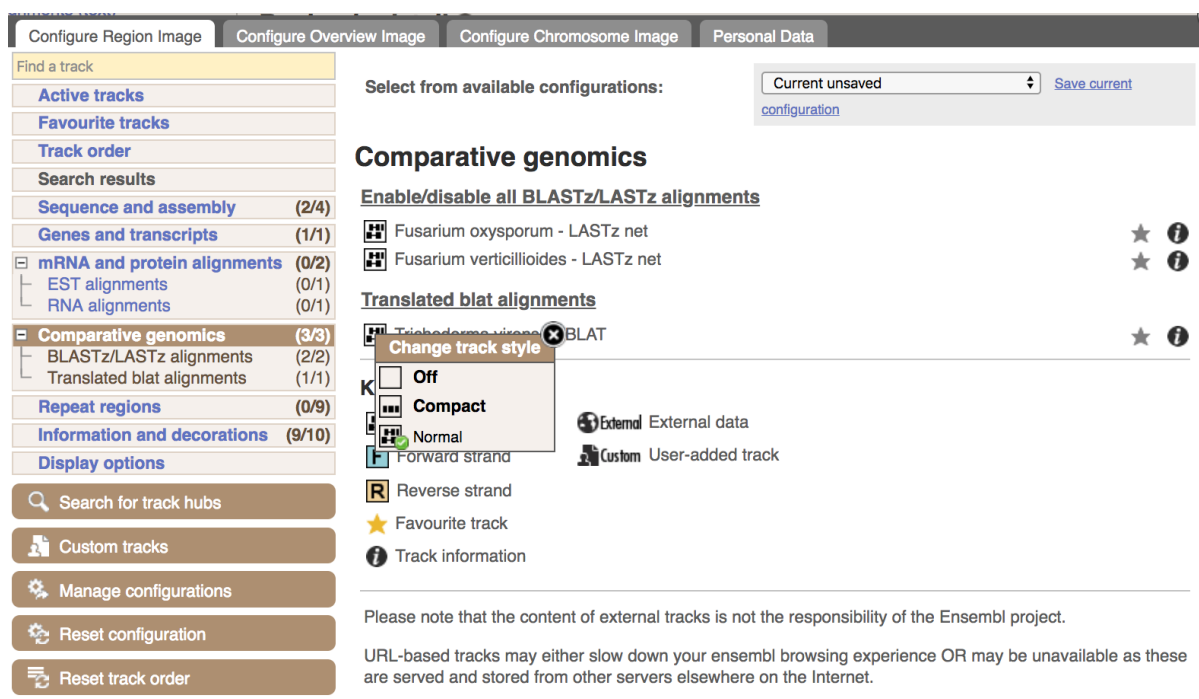


Search: Fusarium solani for

14:1128520-1142558 Go

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

We can also 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.



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 (1/1)
- mRNA and protein alignments (0/2)
  - EST alignments (0/1)
  - RNA alignments (0/1)
- Comparative genomics (3/3)**
  - BLASTz/LASTz alignments (2/2)
  - Translated blat alignments (1/1)
- Repeat regions (0/9)
- Information and decorations (9/10)
- Display options

Search for track hubs

Custom tracks

Manage configurations

Reset configuration

Reset track order

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

### Comparative genomics

[Enable/disable all BLASTz/LASTz alignments](#)

- ☒ Fusarium oxysporum - LASTz net
- ☒ Fusarium verticillioides - LASTz net

[Translated blat alignments](#)

- ☒ **BLAT**

**Change track style**

- ☐ Off
- ☒ Compact
- ☒ Normal
- ☐ Forward strand
- ☐ Reverse strand

☒ Favourite track

☒ Track information

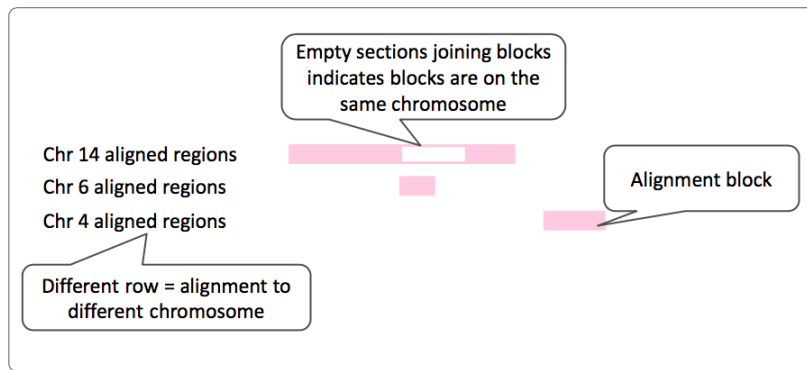
☒ External External data

☒ Custom User-added track

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

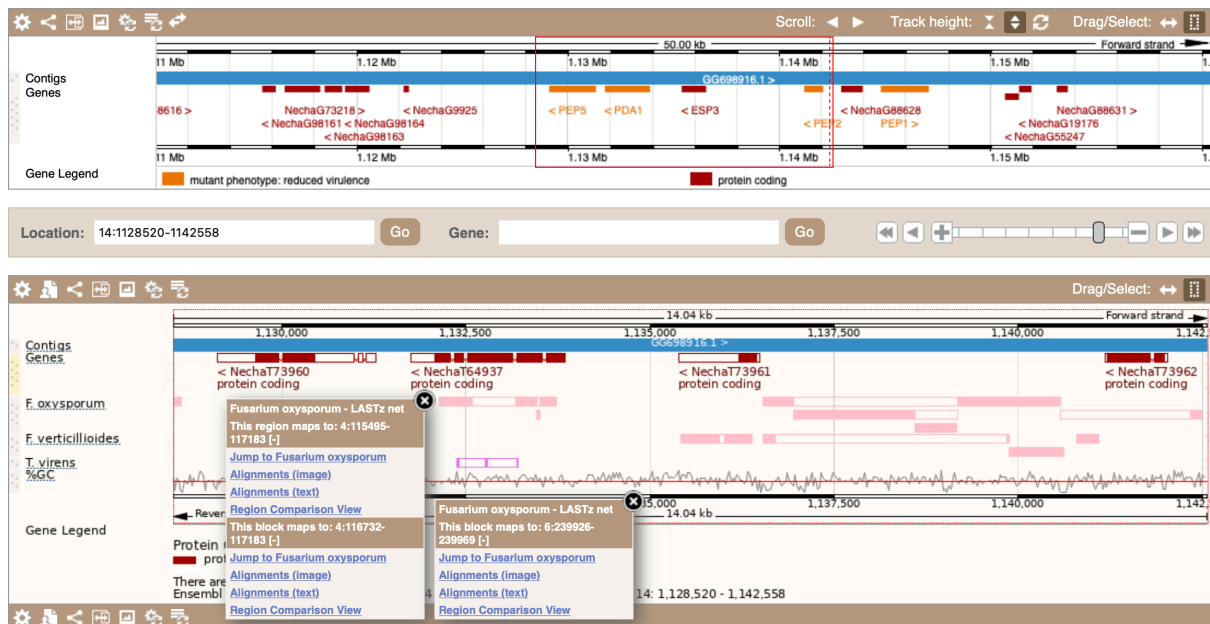
URL-based tracks may either slow down your ensembl browsing experience OR may be unavailable as these are served and stored from other servers elsewhere on the Internet.

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. oxysporum* align to multiple different chromosomes in the other species?

(c) Which chromosome(s) does the *F. solani* *PDA1* gene align to in *F. oxysporum*?



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 alignments text/image and region comparison views. Let's first view a text alignment at this region. Click on [Alignments \(text\)](#) on the left and choose *Fusarium oxysporum* 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 7 alignment blocks have been found. Please select an alignment to view by selecting a Block from the Alignment column.

Show/hide columns		Filter	
Alignment (click to view)	Length (bp)	Location on Fusarium solani	Location on Fusarium oxysporum
<a href="#">Block 1</a>	4035	<a href="#">14:1136535-1140569</a>	<a href="#">3:5089432-5091278</a>
<a href="#">Block 2</a>	2222	<a href="#">14:1136958-1139179</a>	<a href="#">3:4283870-4293377</a>
<a href="#">Block 3</a>	1918	<a href="#">14:1140570-1142487</a>	<a href="#">1:6454070-6459335</a>
<a href="#">Block 4</a>	1597	<a href="#">14:1132137-1133733</a>	<a href="#">4:115495-117183</a>
<a href="#">Block 5</a>	573	<a href="#">14:1138596-1139168</a>	<a href="#">6:1547472-1548044</a>
<a href="#">Block 6</a>	106	<a href="#">14:1128520-1128625</a>	<a href="#">3:5206904-5207009</a>
<a href="#">Block 7</a>	44	<a href="#">14:1133460-1133503</a>	<a href="#">6:239926-239969</a>

Blocks ordered by size, not location

*F. solani* regions all on chromosome 14

*F. oxysporum* regions across the genome

Let's click on [Block 4](#). This takes you to a new page with a sample of the aligned sequence. Then click the button [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:	<input checked="" type="checkbox"/>
Mark alignment start/end:	<input checked="" type="checkbox"/>

```
Fusarium solani      CTTGACAAACCAACACTCGTTCCTCCATGTC-----ATATCCCGGTGTTAACTCT---CGATATCAAAGTTCGGGCAATCTGGGGAATGGCCTTTGACATTTCCAAGATGCTGATG
Fusarium oxysporum  CTTGACAAACCA--AACATCTCCATCAGTACTCAGGATATCCAGACTCTGTATCTGGAAACAAAGTCAAAGTCCGGAACATTTGTGGAAAGCTCCATTAGGCTGATG

Fusarium solani      TTCTTGCCAAATCAGGATCGGGAAACGGCTCCAAACTCTACAGCAGAGCGCTCAGTTACACCGGATTAACTACTGTGATGCCAAGGTCACCTTAC---CGCGAAAGATCCCCAA---TGTT
Fusarium oxysporum  TTCTTGCCCAAGACAGGTACGAGAGCTTTGACCGAAGTTGAAGTAAAGAGTTAGACTAGCGGTAGCGCAATA-TGTTTGGAGATATCACTTACTGTGATGAAATACGCTTCGCGTTCTTT

Fusarium solani      GAT--ATTCTCGTTTGCCTCCAAACACCGCTCGGGCCGGAATATGCTTGATCGTTGCCAAAGATCGCTTTGTTGTGATATAGAGCCCATCGCTTGACACCAACCTCAGTCTGCTCATCA
Fusarium oxysporum  GACCAAGTTCTGGGTAA--TCGAGCCACCTTCGGGCCGGAATACGTGGGCATCATGACCAAAATACCTTGTTGTTGGCGTGGGCTACCCAAGCATTGATGCCAACGACAGTCT---ATCA

Fusarium solani      TTAGTTTGAGCTCAACAC-----TTGAGGCAGACGATTTCGACTTACACCTCGGGGGAAGAACTGTCCCTCGATGACAGGCGACCTTTGGCAGCAGCTCGCGTCAGTTGCGTGCC
Fusarium oxysporum  -GAGTTAGACTACATCAGCAATTATTGTTGATATGAGGAGT---ACATACCCCTGGAGGGAAGTATTGTCCTGCGCAAGTCGACCGCTGTGATGGAACGACCCG.....

Fusarium solani      CACACCCGGATCGAGCCGAGGGCTTCCTTGATAACCGCCTGTAGGTAAAGCATGCTCTGCGATTGCTGAAAACTAATGGGGCCGTCCCTTAACATATCTTTCCAACCTCCTCTCAAGAGT
Fusarium oxysporum  .....

Fusarium solani      GTGCAGAGTACGTGGGTTTGTGTACAGGTAGTACAGGATAGTGTCTGAGCATTGCTGTGATATCAGACCCAGCCCCAATGTTTCAGACCAACAGCCTGTGATGCTCTACCGGAGTGAC
Fusarium oxysporum  .....

Fusarium solani      CGTTCCTCTCTTCCATGAGGAGCAGCTTGGCCAGGAAGTTGTTCTCGCCCTTGAGTGCAGCATCGTCCAGCAACTCGGGCCGCTTGAGCCTGTACTGGATGATTCGTCGCTCGACATA
Fusarium oxysporum  .....

Fusarium solani      CTCGGTCAGGCCCTTGATGGGGACTTCGATCGGTAGGAGTGAAGAGAGACGAGCCACCAAGCGCTGCATGTTTGTGTATATAAGCCATATGGAAGCGTAGTGCCACATGCCGTCCAGGGC
Fusarium oxysporum  .....

Fusarium solani      ACTGACAGCACCCTTTGTATCCGAGTTCGACTCCATCATGCCCATCGACTTGCCAACCTAGCAGAAACACATGTCAGATAATGCTCCACGGCTCGCTTGTGACAGTGAACTCACCCTAAT
Fusarium oxysporum  .....CTCACCCTCAT

Fusarium solani      AACTCCAATGACGCTCAAAGCATAGTACTGGAGGAATCGAGGAGGTCATGACCTGCTTCTGTTGCGAGAACCTCTGC-AGCTGCTCCTCAGGATGGCCGCTCTGGCGCTCGAGCCCT
Fusarium oxysporum  CATGCTTATACGTCGAAGGCATAGCACTGCATCCAGTGGGATATCCACCG-AGGTACCAGACCGAGCAACTCTCTAATCGGTCCCGAAGAACAGCGGAGCATTTATCGATGAAAG

Fusarium solani      CTTCTGAGGATAGCAACGCCCTCATGTTGTACAGAGAGGCAACCTGCTTCTTTATCGCTGAATGACGAGCGGGGTTTTCGCTCGTGAAGAAATTCGGGAACG-----ACGGC
Fusarium oxysporum  GCTCGAGTTGGACCAAGTTGGTCATCGAGTAAGCTGCTGCACCTTCGCTAGCCTGGGCATGGATATGCGGATTCGGTTTCGGCAAGATGTTGGGAAGTGGGCTGATGGGATTGGCGC

Fusarium solani      AGGCCAAA-----GGGTTTATAGTAGT-----CGGCTTTGGGAGGCGCTT-----GCCAATGCGGTAGATGATCTTGAGAGCTTCC
Fusarium oxysporum  TGGCATAATACCATTTGAGACTATCCAAGCTTGTAGCTGTGTTTCTGATAGTATCATGCACTTCGTGACGGACCTTTGTGAATCCTCG.....

Fusarium solani      ATGGTGTCAAAGTCGTACCGCTCGGTCCTATTGCAAGCATGGCTCCTGGTA-AAAAGATATGTTAGTATAAGGACTGCCAATTCCAAGCCACAGACTACCGGTGACGTGGTGTAGAT
Fusarium oxysporum  .....GCTACTCGTTCCGTTGCAATGCGTACAATGGCCCTGGTCTAATCTGTCAGTTGAGTA-----GACATCTCCAAGCGACTTACTAACCATTATTCCTATGGGATTGCGC

Fusarium solani      CCATCATGATCTCGTGGATGTTCCAGTGGCCGCTTTTTCATCTCCAGACTCGGGATATCCGCGCAAGAAAGGACAGGGATCTTTCTCAGACTCGAAAAGAGGAC-----
Fusarium oxysporum  CGATACTGCTCTTGGGTATGTCCTCAAGTAACTGCTTCAGAAGCCATAGTCTTGTGAACCGTGCAAGAAACGGTCCAGGCATCGTCTCA-AGGGGGAACGAGGACATTGACAAGG

Fusarium solani      CGGTAGATGAACCAAG
Fusarium oxysporum  GTCAAAATGAACCAAG
```

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 oxysporum* species by clicking on the name. Close the window.

**Unselected species** <sup>2</sup>

+ Fusarium verticillioides - lastz

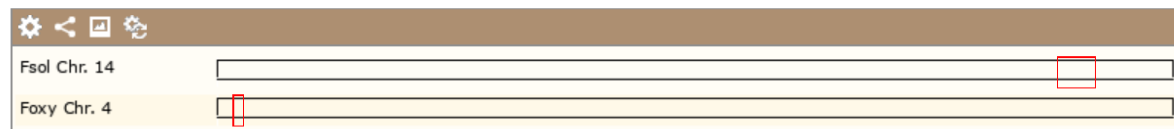
+ Trichoderma virens - translated blat

**Selected species** <sup>1</sup>

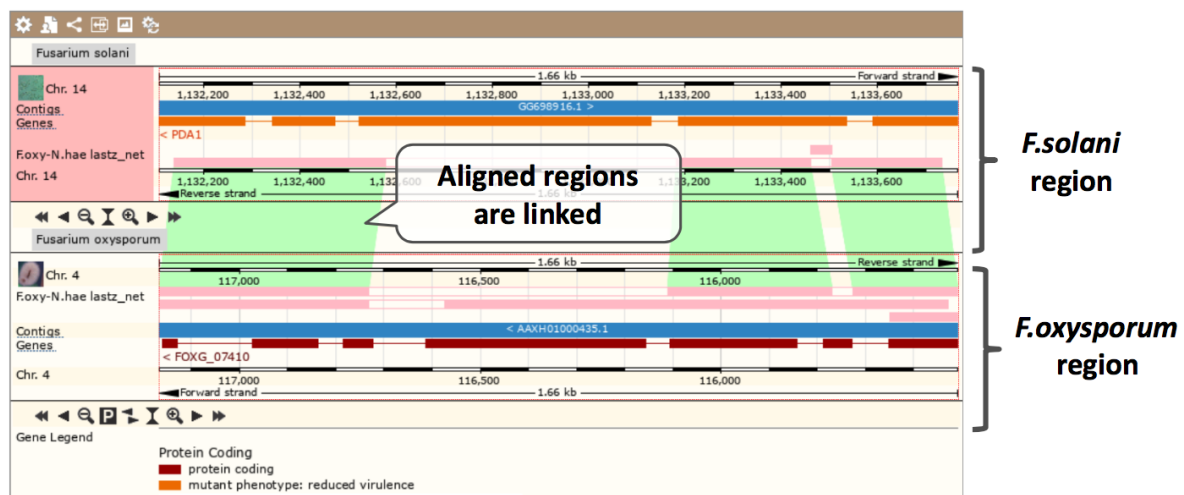
- Fusarium oxysporum - lastz

This page, similar to the region in detail page, shows the chromosome positions first. We can see the location of this alignment on Chromosome 4 in *F. oxysporum*.

### Chromosome 14: 1,132,137-1,133,733



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:**

**Select from available configurations:**

✓ Fusarium solani

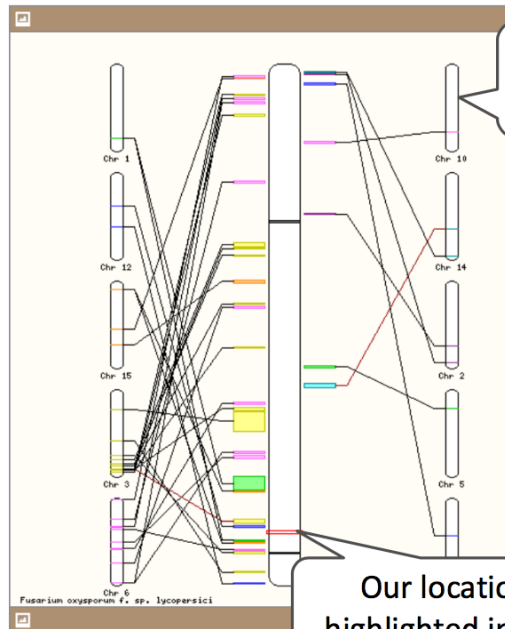
- Fusarium oxysporum

Default

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

## Synteny

Synteny between *Fusarium solani* chromosome 14 and *Fusarium oxysporum*



*F. oxysporum* chromosomes that have alignment to the *F. solani* chromosome 14

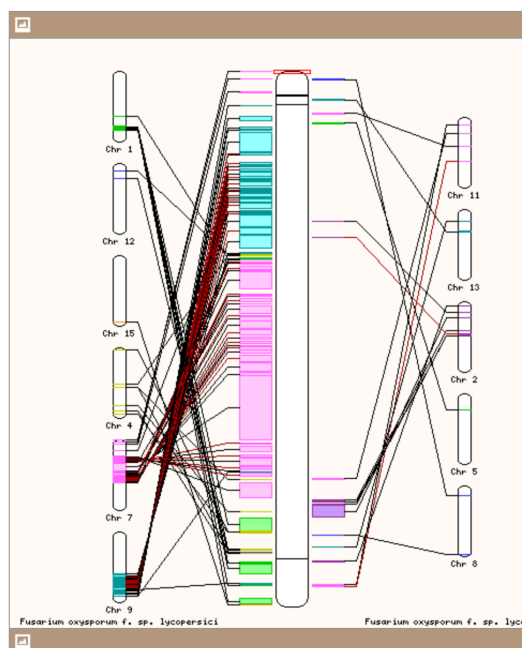
Linking line colours:

- = sequence in same orientation
- = sequence inverted

Our location highlighted in red

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

Synteny between *Fusarium solani* chromosome 5 and *Fusarium oxysporum* Synteny between *Fusarium solani* chromosome 5 and *Fusarium verticillioides*



Change Species:

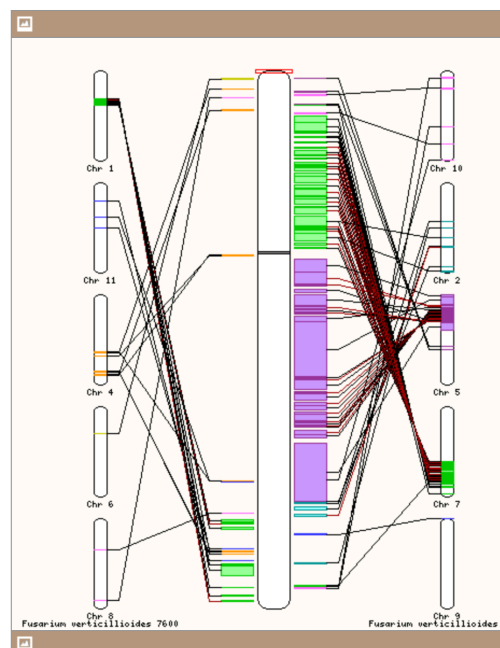
Fusarium oxysporum

Go

Change chromosome:

5

Go



Change Species:

Fusarium verticillioides

Go

Change chromosome:

5

Go

## 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*.

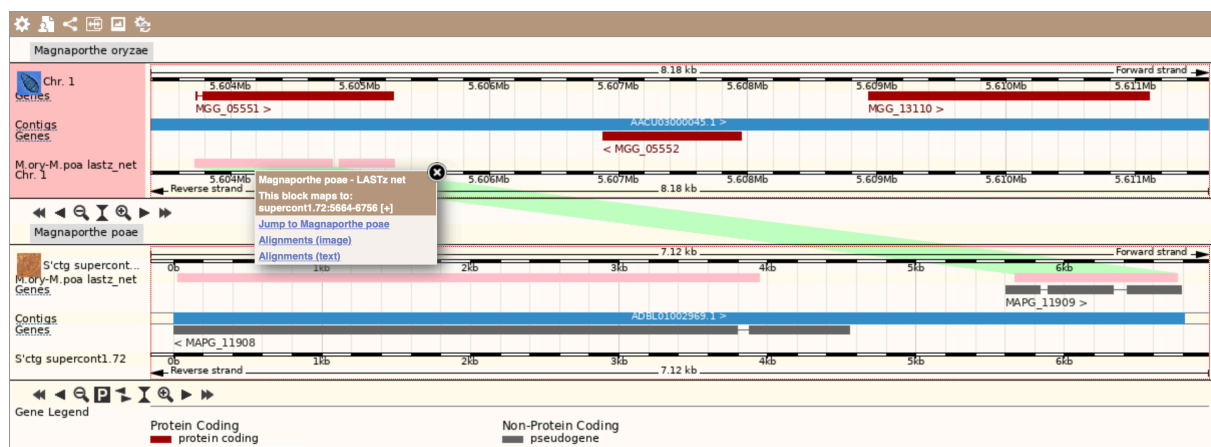
(a) Search for the region **1:5603535-5611402** in *Magnaporthe oryzae*.

Search: 
 for

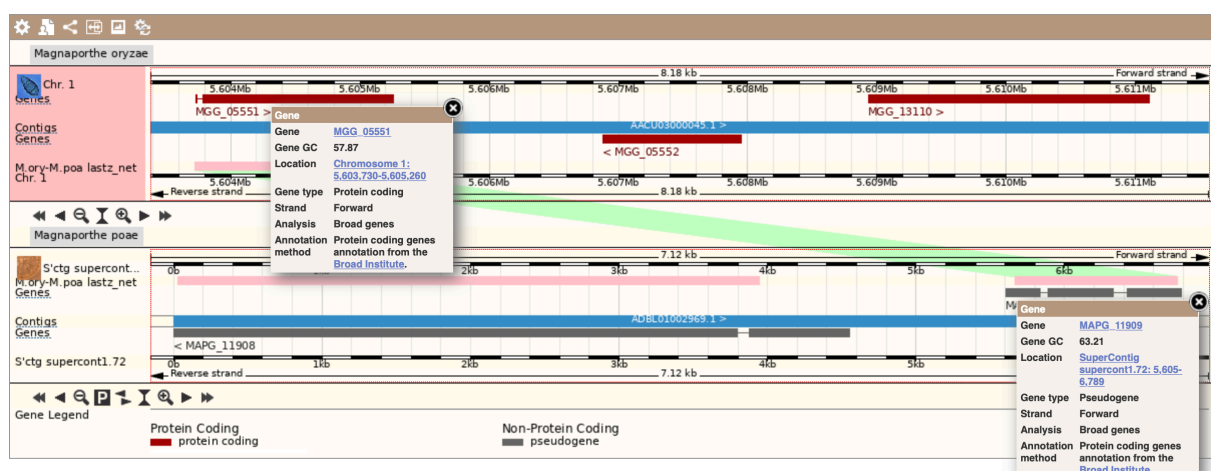
e.g. **NAT2** or **alcohol\***

(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 *Magnaporthe 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*?

