

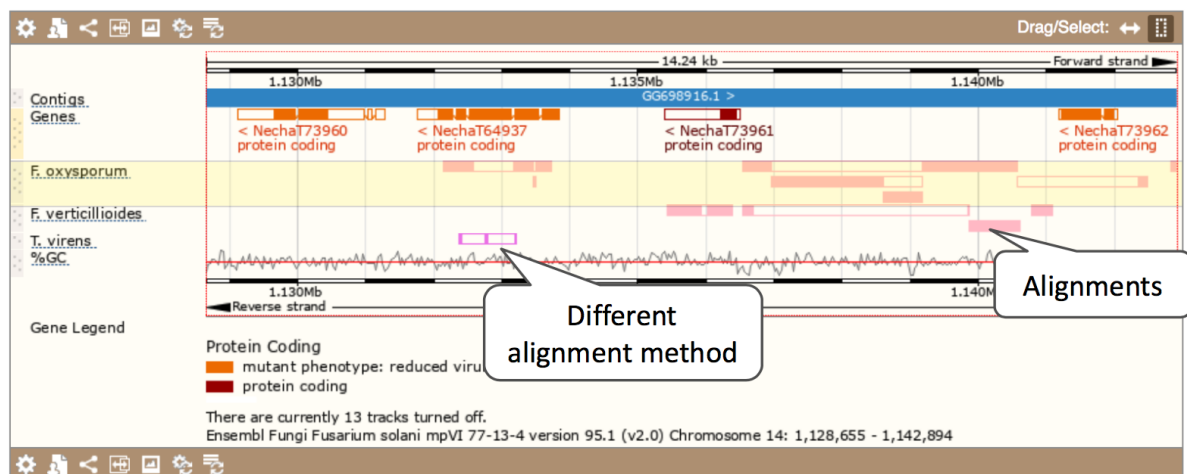
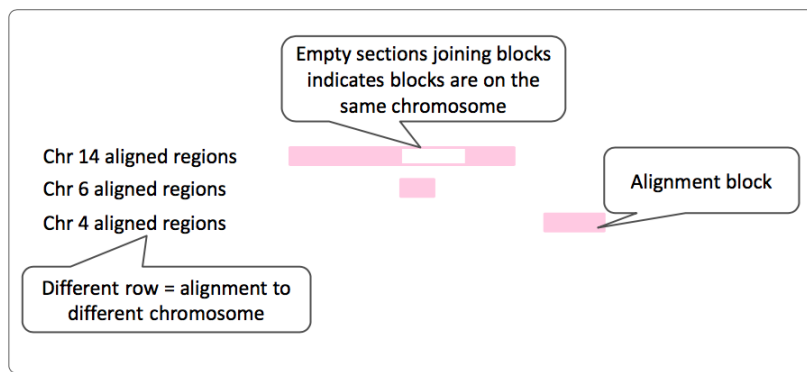
Demo: Ensembl Fungi whole genome alignments

In the BioMart demo in Wednesday's session, we searched for genes that were associated with reduced virulence in *Fusarium solani* that are not present in *Fusarium oxysporum*. 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. Go to the region [14:1128520-1142558](#) in *Fusarium solani*. This region includes the three genes we identified from the BioMart query (PEP2, PEP5 and PDA1) and another called ESP3.

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 format.

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.



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 <i>Fusarium solani</i>	Location on <i>Fusarium oxysporum</i>
Block 1	4035	14:1136535-1140569	3:5089432-5091278
Block 2	2222	14:1136958-1139179	3:4283870-4293377
Block 3	1918	14:1140570-1142487	1:6454070-6459335
Block 4	1597	14:1132137-1133733	4:115495-117183
Block 5	573	14:1138596-1139168	6:1547472-1548044
Block 6	69	14:1142826-1142894	1:5863367-5863438
Block 7	44	14:1133460-1133503	6:239926-239969
Blocks ordered by size, not location		<i>F. solani</i> region all on Chromosome 14	<i>F. oxysporum</i> 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 to [View 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.

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

Unselected species ²

+ Fusarium verticillioides - lastz

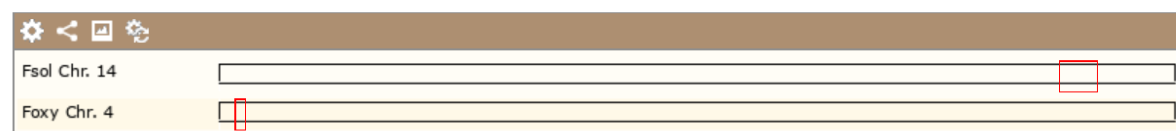
+ Trichoderma virens - translated blat

Selected species ¹

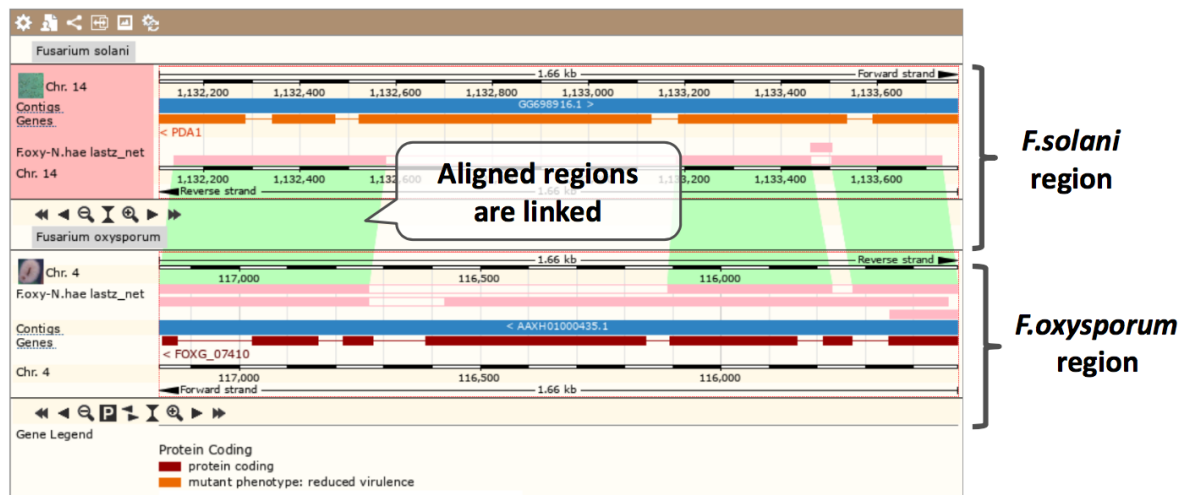
- Fusarium oxysporum - lastz

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:

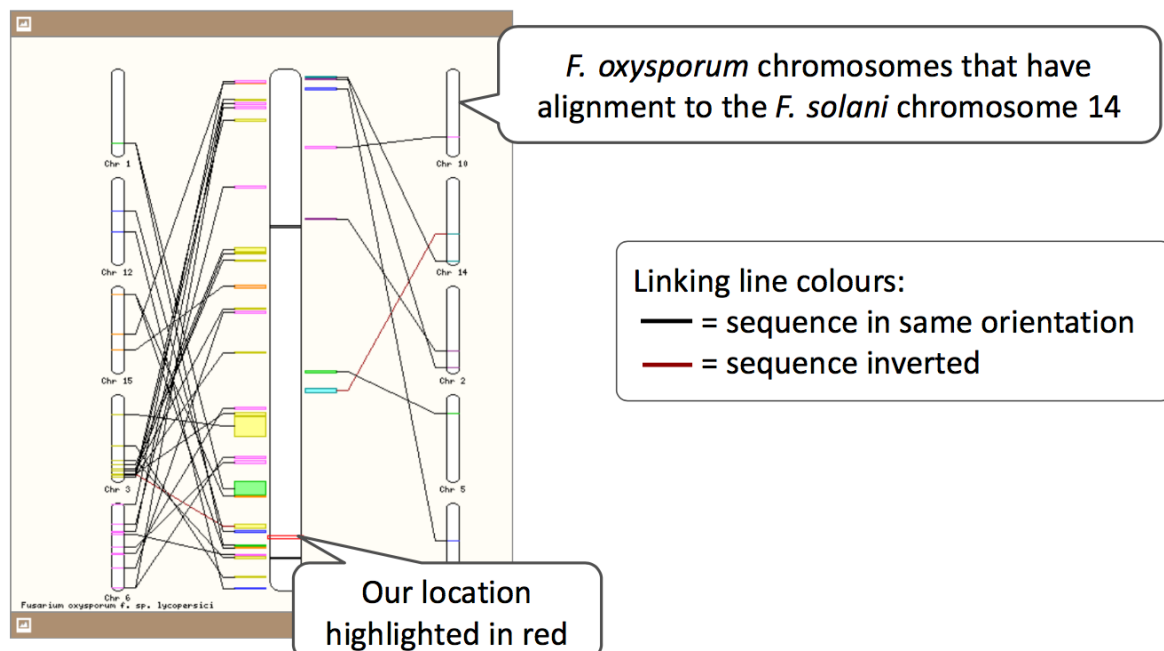
✓ *Fusarium solani*
Fusarium oxysporum

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*



Exercises: Ensembl Fungi whole genome alignments

WGA Exercise 1 - 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*.
- (b) Click on [Region comparison](#) and choose *Magnaporthe poae* from the select species or regions pop-up to perform an alignment.
- (c) To what region (chromosome/scaffold/contig) does this region align to on the *Magnaporthe poae* assembly?
- (d) Scroll down to the most detailed image. 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*?

WGA Exercise 2 – Whole genome alignments

- (a) Find the 7:2007000-2026000 region in *Fusarium oxysporum* and go to the [Region in detail](#) page.
- (b) Turn on the [LASTZ-net alignment](#) tracks for *Fusarium solani* and *Fusarium verticillioides*.
In which species can you see in the most gaps in the alignment?
Looking at the pink alignment blocks, does this region in *F. oxysporum* align to multiple different chromosomes in the other species, how can you tell?
- (c) Click on Synteny.
Which chromosome in *F. solani* is most similar to *F. oxysporum* chromosome 7?
Change the display to show *F. verticillioides*. Does this give you the same answer as for *F. solani*?