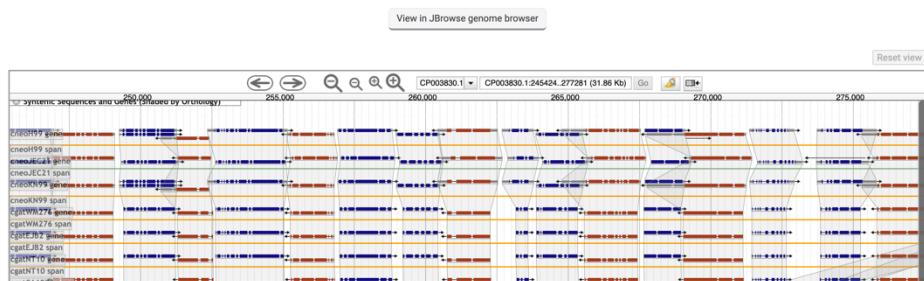


FungiDB: Synteny in JBrowse

- Navigate to the gene record page for **Gat201** in *Cryptococcus neoformans* H99 and examine the evidence within the Orthology and Synteny section.

1. Use site search to locate the gene record page.
2. Use the contents menu on the left to navigate to the Orthology and Synteny section.



3. Filter for *Cryptococcus* species in the Orthology and Synteny table.

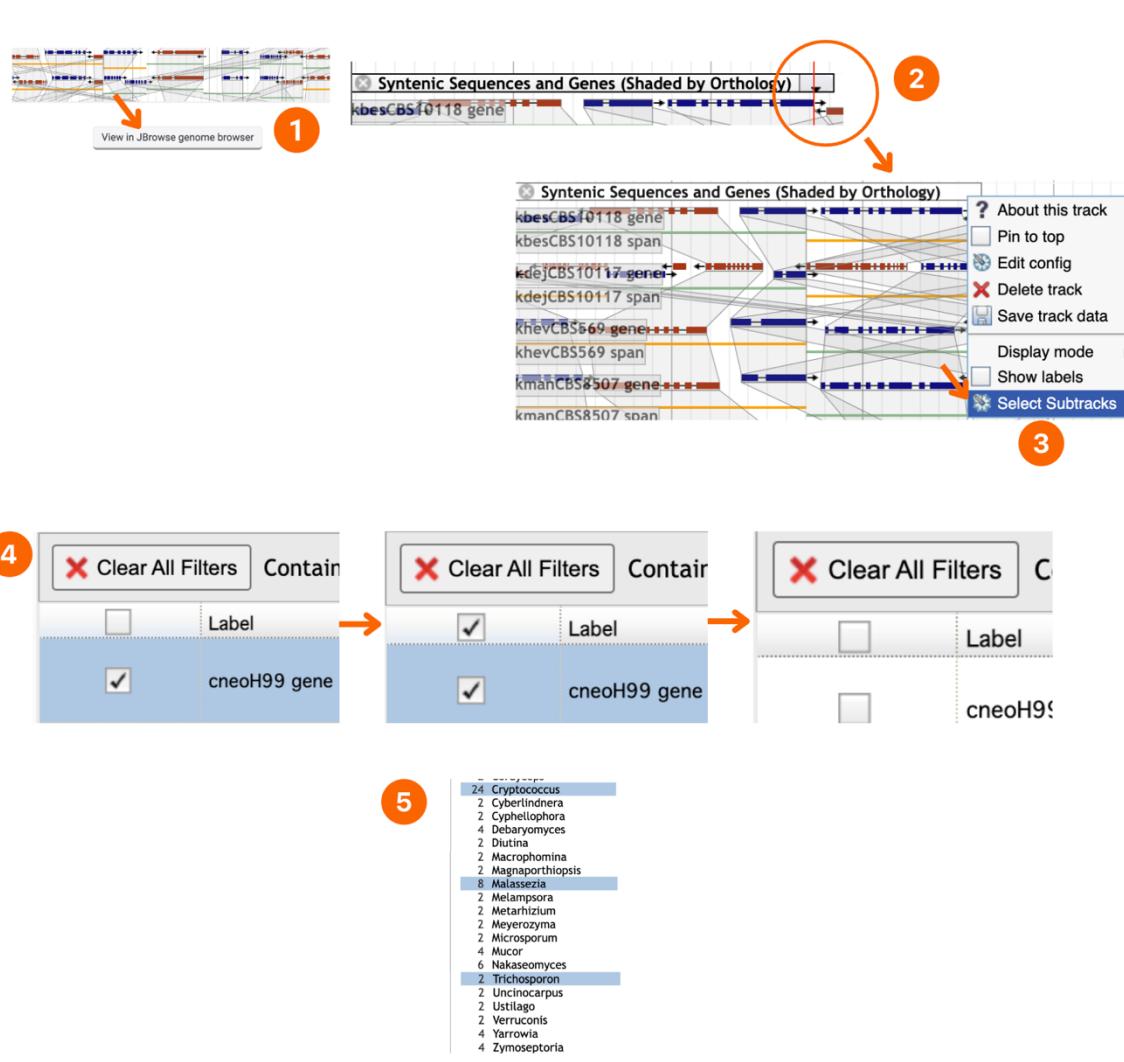
- What can you tell about its conservation across *Cryptococcus* species?

The figure shows a screenshot of the 'Orthology and Synteny' table in FungiDB. The table has three columns: 'Ortholog Group' (with a dropdown menu for 'OG6_531912'), 'Product' (with a dropdown menu for 'Data sets'), and 'To run Clustal Omega, select genes from the table below. Then choose the sequence type and initiate the analysis.' A search bar at the bottom is set to 'Crypto'. The table lists four entries:

Ortholog Group	Product	
OG6_531912	D1P53_003607	unspecified product
	L203_05099	GATA-type domain-containing protein [Source:UniProtKB/TEMBL;Acc:ADATE3 9A1]
	I314_00715	hypothetical protein
	I306_00505	hypothetical protein

- Navigate to JBrowse and create a custom JBrowse view for this gene's synteny across *Cryptococcus*, *Malassezia*, and *Trichosporon*.

1. Click on the “View in JBrowse gene browser” button.
2. When in JBrowse, left click at the end of the “Syntenic sequences and Genes (Shaded by Orthology)” tracks to bring up the pull-down menu.
3. Click on the “Select subtracks” option.
4. Use the main check box to clear all selections.
5. Select tracks for *Cryptococcus*, *Malassezia*, and *Trichosporon* (*and don't forget save your choices by clicking on the “save” option at the bottom of the track*).



Gat201 is a positive regulator of titanization under specific conditions in *Cryptococcus*. Titan cell formation is a rare phenomenon in *C. neoformans/C. gattii* species complex. What can you conclude about the conservation of this gene across the selected fungal pathogens? Do the results make sense based on what you know about Gat201?

Examine neighboring genes in *Cryptococcus* species. Can you spot any genes that have undergone expansions, possible truncations or simply not present in all gene models?

Mining synteny and orthology information for hypothetical genes.

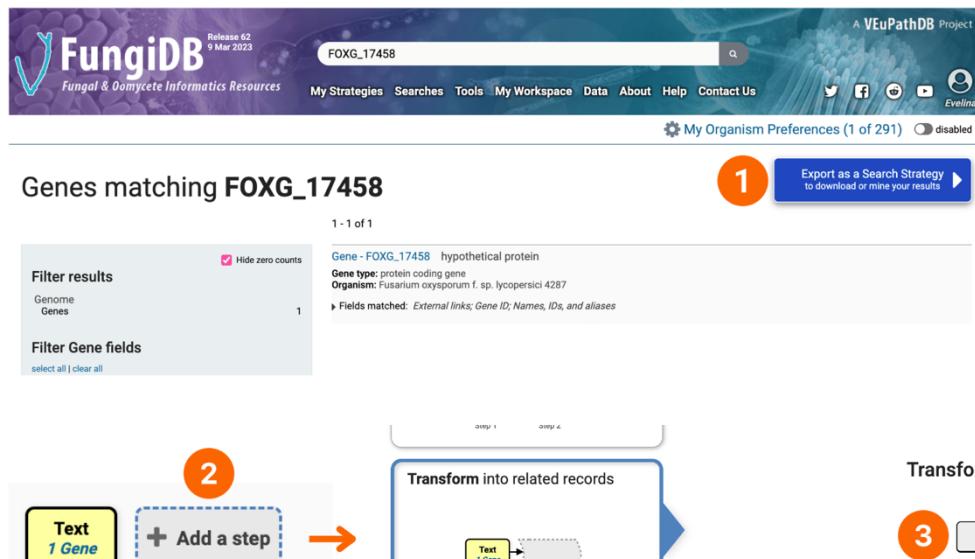
- Navigate to **FOXG_17458** gene record page in FungiDB and view the Orthology and Synteny section.



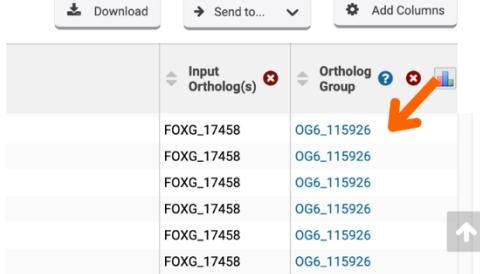
Notice that this hypothetical protein in *Fusarium oxysporum* f. sp. *lycopercisi* 4287 has no syntenic orthologs. Why do you think this is?

How can you test if there are orthologs of this gene in other *Fusarium* species?

- Create a search strategy looking for orthologs of **FOXG_17458** in *Fusarium* species.
 1. Use site search and export FOXG_17458 as a strategy step.
 2. Click on the Add Step button.
 3. Deploy the “Transform into related record” search and choose to transform genes into “Orthologs
 4. Select all *Fusarium* species and click on the “Run Step” button.



- Examine phyletic distribution by clicking on the “Ortholog Group” link within the results table.



	Input Ortholog(s)	Ortholog Group
FOXG_17458	OG6_115926	

▼ Phylogenetic Distribution of Proteins

Numbers refer to the number of proteins in that organism or taxonomic group.

Hide zero counts

fusarium

Eukaryota (EUKA)

Fungi (FUNG)

Ascomycota (ASCO)

Fusarium circinatum NRRL 25331 (fcir)	7
Fusarium fujikuroi IMI 58289 (ffuj)	7
Fusarium graminearum PH-1 (fgra)	2
Fusarium mangiferae MRC7560 (fman)	6
Fusarium odoratissimum NRRL 54006 (foxc)	9
Fusarium odoratissimum strain race 4 (foxt)	9
Fusarium oxysporum Fo47 (foxf)	3
Fusarium oxysporum NRRL 32931 (foxa)	4
Fusarium oxysporum f. sp. conglutinans Fo5176 (focf)	10
Fusarium oxysporum f. sp. cubense race 1 (foxr)	6
Fusarium oxysporum f. sp. lycopersici 4287 (foxy)	14
Fusarium oxysporum f. sp. melonis 26406 (foxm)	8
Fusarium proliferatum ET1 (fpzo)	8
Fusarium proliferatum strain NRRL62905 (fprn)	6
Fusarium vanettenii 77-13-4 (fvan)	8
Fusarium verticillioides 7600 (fver)	4

Is there evidence of possible expansion across different Fusarium species?

- Examine evidence for non-syntenic orthologs in MycoCosm.

1. Navigate to [Mycocosm](#) main page and select a *Fusarium oxysporum* f. sp. *lycopersici* strain 4287 genome. [mycocosm.jgi.doe.gov/Fusox2]

Home • *Fusarium oxysporum* f. sp. *lycopersici* 4287 v2

SEARCH BLAST BROWSE ANNOTATIONS ▾ MCL CLUSTERS SYNTENY DOWNLOAD INFO HOME HELP!



The genome of *Fusarium oxysporum* f. sp. *lycopersici* strain 4287 (race 2, VCG 0030) was sequenced by the Broad Institute and the text below is copied from there. In order to allow comparative analyses with other fungi, a copy of this genome was imported into MycoCosm.

Fungi of the *Fusarium oxysporum* species complex (FOSC) are ubiquitous soil and plant inhabiting microbes. As plant pathogens, FOSC strains can cause wilt and root rot diseases on over 120 plant species (Michelise and Rep, 2009). Many FOSC strains can infect plant roots without apparent effect or can even protect plants from subsequent infection (Alabouvette et al., 2009). FOSC isolates also have been identified as human pathogens causing localized or disseminated infections that may become life-threatening in neutropenic individuals (O'Donnell et al., 2004).

The first genome made available in 2007 was from a tomato wilt strain FOL 4287 (NRRL 34936) which was used for comparative analysis with the genomes of *F. graminearum* and *F. verticillioides*. Results of this comparison led to the discovery of mobile supernumerary chromosomes in this strain of *F. oxysporum* f. sp. *lycopersici* (race 2 - VCG 0030) containing genes required for host specific infection and disease (Ma et al., 2010).

References :

- Alabouvette,C., Olivain,C., Micheli,Q., and Steinberg,C. (2009) Microbiological control of soil-borne phytopathogenic fungi with special emphasis on wilt-inducing *Fusarium oxysporum*. *New Phytologist* 184: 529-544.
- Ma,L.J., van der Does,H.C., Borkovich,K.A., Coleman,J.J., Daboussi,M.J., Di Pietro,A. et al. (2010) Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*. *Nature* 464: 367-373.
- O'Donnell,K., Sutton,D.A., Rinaldi,M.G., Magnon,K.C., Cox,P.A., Revankar,S.G. et al. (2004) Genetic diversity of human pathogenic members of the *Fusarium oxysporum* complex inferred from multilocus DNA sequence data and amplified fragment length polymorphism analyses: Evidence for the recent dispersion of a geographically widespread clonal lineage and nosocomial origin. *Journal of Clinical Microbiology* 42: 5109-5120.

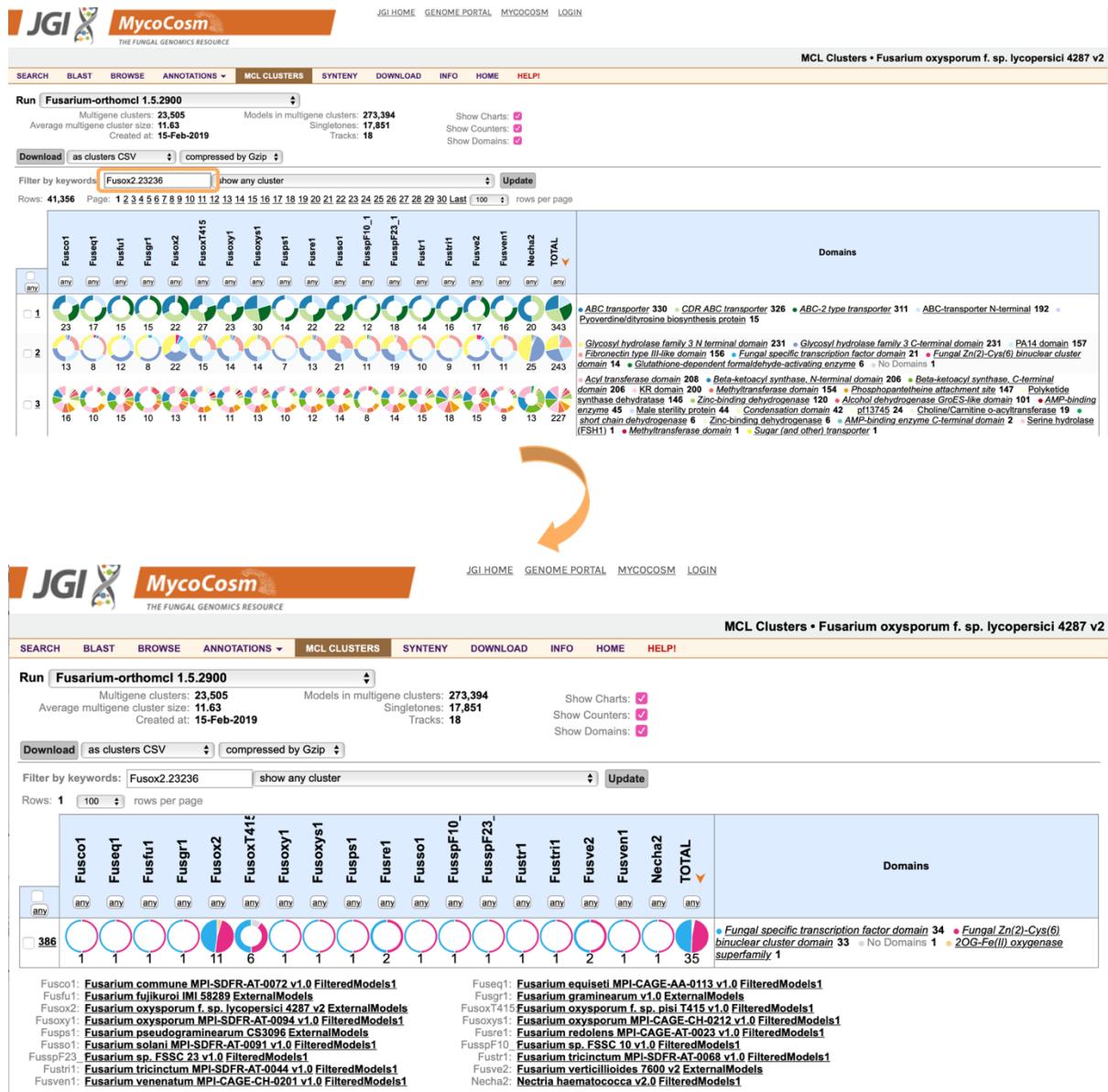
2. Use the Fusox2 portal's search page to identify the proteinID of "FOXG_17458T0" (Transcript 0 of FOXG_17458). You will find that the proteinID of FOXG_17458 in Fusox2 is 23236.

Gene	Gene Ontology	Annotations
Portal: Fusox2 Portal Name: Fusarium oxysporum f. sp. lycopersici 4287 v2 Protein Id: 23236 Transcript Id: 23236 Location: Scaffold_51:76759-80046 (+) Model Name: FOGX_17458T0 Track: ExternalModels	GO:0003677 • DNA binding GO:0003700 • transcription factor activity, sequence-specific DNA binding GO:0005634 • nucleus GO:0006351 • transcription, DNA-templated GO:0006355 • regulation of transcription, DNA-templated GO:0008270 • zinc ion binding	PF04082 • Fungal specific transcription factor domain PF00172 • Fungal Zn(2)-Cys(6) binuclear cluster domain IPR007219 • Transcription_factor_dom_fun IPR001138 • Zn2-C6_fun-type_DNA-bd IPR002409 • missing_ipr002409

3. Click on MCL clusters tab and then use the pull down menu to select clustering run "Fusarium-orthomcl 1.5.2900".

<https://mycocosm.jgi.doe.gov/clm/run/Fusarium-orthomcl.2900?organism=Fusox2>

4. Enter keyword Fusox2.23236 (databaseID.proteinID) to find clusters with that protein in it. Remember, for FOXG_17458 (FOGX_17458T0 protein ID in MycoCosm is 23236 and genome ID is Fusox2)



This will bring up cluster #386. Notice that this family is expanded only in the two known pathogens of the *Fusarium oxysporum* species complex with dispensable chromosomes (*Fusox2* and *FusoxT415*), but not in other *Fusarium* species including endophytic *Fusarium oxysporum* like *Fusoxys1* and *Fusoxyl*.

Now having this information at hand, you can either return to FungiDB and examine underlying transcriptomics, proteomics, etc. data or use other databases to enrich your analysis. For example:

- Navigate to Ensembl Fungi, search for FOXG_17458 and visualize the gene-tree:

EnsemblFungi - HMMER | BLAST | BioMart | Tools | Downloads | Documentation | Website help

Fusarium oxysporum (FO2) ▾

Location: 14:1,108,371-1,111,923 Gene: FOXG_17458 Transcript: FOXG_17458T0 Jobs ▾

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Gene alleles
- Sequence
- Secondary Structure
- Gene families
- Literature
- Fungal Compara
- Genomic alignments
- Gene tree**
- Gene gain/loss tree
- Orthologues
- Paralogues
- Pan-Taxonomic Compara
- Gene Tree
- Orthologues
- Ontologies
- GO: Biological process
- GO: Molecular function
- GO: Cellular component
- PHI: Phibase identifier
- Phenotypes
- Genetic Variation
- Variant table
- Variant image
- Structural variants
- Gene expression
- Pathway
- Regulation
- External references

Gene: FOXG_17458

Description: conserved hypothetical protein [Source:BROAD_F_oxysporum;Acc:FOGX_17458]

Location: Chromosome 14: 1,108,371-1,111,923 forward strand. FO2:CM000602.1

About this gene: This gene has 1 transcript (splice variant), 318 orthologues, 15 paralogues and is a member of 2 Ensembl protein families.

Transcripts: Hide transcript table

Name	Transcript ID	bp	Protein	Biotype	UniProt	Flags
Novel	FOGX_17458T0	2832	943aa	Protein coding	J9NQH9	

Gene tree

GeneTree ENSGT00930000001158

Number of genes: 345
 Number of speciation nodes: 270
 Number of duplication nodes: 47
 Number of ambiguous nodes: 26
 Number of gene split events: 1
 Highlight annotations: Hide annotations table

leotiomycetes: 51 homologs

Sordariomycetidae: 12 homologs

Microascales: 4 homologs

Hypocreales: 37 homologs

FOXG_17123, Fusarium oxysporum

FOXG_17458, Fusarium oxysporum

FOXG_16414, Fusarium oxysporum

FOXG_17084, Fusarium oxysporum

FOXG_12539, Fusarium oxysporum

FOXG_12589, Fusarium oxysporum

FOXG_14000, Fusarium oxysporum

FOXG_14422, Fusarium oxysporum

FOXG_15059, Fusarium oxysporum

FOXG_14257, Fusarium oxysporum

FOXG_09390, Fusarium oxysporum

Fusarium fujikuroi species complex: 2 homologs

NechaG47027, Fusarium solani

AK830_g8859, fungi_ascomycota3

Glomerellales: 8 homologs

Sordariomycetidae: 8 homologs

Xyariales: 7 homologs

Eurotiomycetes: 71 homologs

leotiomyceta: 2 homologs

Pezizomycotina: 6 homologs

Ascomycetes: 5 homologs

Budding yeasts: 5 homologs

saccharomyces: 7 homologs

Fungi incertae sedis: 71 homologs

LEGEND

Branch Length

- x1 branch length
- x10 branch length
- x100 branch length

Genes

- Gene ID gene of interest
- Gene ID within-sp. paralog

Nodes

- gene node
- speciation node
- duplication node
- ambiguous node
- gene split event

Collapsed Nodes

- collapsed sub-tree
- collapsed (paralog)
- collapsed (gene of interest)

Collapsed Alignments

- 0 - 33% aligned AA
- 33 - 66% aligned AA
- 66 - 100% aligned AA

Take a look at the between species paralogues. Is your data consistent with observations in MycoCosm? (Hint: look for duplication nodes).

- Click on the link at the bottom of the gene tree image to view all paralogues on the tree:

Expanded Alignments

gap
aligned AA

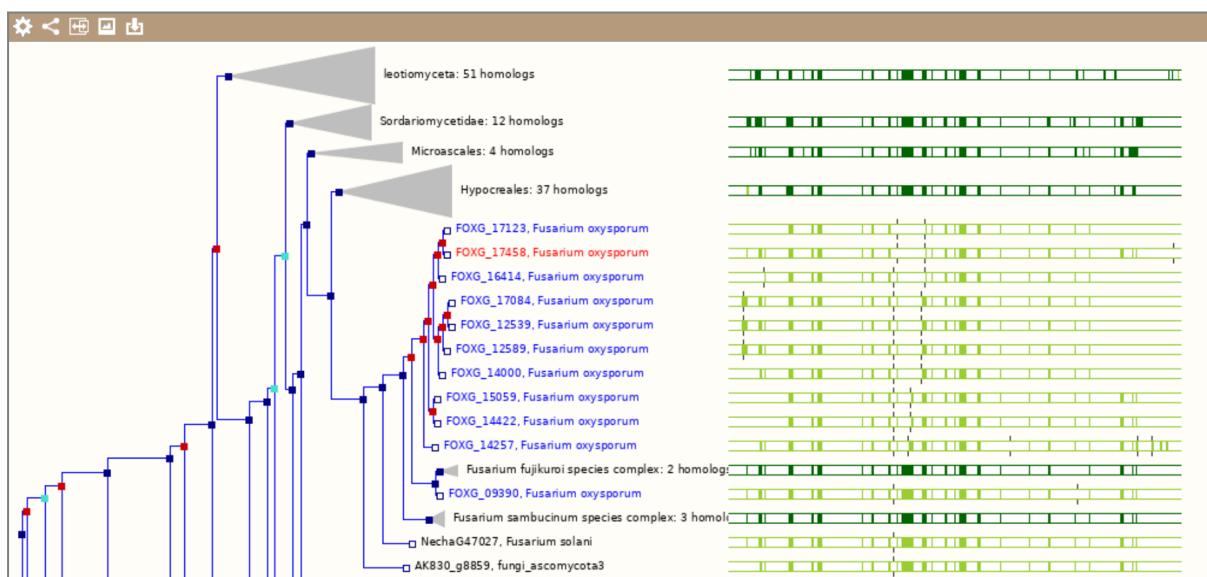
Add/remove tracks | Share | Resize image | Export image | Export

View options:

- [View current gene only](#) (Default)
- [View paralogues of current gene](#)
- [View all duplication nodes](#)
- [View fully expanded tree](#)
- Collapse all the nodes at the taxonomic rank

Use the 'configure page' link in the left panel to set the default. Further options are available from menus on individual tree nodes.

Ensembl Fungi release 56 - Feb 2023 © EMBL-EBI



- To export this data you can click on the *Download data for this image* button and choose form multiple formats:



File name: FOXG_17458_gene_tree

File format: FASTA

Preview Download Download Compressed

Guide to file formats

CLUSTALW	FASTA	Mega	MSF	Newick
<pre>CLUSTAL W(1.81) multiple sequence [TITLE: ProjectedMultiAlign] homo_sapiens/1-465588 CCTCAGGAC pan_tragiolytes/1-465588 CCCAGGCC *** **** homo_sapiens/1-465588 CCCAGGCC pan_tragiolytes/1-465588 CCCAGGCC *****</pre>	<pre>>homo_sapiens/1-464308 CCTCAGGACGCCAGGCCAAACCAACCGA CCCAGTCCTGCATGCCCTCTGGGCC TGCCATGCCATGCCATGCCATGCCATGCC AGAGGCCGCCAGGCCAGGCCAGGCCAGGCC CCAGCTGGATCTGTATTTGGCACCTG CCAGCTCTGTGCAAAAGGTGCTGTG/ AGGAAGACCCCTGGTGCCTCTGCCCTGTG/ AAAGATGGGGGGTGGTGGTGGTGGTCCCTCT GGGAGAGGGAGAGAGAAAGGGCCCTGGG TAGCCCCCTGGGCTCTAGCCCCACTGGGG</pre>	<pre>#mega !Title: ProjectedMultiAlign; !Format datatype=dna identical=- #homo_sapiens CCTCAGGAC GACGGCAAAC #pan_tragiolytes #homo_sapiens CCCAGTCCT TGCACTGCCT #pan_tragiolytes #homo_sapiens TGGGACAGAG AGAGAACAC</pre>	<pre>ProjectedMultiAlign MSF: 2 Type: Name: homo_sapiens/1-465588 Leri Name: pan_tragiolytes/1-465588 Leri // homo_sapiens/1-465588 CCTCAGGAC GACGGCAAAC #pan_tragiolytes/1-465588 CCCAGGCC homo_sapiens/1-465588 GGTCAACAC CI</pre>	<pre>(((((ENSTRUP0000015030_Trib_0_07 ENSTNP0000002493_Trig_0_10_49)0_0 ENSTNP0000002494_Trig_0_10_49)0_0 ((ENSPYPO0000001575_Pfor_0_042925, ENSMAP0000006983_Xmac_0_044847)0_0 ENSNTP0000006940_Ori_0_29811)0_0 ENSNTP0000006941_Ori_0_29811)0_0 ENSNTP0000006942_Ori_0_29811)0_0 ENSNTP00000010385_Gmor_0_34066)0_1 (ENSAKMP00000013460_Amor_0_474771, ENSDAXP00000099674_Drer_0_588918)0_0 ENSGAIP00000015990_Mgal_0_043749)0_0 ((((((ENSGALP000000272524_Ogal_0_03 ENSGAIP00000015990_Mgal_0_043749)0_0 ENSAFLP0000007411_Apla_0_128777)0_0</pre>
Nexus	OrthoXML	Pfam	Phylip	
<pre>#NEXUS [TITLE: ProjectedMultiAlign] begin data; dimensions ntax=2 nchar=465588; format interleave datatypes=none gap=- matrix homo_sapiens CCTCAGGAC ; pan_tragiolytes CCCAGGCC ; homo_sapiens GGGTCAACAC ; pan_tragiolytes GGGCCAACAC ;</pre>	<pre><?xml version="1.0" encoding="UTF-8"?> <xsi> <orthoXML xsi:schemaLocation="http://www.w3.org/2005/10/XMLSchema-Instances.xsd" xsi:type="orthoxml"> <orthoxML xsi:schemaLocation="http://www.w3.org/2005/10/XMLSchema-Instances.xsd" xsi:type="orthoxML"> <species NCBITaxId="925"> <database name="Unkno <genes> <gene id="6053741" <gene id="5945247 </genes></pre>	<pre>homo_sapiens/1-465588 CCTCAGGAC pan_tragiolytes/1-465588 CCCAGGCC</pre>	<pre>2 465588 homo_sapien CCTCAGGAC GACGGCAA pan_tragioly CCCAGGCC GACGGCAA GGTCAACAC CCCAGGCC GGCCAACAC CCCAGGCC ACTGTGTGG TTCAACCTA ACTGTGTGG TTCAACCTA GCTCGGGGGA CCTCTGGAT GCTCGGGGGA CCTCTGGAT</pre>	
PhyloXML	PSI	Stockholm	Text	
<pre><?xml version="1.0" encoding="UTF-8"?> <phyloxml xsi:schemaLocation="http://w3.org/1999/02/22-owl#&gt; type="gene"></pre>	<pre>homo_sapiens CCTCAGGACGCCAGGCCAA pan_tragiolyt CCCAGGCCAGGCCAGGCCA</pre>	<pre># STOCKHOLM 1.0</pre>	<pre>(B=0 T=Buteleostomi 10335 ---(B=67 T=Neopterygii 1; ---(B=2 T=Clupeonidae)</pre>	

Or you can choose to download the image as shown by clicking on the Export this image button:

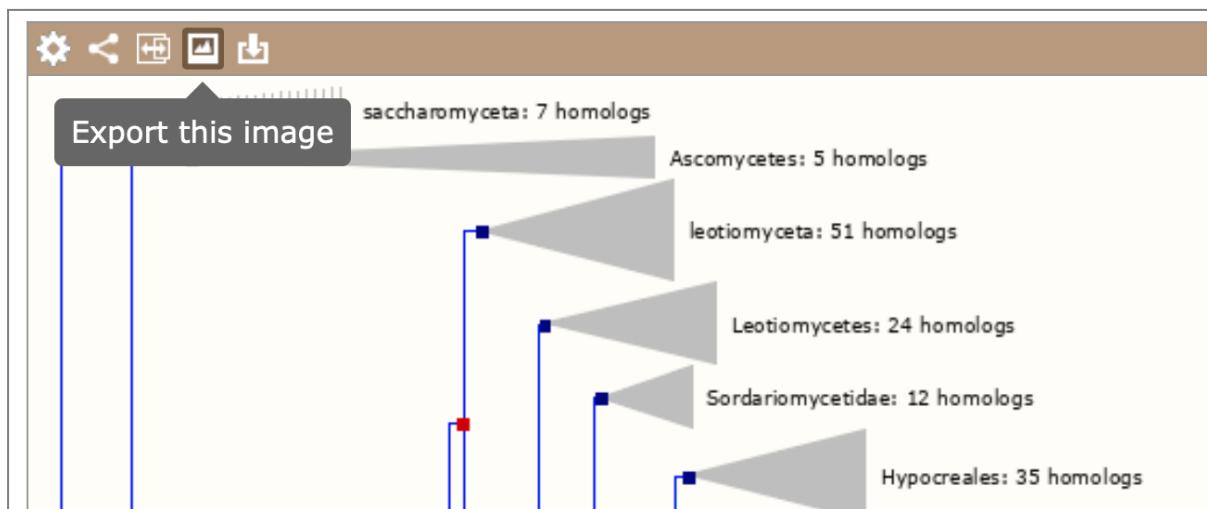


Image download

File name: Fusarium oxysporum_FOXG_17458.pc

Select Format

- PDF file** - Standard image as PDF file
- Presentation** - Saturated image, better suited to projectors
- Poster** - Very high resolution, suitable for posters and other large print uses
- Journal/report** - High resolution, suitable for printing at A4/letter size
- Web** - Standard image, suitable for web pages, blog posts, etc.
- Custom image** - Select from a range of formats and sizes

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