

FungiDB: Synteny in JBrowse

Fungal organisms produce a wide range of extracellular enzymes to break down organic materials. Glycoside hydrolases (GH) is a large family of enzymes that facilitate degradation processes.

1. Using Synteny tracks in FungiDB

- Initiate a gene search for Glycosyl hydrolase family 47 proteins in *Cryptococcus gattii* R265. Use the InterPro Domain search and enter **PF01532**.

Identify Genes based on InterPro Domain

cryp

☐ Fungi

☐ Basidiomycota

☐ Tremellomycetes

☐ Cryptococcaceae

☒ Cryptococcus

☒ Cryptococcus gattii VGI

☒ Cryptococcus gattii EJR2

☒ Cryptococcus gattii NT-10

☒ Cryptococcus gattii WM276

☒ Cryptococcus gattii R265

☒ Cryptococcus gattii VGII

☒ Cryptococcus gattii CA1873

☒ Cryptococcus gattii VGIH INO107

☒ Cryptococcus neoformans

☒ Cryptococcus neoformans var. grubii H99

☒ Cryptococcus neoformans var. grubii KNV9

☒ Cryptococcus neoformans var. neoformans B-3501A

☒ Cryptococcus neoformans var. neoformans JEC21

☐ Kwonella

☐ Kwonella bestiolae CBS 10118

☐ Kwonella dejecticola CBS 10117

☐ Kwonella hevenensis CBS 569

add these | clear these | select only these
select all | clear all

Domain Database

PFAM

Specific Domain(s)

PF01532: Glyco_hydro_47 Glycosyl hydrolase family 47

- Navigate to the gene page of CNBG_9313. This gene belongs to the family of CAZy genes

InterPro Domains

Step 1

3 Genes (2 ortholog groups) [Review this search]

Gene Results [Genomic View] [Annotate Results]

Rows per page: 1000

Gene ID	Transcript ID	Organism	Genomic Location (Gene)	Product Description	Score / E value
CNBG_2391	CNBG_2391-CDL1	Cryptococcus gattii VGIH R265	KQ410561.940.016..942.011(+)	mannosyl-oligosaccharide 1,2-alpha-mannosidase	.000E+00
CNBG_5230	CNBG_5230-CDL1	Cryptococcus gattii VGIH R265	KQ410571.140.140..142.781(+)	mannosyl-oligosaccharide alpha-1,2-mannosidase	.000E+00
CNBG_9313	CNBG_9313-CDL1	Cryptococcus gattii VGIH R265	KQ410563.85.561..89.006(+)	carbohydrate binding protein	.000E+00

- Click on the Synteny shortcut to examine tracks in closely related species.

Shortcuts

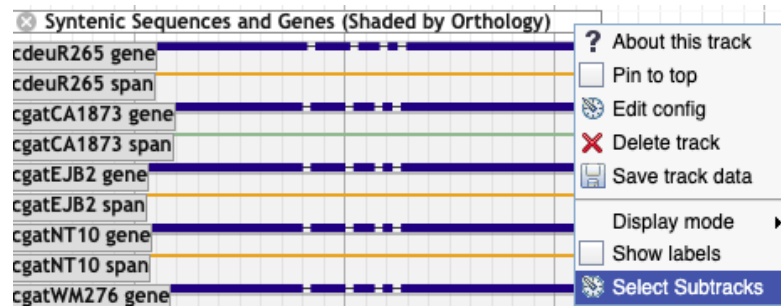
Synteny BLAT Alignments SNPs Transcriptomics

Protein Features

Also see Afu4g12470 in the [Genome Browser](#) or [Protein Browser](#)

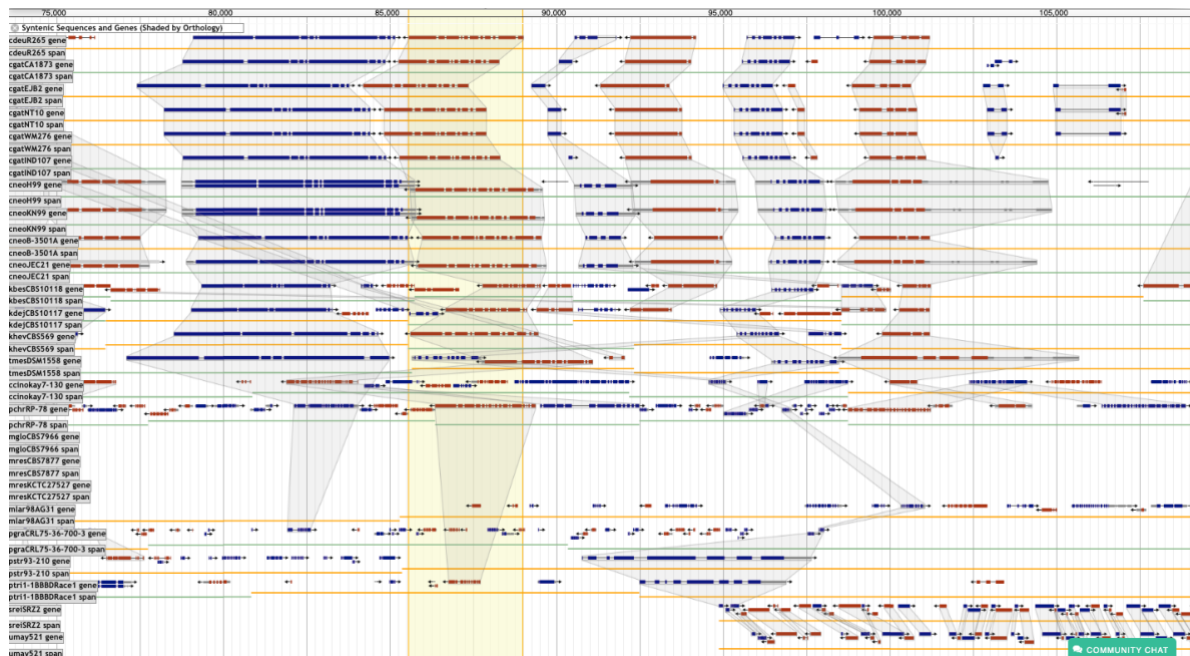
Expand All | Collapse All

Let's explore synteny in Basidiomycota. Click on the *View in genome browser* button to be re-directed to a JBrowse session and the activate custom tracks by clicking on the *Select subtracks* tab.



✖ Clear All Filters Contains text **basidio** ✖ 50 matching tracks

Is the region containing this gene syntenic in all species you selected?



- What can you conclude about the conservation of this gene across various species?
- What is the direction of the CNBG_9313 (highlighted in yellow) gene relative to the chromosome?
- Do you observe changes in the number of exons in different species?
- Notice that some of the genomes have contigs that are not contiguous. Why is that?
- Mouse over the two contigs and look at the information in the popups – do these pieces belong to the same chromosome? What does this mean?
- Observe the last track on the bottom of the screen – *Ustilago maydis*. Why do you think this gene is not detected here? *Hint: examine contigs.*

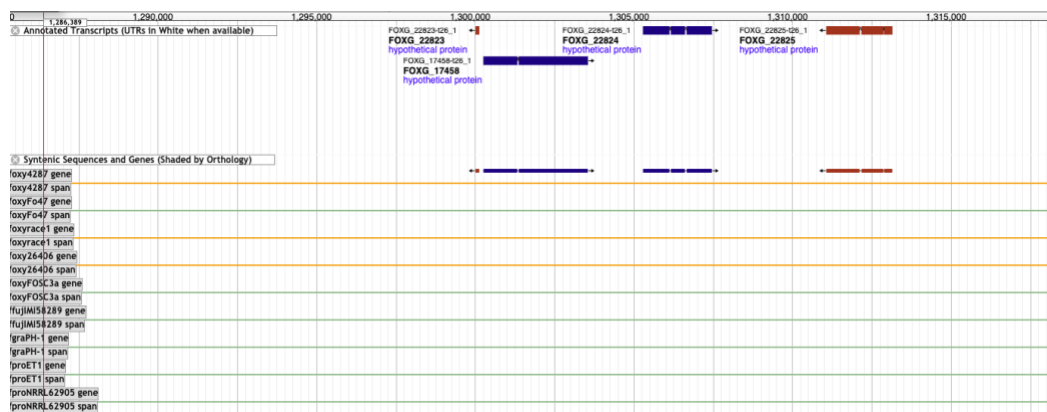
- Examine neighboring genes in *Cryptococcus* species. Which genes have undergone expansions or possible truncations?

Mining synteny and orthology information for hypothetical genes.

- Navigate to FOXG_17458, a hypothetical protein in *Fusarium oxysporum* f. sp. *lycopercisi* 4287
- View of syntenic genes in *Fusarium* species only:

✖ Clear All Filters
Contains text **fusarium**
✖ 24 matching tracks

Notice that there are no syntenic genes shown for FOXG_17458:



- Why do you think this is?
 - Look into non-syntenic *Fusarium* orthologs in FungiDB and examine Fusarium resources offered at MycoCosm.
- Using FungiDB site search, search for FOXG_17458 and export your results into the search strategy and look for non-syntenic orthologs in *Fusarium* species:

Text
1 Gene

Edit

+ Add a step

Step 1

1 Gene

Step 1

Step 2

Transform into related records

Text
1 Gene

Step 1

Step 2

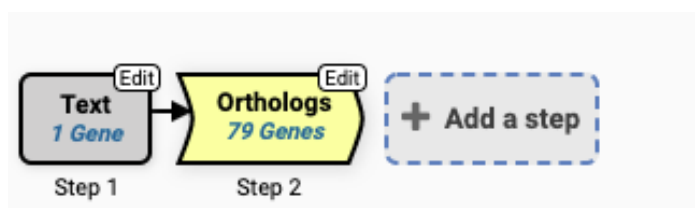
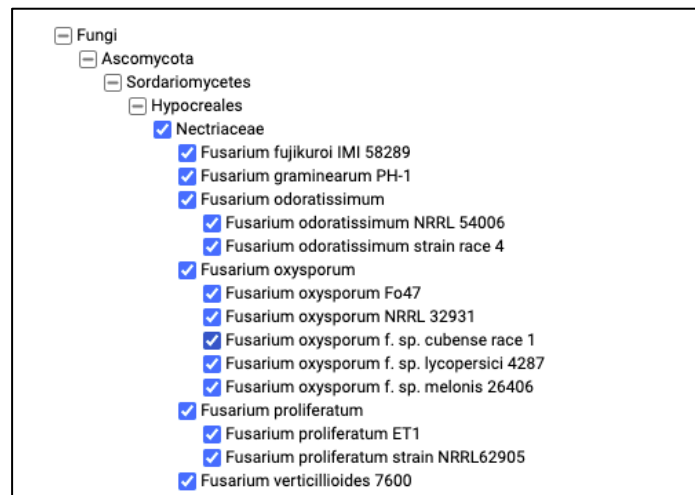
Use Genomic Colocation to

Transform 1 Gene into...

Orthologs

Metabolic Pathways

Compounds



- Examine your results. What can you conclude about conservation and function of this gene?
- Navigate to [Mycocosm](http://mycocosm.jgi.doe.gov/Fusox2) 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**

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Fusarium wilt of tomato caused by *Fusarium oxysporum* f. sp. *lycopersici*.
Image Credit: David B. Langston, University of Georgia, Bugwood.org

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 (Michiels 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., Migheli, 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.

- 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.

FOXG_17458T0 Search

Search By: Keywords Across: Default Terms: exact - fast

Download as CSV compressed by Gzip

Total genes found: 1 25

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: FOXG_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

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

MCL Clusters • Fusarium oxysporum f. sp. lycopersici 4287 v2

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Run **Fusox2 comparative clustering.829**

Cylol1 comparative clustering.2522
 Daces1 comparative clustering.2372
 Dacma1 comparative clustering.2494
 Dikarya 2017-01.1797
Fusarium-orthomcl 1.5.2900
 Fusco1 comparative clustering.2398
 Fuseq1 comparative clustering.2370
 Fusox2 comparative clustering.829
 FusoxT415 comparative clustering.2662
 Fusoxy1 comparative clustering.2154
 Fusoxys1 comparative clustering.2432
 Fusps1 comparative clustering.2026
 Fusre1 comparative clustering.1996
 Fusso1 comparative clustering.2371
 FusspF10_1 comparative clustering.2726
 FusspF11_1 comparative clustering.2896
 FusspF23_1 comparative clustering.2732
 Fustr1 comparative clustering.2430
 Fustr1 comparative clustering.2431
 Fusven1 comparative clustering.2486

gene clusters: **76,126**
 Singletons: **5,743**
 Tracks: **5**

Show Charts: ☒
 Show Counters: ☒
 Show Domains: ☒

100 rows per page

Domains

dehydrogenase 363 * No Domains 6 * [Zinc-binding dehydrogenase 3](#) * [Shikimate /](#)
 nase 1

superfamily 262 * No Domains 95 * [Sugar \(and other\) transporter 4](#) *

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

- Enter keyword Fusox2.23236 (databaseID.proteinID) to find clusters with that protein in it. Remember, for FOXG_17458 (FOXG_17458T0 protein ID in MycoCosm is 23236 and genome ID is Fusox2)

JGI MycoCosm THE FUNGAL GENOMICS RESOURCE

MCL Clusters • *Fusarium oxysporum* f. sp. lycopersici 4287 v2

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Run *Fusarium-orthomcl* 1.5.2900

Multigene clusters: 23,505 Models in multigene clusters: 273,394
Average multigene cluster size: 11.63 Singletons: 17,851
Created at: 15-Feb-2019 Tracks: 18

Show Charts: ☒
Show Counters: ☒
Show Domains: ☒

Download as clusters CSV compressed by Gzip

Filter by keywords: Fusox2.23236 show any cluster Update

Rows: 41,356 Page: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 Last (100) rows per page

	Fusox1	Fusox2	Fusox3	Fusox4	Fusox5	Fusox6	Fusox7	Fusox8	Fusox9	Fusox10	Fusox11	Fusox12	Fusox13	Fusox14	Fusox15	Fusox16	Fusox17	Fusox18	Fusox19	Fusox20	Fusox21	Fusox22	Fusox23	Fusox24	Fusox25	Fusox26	Fusox27	Fusox28	Fusox29	Fusox30	Fusox31	Fusox32	Fusox33	Fusox34	Fusox35	Fusox36	Fusox37	Fusox38	Fusox39	Fusox40	Fusox41	Fusox42	Fusox43	Fusox44	Fusox45	Fusox46	Fusox47	Fusox48	Fusox49	Fusox50	Fusox51	Fusox52	Fusox53	Fusox54	Fusox55	Fusox56	Fusox57	Fusox58	Fusox59	Fusox60	Fusox61	Fusox62	Fusox63	Fusox64	Fusox65	Fusox66	Fusox67	Fusox68	Fusox69	Fusox70	Fusox71	Fusox72	Fusox73	Fusox74	Fusox75	Fusox76	Fusox77	Fusox78	Fusox79	Fusox80	Fusox81	Fusox82	Fusox83	Fusox84	Fusox85	Fusox86	Fusox87	Fusox88	Fusox89	Fusox90	Fusox91	Fusox92	Fusox93	Fusox94	Fusox95	Fusox96	Fusox97	Fusox98	Fusox99	Fusox100	Fusox101	Fusox102	Fusox103	Fusox104	Fusox105	Fusox106	Fusox107	Fusox108	Fusox109	Fusox110	Fusox111	Fusox112	Fusox113	Fusox114	Fusox115	Fusox116	Fusox117	Fusox118	Fusox119	Fusox120	Fusox121	Fusox122	Fusox123	Fusox124	Fusox125	Fusox126	Fusox127	Fusox128	Fusox129	Fusox130	Fusox131	Fusox132	Fusox133	Fusox134	Fusox135	Fusox136	Fusox137	Fusox138	Fusox139	Fusox140	Fusox141	Fusox142	Fusox143	Fusox144	Fusox145	Fusox146	Fusox147	Fusox148	Fusox149	Fusox150	Fusox151	Fusox152	Fusox153	Fusox154	Fusox155	Fusox156	Fusox157	Fusox158	Fusox159	Fusox160	Fusox161	Fusox162	Fusox163	Fusox164	Fusox165	Fusox166	Fusox167	Fusox168	Fusox169	Fusox170	Fusox171	Fusox172	Fusox173	Fusox174	Fusox175	Fusox176	Fusox177	Fusox178	Fusox179	Fusox180	Fusox181	Fusox182	Fusox183	Fusox184	Fusox185	Fusox186	Fusox187	Fusox188	Fusox189	Fusox190	Fusox191	Fusox192	Fusox193	Fusox194	Fusox195	Fusox196	Fusox197	Fusox198	Fusox199	Fusox200	Fusox201	Fusox202	Fusox203	Fusox204	Fusox205	Fusox206	Fusox207	Fusox208	Fusox209	Fusox210	Fusox211	Fusox212	Fusox213	Fusox214	Fusox215	Fusox216	Fusox217	Fusox218	Fusox219	Fusox220	Fusox221	Fusox222	Fusox223	Fusox224	Fusox225	Fusox226	Fusox227	Fusox228	Fusox229	Fusox230	Fusox231	Fusox232	Fusox233	Fusox234	Fusox235	Fusox236	Fusox237	Fusox238	Fusox239	Fusox240	Fusox241	Fusox242	Fusox243	Fusox244	Fusox245	Fusox246	Fusox247	Fusox248	Fusox249	Fusox250	Fusox251	Fusox252	Fusox253	Fusox254	Fusox255	Fusox256	Fusox257	Fusox258	Fusox259	Fusox260	Fusox261	Fusox262	Fusox263	Fusox264	Fusox265	Fusox266	Fusox267	Fusox268	Fusox269	Fusox270	Fusox271	Fusox272	Fusox273	Fusox274	Fusox275	Fusox276	Fusox277	Fusox278	Fusox279	Fusox280	Fusox281	Fusox282	Fusox283	Fusox284	Fusox285	Fusox286	Fusox287	Fusox288	Fusox289	Fusox290	Fusox291	Fusox292	Fusox293	Fusox294	Fusox295	Fusox296	Fusox297	Fusox298	Fusox299	Fusox300	Fusox301	Fusox302	Fusox303	Fusox304	Fusox305	Fusox306	Fusox307	Fusox308	Fusox309	Fusox310	Fusox311	Fusox312	Fusox313	Fusox314	Fusox315	Fusox316	Fusox317	Fusox318	Fusox319	Fusox320	Fusox321	Fusox322	Fusox323	Fusox324	Fusox325	Fusox326	Fusox327	Fusox328	Fusox329	Fusox330	Fusox331	Fusox332	Fusox333	Fusox334	Fusox335	Fusox336	Fusox337	Fusox338	Fusox339	Fusox340	Fusox341	Fusox342	Fusox343	Fusox344	Fusox345	Fusox346	Fusox347	Fusox348	Fusox349	Fusox350	Fusox351	Fusox352	Fusox353	Fusox354	Fusox355	Fusox356	Fusox357	Fusox358	Fusox359	Fusox360	Fusox361	Fusox362	Fusox363	Fusox364	Fusox365	Fusox366	Fusox367	Fusox368	Fusox369	Fusox370	Fusox371	Fusox372	Fusox373	Fusox374	Fusox375	Fusox376	Fusox377	Fusox378	Fusox379	Fusox380	Fusox381	Fusox382	Fusox383	Fusox384	Fusox385	Fusox386	Fusox387	Fusox388	Fusox389	Fusox390	Fusox391	Fusox392	Fusox393	Fusox394	Fusox395	Fusox396	Fusox397	Fusox398	Fusox399	Fusox400	Fusox401	Fusox402	Fusox403	Fusox404	Fusox405	Fusox406	Fusox407	Fusox408	Fusox409	Fusox410	Fusox411	Fusox412	Fusox413	Fusox414	Fusox415	Fusox416	Fusox417	Fusox418	Fusox419	Fusox420	Fusox421	Fusox422	Fusox423	Fusox424	Fusox425	Fusox426	Fusox427	Fusox428	Fusox429	Fusox430	Fusox431	Fusox432	Fusox433	Fusox434	Fusox435	Fusox436	Fusox437	Fusox438	Fusox439	Fusox440	Fusox441	Fusox442	Fusox443	Fusox444	Fusox445	Fusox446	Fusox447	Fusox448	Fusox449	Fusox450	Fusox451	Fusox452	Fusox453	Fusox454	Fusox455	Fusox456	Fusox457	Fusox458	Fusox459	Fusox460	Fusox461	Fusox462	Fusox463	Fusox464	Fusox465	Fusox466	Fusox467	Fusox468	Fusox469	Fusox470	Fusox471	Fusox472	Fusox473	Fusox474	Fusox475	Fusox476	Fusox477	Fusox478	Fusox479	Fusox480	Fusox481	Fusox482	Fusox483	Fusox484	Fusox485	Fusox486	Fusox487	Fusox488	Fusox489	Fusox490	Fusox491	Fusox492	Fusox493	Fusox494	Fusox495	Fusox496	Fusox497	Fusox498	Fusox499	Fusox500	Fusox501	Fusox502	Fusox503	Fusox504	Fusox505	Fusox506	Fusox507	Fusox508	Fusox509	Fusox510	Fusox511	Fusox512	Fusox513	Fusox514	Fusox515	Fusox516	Fusox517	Fusox518	Fusox519	Fusox520	Fusox521	Fusox522	Fusox523	Fusox524	Fusox525	Fusox526	Fusox527	Fusox528	Fusox529	Fusox530	Fusox531	Fusox532	Fusox533	Fusox534	Fusox535	Fusox536	Fusox537	Fusox538	Fusox539	Fusox540	Fusox541	Fusox542	Fusox543	Fusox544	Fusox545	Fusox546	Fusox547	Fusox548	Fusox549	Fusox550	Fusox551	Fusox552	Fusox553	Fusox554	Fusox555	Fusox556	Fusox557	Fusox558	Fusox559	Fusox560	Fusox561	Fusox562	Fusox563	Fusox564	Fusox565	Fusox566	Fusox567	Fuso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Domains

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 29

EnsemblFungi | HMMER | BLAST | BioMart | Tools | Downloads | Documentation | Website help | Search Ensembl Fungi...

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:FOXG_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](#).

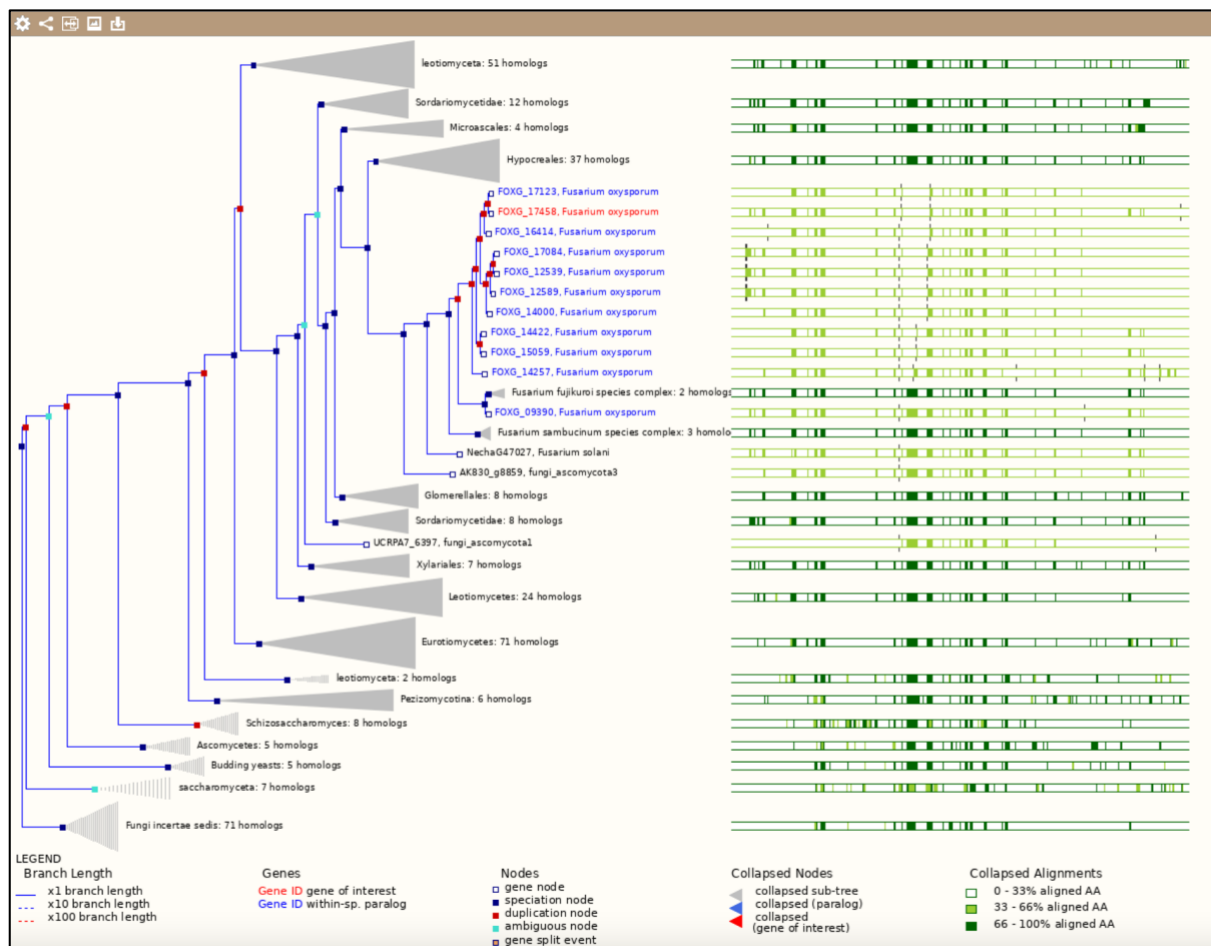
Transcripts [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Biotype	UniProt	Flags
Novel	FOXG_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

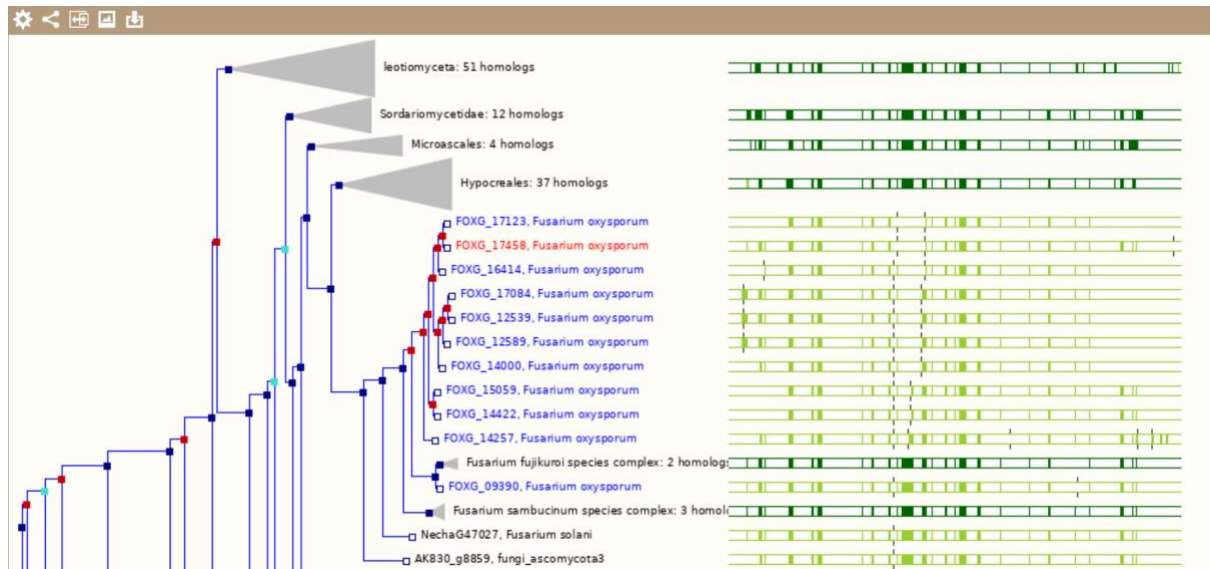


Take a look at the between species paralogues. Is your data consistent with observations in MycoCosm? (Hint: look for duplication nodes).

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

View options:

- [View current gene only](#) (Default)
- [View paralogs of current gene](#)
- [View all duplication nodes](#)
- [View fully expanded tree](#)



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



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