

FungiDB: Navigating gene record pages

Learning objectives

- Become familiar with gene page structure and content
- Navigate to and from the gene pages

1. Navigation to the Gene pages.

Navigate to the gene record page of [Afu2g13260](#), which is a gene known to be important for the virulence of the filamentous fungus *Aspergillus fumigatus*.



The panel on the left provides a summary of all record types that match **Afu2g13260**

Genes matching **Afu2g13260**

1 - 1 of 1

Click on the link to navigate to the gene record page for **Afu2g13260**

Export as a Search Strategy
to download or mine your results ►

Filter results
Genome Genes 1
External links 1
Gene ID 1

Filter Gene fields
select all | clear all
External links 1
Gene ID 1

Filter organisms
select all | clear all | expand all | collapse all
Type a taxonomic name ?
Fungi 1
Ascomycota 1

Gene - Afu2g13260 Putative regulator of adherence, host cell interactions and virulence

Gene name or symbol: medA
Organism: *Aspergillus fumigatus* Af293

► Fields matched: External links; Gene ID

Gene - Afu2g13260 Putative regulator of adherence, host cell interactions and virulence

Gene name or symbol: medA
Organism: *Aspergillus fumigatus* Af293

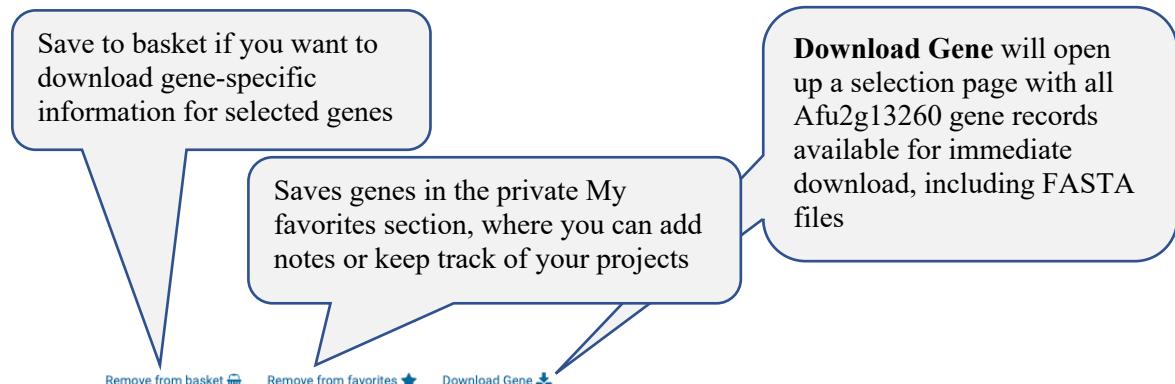
► Fields matched: External links; Gene ID

Clicking on this button will transform your search into a search strategy.

Note: If the button is shaded/inactive, limit your search to a single data type from the Filter results panel on the left.

2. Gene page components

The top section of the page provides a snapshot of the information available for this gene and offers several shortcuts:



Afu2g13260 Putative regulator of adherence, host cell interactions and virulence

Name: medA
Type: protein coding gene
Chromosome: 2
Location: Chr2_A_fumigatus_Af293:3,408,135..3,413,423(-)

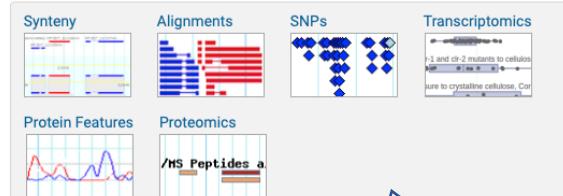
Species: *Aspergillus fumigatus*
Strain: Af293
Status: Curated Reference Strain

[View this gene at GeneDB](#)
[Add the first user comment](#)

Model Organism Orthologs
CGD: C3_01180C_A

Submit a comment about gene function or a knockout mutant phenotype (a separate form is available for bulk user submissions under About > Submit data)

Shortcuts



Also see Afu2g13260 in the [Genome Browser](#) or [Protein Browser](#)

Shortcuts panel contains a number of datasets available within a given category. Clicking on the magnifying glass symbol within the thumbnail will open evidence preview screen

Explore the content of this gene record page. Below are the navigational highlights.

The **Contents** section contains a list of links to various sections in the gene record page and is searchable. Sub-sections of the Contents menu can be hidden by checking the box to the right.

Afu2g13260

expand all | collapse all

Search section names...

• 1 Gene models
• 2 Annotation, curation and identifiers
• 3 Link outs
• 4 Genomic Location
• 5 Literature
• 6 Taxonomy
• 7 Ontology and synteny
• 8 Phenotype
• 9 Genetic variation
• 10 Transcriptomics
11 Sequence analysis
• 12 Sequences
• 13 Structure analysis
• 14 Protein features and properties
• 15 Function prediction
• 16 Pathways and interactions
• 17 Proteomics
• 18 Immunology

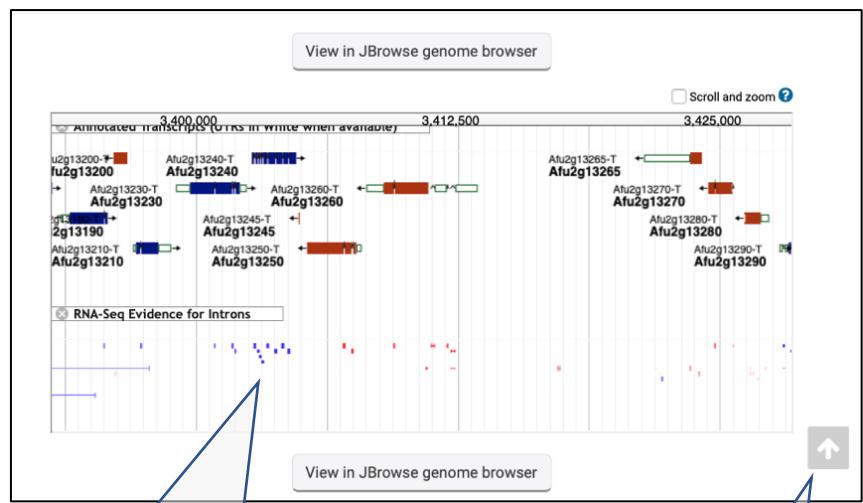
expand all | collapse all

Search Box

Customize the Contents menu

3. Explore the gene model section.

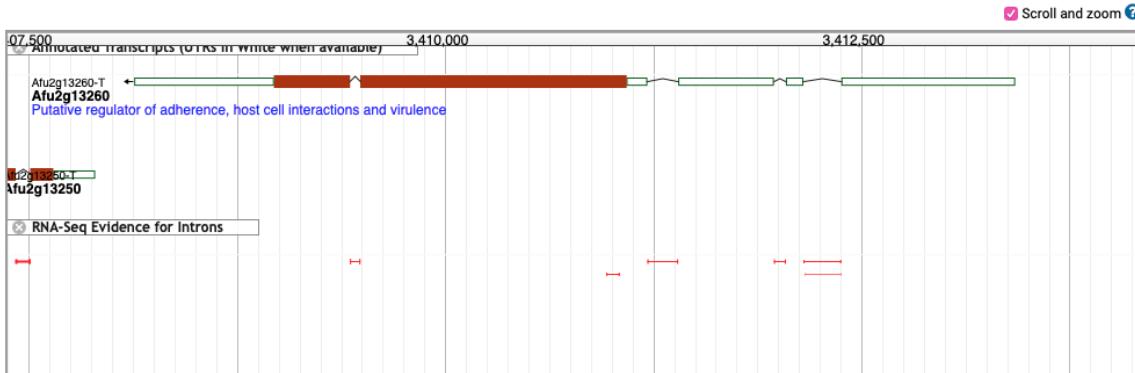
The **Gene Models** section is the first section of the gene record page and it contains information about the structure of the gene (e.g. exon count, transcript number, annotated UTRs and introns (when available), alternative transcripts) displayed within the genome browse JBrowse wrapper. To scroll within the JBrowse frame and zoom in onto the gene, check the “Scroll and zoom” window and use click and drag motion to select the area of interest. The **View in JBrowse genome browser** button opens a separate tab with the JBrowse session where you can activate additional tracks.



Introns that are matching transcript annotation for which there is an abundance of supporting data from aligned RNA-Seq reads are displayed in bold colours (Blue for a forward gene and red for a gene located on the reverse strand).

Click this button to navigate to the top of the gene record page

- Zoom in on Afu2g13260. To do this, activate scroll and zoom function within the JBrowse wrapper to zoom in on the gene.



- Click on one of the introns within the **RNA-Seq Evidence for Introns** track. The pop-up window contains a table showing all experiments and samples that provide evidence for this intron junction (generated by in-house automated pipelines):

Intron Spanning Reads (ISR): The total number of uniquely mapped reads (all samples) which map across the junction and are on the appropriate strand. GSNAP uses splice site consensus sequences to determine the strand of the mapped read.

ISR per million (ISRPm):
Intron Spanning Reads Per Million intron spanning reads and thus represents a normalized count of unique reads.

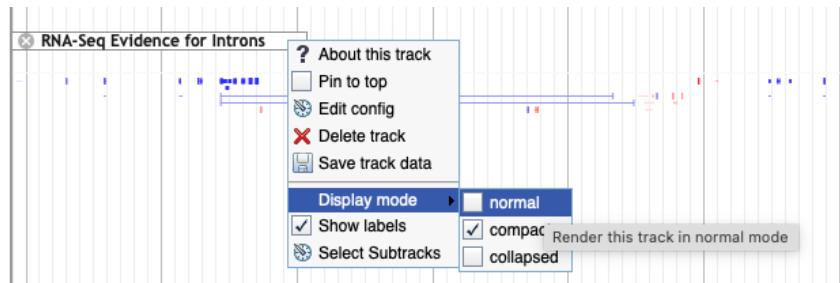
% of Most Abundant Intron (MAI): The percentage (ISRPm of this junction / ISRPm of maximum junction for this gene) of this junction over the maximum for this gene.

Score=1336 details						
Intron Location:	3411216 - 3411400 (185 nt)					
Intron Spanning Reads (ISR):	1336					
ISR per million (ISRPm):	419.8					
Gene assignment:	Afu2g13260 - annotated intron					
% of Most Abundant Intron (MAI):	74.2					
Most abundant in:	Gene expression under oxidative and iron stresses : Af Fe-starved					
ISRPm (ISR / gene coverage)	49.46 (.7489)					
Experiment	Sample	Unique ISRPm	ISR/Cov	% MAI		
Adaptation to different growth environments (blood)	pre	110	.17.96	.4737	73.8	
	B30	48	.7.85	.3363	47.5	
	B180	14	.3.07	.1285	43.8	
	M180	71	.11.31	.6684	47.7	
	M30	133	.17.46	.8012	72.3	
Adaptation to oxygen limitation	0 min 100% O2	17	.9.35	.9379	100	
	15 min 5% O2	5	.3.7	.5475	62.5	
	30 min 5% O2	16	.10.32	.9247	94.1	
	75 min 100% O2	22	.12.43	.963	95.7	
Comparative transcriptomics of dormant and germinating conidia	hyphae	39	.23.9	.1.8544	95.1	
	conidia	1	.7.72	.2793	33.3	
	germinated conidia	2	.5.59	.2841	22.2	
Gene expression under oxidative and iron stresses	Af control	18	.15.85	.1.1567	100	
	Af Fe-starved	49	.49.46	.7489	69	
	Af H2O2-treated	13	.11.45	.7677	61.9	
	Af Fe-starved and H2O2-treated	5	.5.38	.1764	41.7	
Transcriptome of wild-type vs veA and mtfA deletion mutants	Delta-mtfA TTDS4.1	22	.6.96	.8021	81.5	
	WT CEA10 mtfA matched	28	.10	.1.0062	82.4	

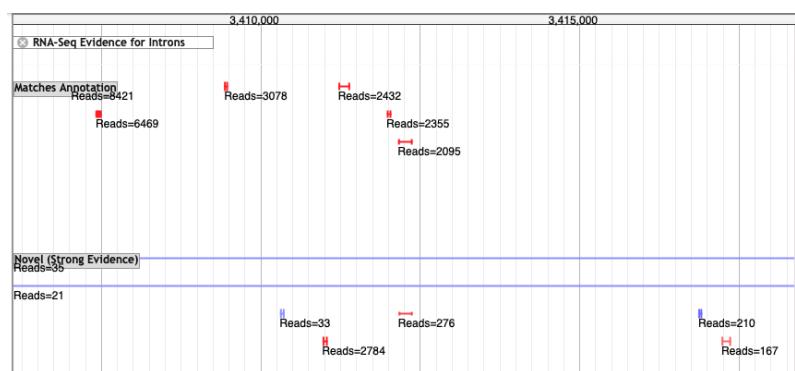
Most abundant in: The experiment and sample that has the highest ISRPm for this gene.

ISRPm, (ISR / coverage): ISRPm from the sample with the highest ISRPm and the ISR/coverage for that same sample.

- Notice that some introns reported within the track do not match the current gene model. You can further evaluate the intron evidence by left-clicking at the end of the **RNA-Seq Evidence for Introns** track and selecting “normal” from the Display mode options.



- The track is updated with 2 sub-tracks: RNA-Seq read mapping that matches current annotation and novel predicted introns with strong evidence.



3. Explore other content within the page.

- The track is updated with 2 sub-tracks: RNA-Seq read mapping that matches current annotation and novel predicted introns with strong evidence.

2 Annotation, curation and identifiers															
▼ Annotated Product Descriptions Data sets															
Transcript ID(s)	Product	Evidence Code	Reference	Support for Evidence Code Assignment											
Afu2g13260-T	Putative regulator of adherence, host cell interactions and virulence	N/A	N/A	N/A											
▼ Alternate Product Descriptions Data sets															
No data available															
External DB Version 2015-09-27															
Gene Name or Symbol medA															
▼ Names, Previous Identifiers, and Aliases Download Data sets															
<table border="1"> <thead> <tr> <th>Search this table...</th> </tr> </thead> <tbody> <tr> <td>Name/ID/Alias</td><td>Type</td></tr> <tr> <td>MEDA</td><td>name</td></tr> <tr> <td>AFUA_2G13260</td><td>previous ID</td></tr> <tr> <td>AFUB_028890</td><td>previous ID</td></tr> <tr> <td>CADAFUAG00004866</td><td>previous ID</td></tr> </tbody> </table>					Search this table...	Name/ID/Alias	Type	MEDA	name	AFUA_2G13260	previous ID	AFUB_028890	previous ID	CADAFUAG00004866	previous ID
Search this table...															
Name/ID/Alias	Type														
MEDA	name														
AFUA_2G13260	previous ID														
AFUB_028890	previous ID														
CADAFUAG00004866	previous ID														

The **Annotation, curation and identifiers** section offers alternate product descriptions, previous identifiers, and aliases, and is populated using data from internal curation, other fungal resources (*e.g.* AspGD, Ensembl, *etc.*), or user-submitted data (user comments).

The **Link outs** section offers redirection to other resources (*e.g.* CGD, Ensembl, MycoCosm, *etc.*).

▼ External Links Download Data sets	
Search this table...	
Database	External ID
AspGD	Afu2g13260
EnsemblFungi	AFUA_2G13260
Entrez Gene	3513134
GeneDB: The Sanger Institute Pathogen Genomics Database	Afu2g13260
NCBI RefSeq	XP_755658.1
PHI-base	PHI:2661
PubMed from Genome Annotations	19527167
PubMed from Genome Annotations	19889083
PubMed from Genome Annotations	20974273
PubMed from Genome Annotations	21646428
PubMed from Genome Annotations	21784698
PubMed from Genome Annotations	23031507
PubMed from Genome Annotations	23185496
PubMed from Genome Annotations	23925951
PubMed from Genome Annotations	23990787
The Universal Protein Resource (UniProt)	Q4X0J5

- Find curated information for host-pathogen interactions
 - Hint: Expand the External Links section and click on the link to the Pathogen-Host Interaction Database (PHI-Base).*

Pathogen Gene	Mutant Phenotype	Pathogen Species	Disease	Host Species
- MedA	reduced virulence	Aspergillus fumigatus	Invasive Pulmonary Aspergillosis	Galleria mellonella (related: greater wax moth)
Pathogen Gene Allele				
Gene:MedA		Pathogen species:Aspergillus fumigatus		Host species:Galleria mellonella (related: greater wax moth)
PHI-base entry:PHI:2661		Pathogen ID: 746128		Host classification:Moths
Gene ID:EAL93620		Pathogen strain:Af293		Host ID: 7137
Protein ID: Q4X0J5		Pathogen strain ID: 330879		Tissue:larva
Sequence strain:Af293				
Gene function:Developmental Regulator				
Essential gene/no				
Reference	Comments	PHI Phenotype	Pathogen Phenotype	
Pmid:23185496		Phenotype:reduced virulence		
Ref source:Pubmed		Disease name:Invasive Pulmonary Aspergillosis		
Year:2012		Tissue:larva		
DOI: 10.1371/journal.pone.0049959		Experimental technique:Gene mutation: characterised; gene complementation		
Author reference:Q A Abdallah 2012				

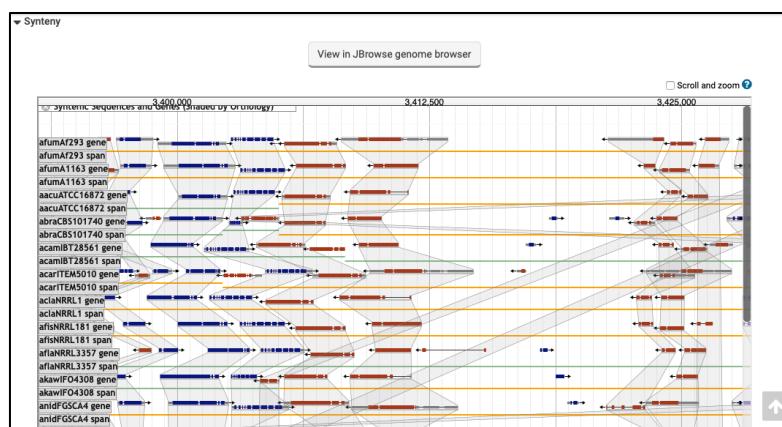
- What species are mentioned in the PHI-Base host section?
- Is this an essential gene in *A. fumigatus*?

The **Orthology and Synteny** section provides a table of Orthologs and Paralogs within FungiDB produced by OrthoMCL (www.orthomcl.org).

The table has a search box for creating a custom display of orthologs and also deploy the ClustalOmega analysis. The output of this tool can be used to build phylogenetic trees (e.g. iTOL).

The **Orthology and Synteny** section also contains synteny graphs in JBrowse:

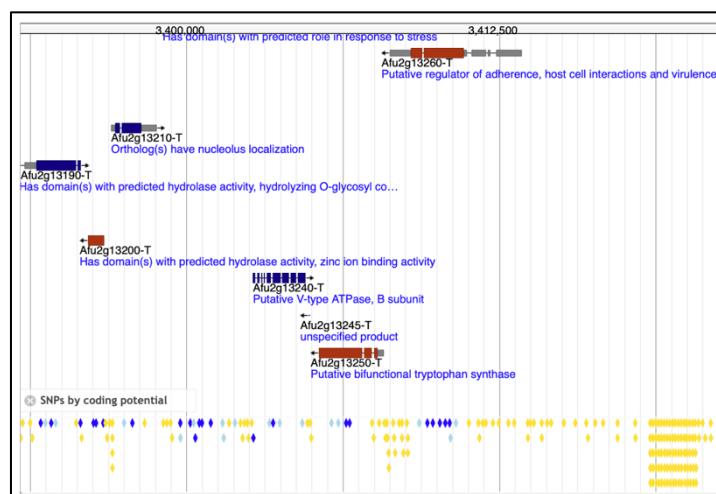
The screenshot shows the Orthology and Synteny section of FungiDB. At the top, there is a search bar labeled "Cocci". Below it is a table titled "Orthology Group OG_189343" with columns for "Protein cluster", "Gene", "Organism", "Product", "Is syntetic", and "Has comments". A red arrow points to the search bar with the text "Use search box to limit to a species of interest". Below the table is a button "Run clustal Omega for selected genes | Check All | Uncheck All" with a red arrow pointing to it and the text "Run ClustalOmega to generate protein sequence alignments and a .dnd file for building phylogenetic trees". To the right of the table is a ".dnd file" box containing several lines of text.



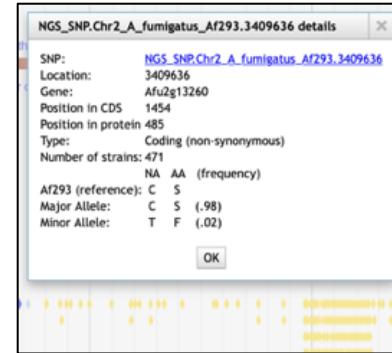
- Does this gene have syntenic orthologs in other *Aspergillus* species (hint: syntenic genes are highlighted in grey)?

The **Genetic Variation** section summarizes integrated SNP data for a given region and classifies SNPs based on the effect on gene function:

- noncoding (yellow diamonds)
- non-synonymous (dark blue)
- synonymous (light blue)
- nonsense (red)



- Left-click on the non-synonymous SNP positioned next to the intron and click on the SNP ID link at the top of the pop-up window to examine SNP evidence generated from the genomic data integrated into FungiDB.



Major allele is the most common allele in the studied population/isolates.

SNP: NGS_SNP.Chr2_A_fumigatus_Af293.3409636

Organism: Aspergillus fumigatus Af293
Location: Chr2_A_fumigatus_Af293: 3,409,636
Type: coding
Number of Strains: 48
Gene ID: Afu2g13260
Gene Strand: reverse
Major Allele: G (0.98)
Minor Allele: A (0.02)
Distinct Allele Count: 2
Reference Allele: G
Reference Product: S 485
Allele (gene strand): C
SNP context: AAGAAGTCTTCACTGTGCTTGGCTTG**G**GACACGGTGAGGGGTCGGAACCCCTCCAGAT
SNP context (gene strand): ATCTGGAGGGTTCCGACCCCTCACCGT**C**AAAGCCAAGCAGACAGTGAAGACTTCTT

Minor allele frequency is the frequency of the second most common allele occurring in a given population or a group of isolates.

Minor allele frequency is useful when looking for rare variants or disease-causing SNPs. However, there can be exceptions when minor allele frequency increases under selective pressure (e.g. development of drug resistance)

- Determine the minor allele frequency.
- What is the geographical origin of the isolate where this SNP occurs?

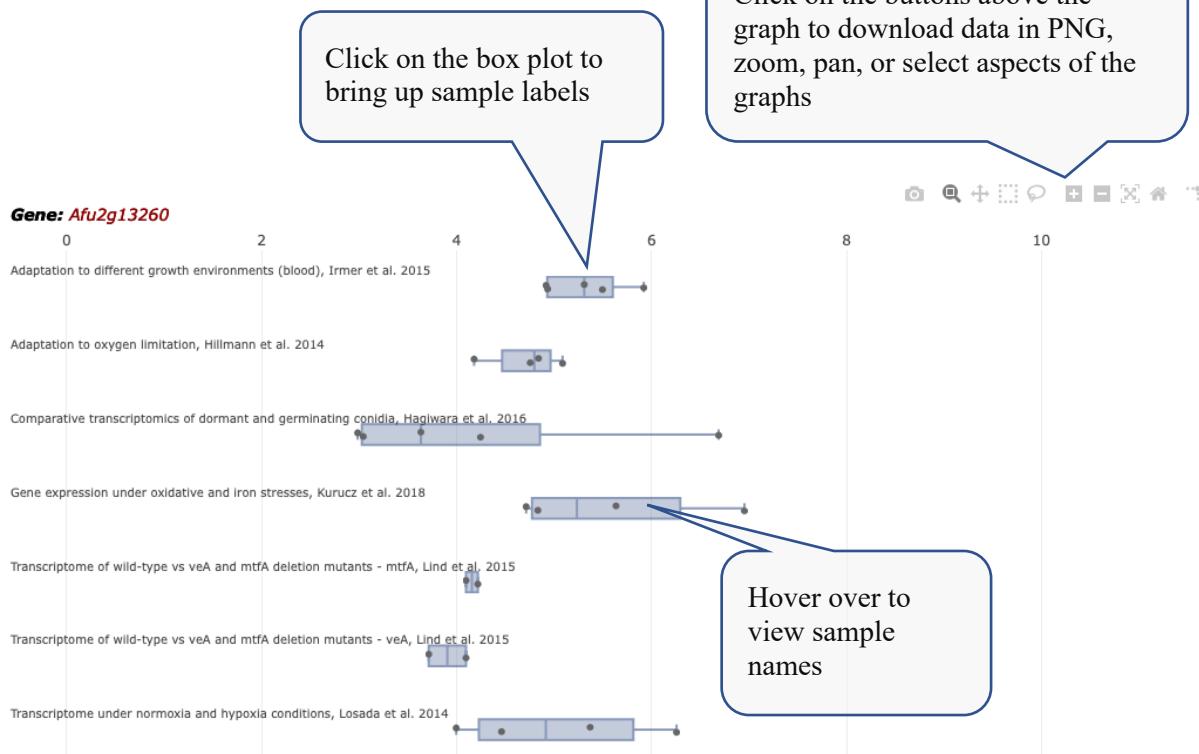
2.1 DNA polymorphism							
Allele Summary							
Download Data sets							
Search this table...	Allele	Allele Frequency	Allele Count	Average Coverage	Average Read Percent		
	G	0.98	47	77.8	100		
	A	0.02	1	90	98.8		
Country Summary							
Download Data sets							
Search this table...	Geographic Location	Allele	Major Allele	Minor Allele	Other Allele		
	unknown	G	G (0.98)	A (0.02)			
	United Kingdom	G	G (0.98)	A (0.02)			
	Kingdom of the Netherlands	G	G (0.98)				
	India	G	G (0.98)				
	United States of America	G	G (0.98)				
Strain / Samples							
Download Data sets							
Search this table...	Geographic Location	Strain	Sample	Allele	Allele (gene strand)	Product	Coverage
	AF293 (reference)			G	C	S	100
	India	Af_1542-09	EUSMPL0007-1-18	G	C	S	108
	India	Af_1542-111	EUSMPL0007-1-18	G	C	S	113
	India	Af_1546-111	EUSMPL0007-1-20	G	C	S	96
	India	Af_1548-111	EUSMPL0007-1-22	G	C	S	107
	India	Af_1549-111	EUSMPL0007-1-21	G	C	S	102
	India	Af_1549-P-11	EUSMPL0007-1-17	G	C	S	78
	India	Af_1591-12	EUSMPL0007-1-18	G	C	S	84
	India	Af_1591-12	EUSMPL0007-1-18	G	C	S	128
	Kingdom of the Netherlands	08-19-02-13	EUSMPL0007-1-18	G	C	S	94
	Kingdom of the Netherlands	08-19-02-10	EUSMPL0007-1-18	G	C	S	118
	Kingdom of the Netherlands	08-19-02-09	EUSMPL0007-1-11	G	C	S	123
	Kingdom of the Netherlands	08-19-02-46	EUSMPL0007-1-13	G	C	S	126
	Kingdom of the Netherlands	08-19-02-41	EUSMPL0007-1-10	G	C	S	130
	Kingdom of the Netherlands	08-31-09-91	EUSMPL0007-1-9	G	C	S	94
	Kingdom of the Netherlands	08-30-03-25	EUSMPL0007-1-8	G	C	S	138
	Kingdom of the Netherlands	10-01-02-27	EUSMPL0007-1-12	G	C	S	117
	United Kingdom	09-7500006	EUSMPL0007-1-6	A	T	F	90
	United Kingdom	12-7504462	EUSMPL0007-1-6	G	C	S	111

The **Transcriptomics** section (RNA-Seq and microarray data) provides the Transcript Expression Summary section that helps identify experiments in which the current gene is highly regulated.

▼ RNA-Seq Transcription Summary **NEW** 

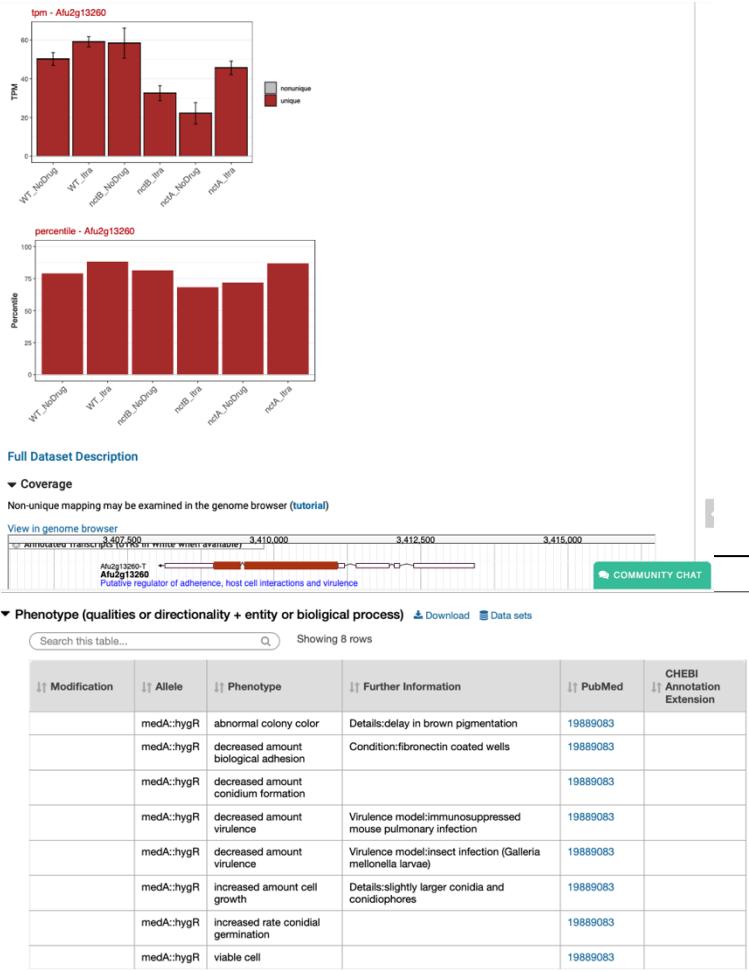
▼ *Summary of expression values. Each row represents a distinct RNA-Seq experiment. [Click to read more...](#)*

- Each black dot represents expression in a sample. A boxplot is shown, with the box representing the median and upper/lower quartiles, and the whiskers representing the max/min values (or 1.5 times the interquartile range, in which case values beyond the whiskers are considered outliers).
- Use the toggle button to switch from Log Scale to Linear Scale.
- Log Scale values are $\log_2(\text{TPM}+1)$ for these reasons:
 1. TPM+1: to de-emphasize low noisy TPM values (i.e., <1).
 2. log2: so that each unit on the x-axis represents a 2-fold difference.
- Navigation buttons are located at the top right: zoom in to see adjacent samples or smaller fold-changes; zoom out by double-clicking within the graph.
- This graph was created with Plotly. [Get more help at their website.](#)



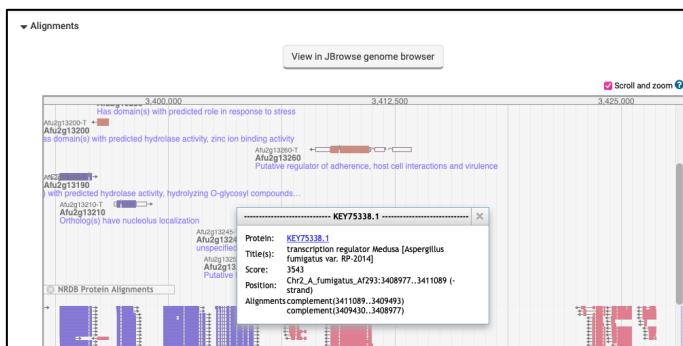
- Which dataset/sample corresponds to the lowest gene expression?

The Transcript Expression section, which is located under the RNA-Seq summary section, can be expanded to view the expression graph (TPM), full dataset description and a link out to view unique and non-unique coverage plots in JBrowse.



Phenotypes section includes manually curated, community submitted, and other datasets (e.g. integrated from other resources).

The Sequences, Sequence analysis, Structure analysis.



These sections offer sequence information (DNA, RNA, and protein), an interactive summary of EST alignments and BLAT hits against the nonredundant protein sequence database (NRDB), 3D structure predictions and similar Protein Data Bank (PDB) chains, when available, etc.

Protein features and properties offer protein domains identifications (InterPro), signal and transmembrane predictions graphics, BLASTP hits, and also a selection of tools that can be deployed directly from the gene record page using the amino acid sequence of interest:

- BLASTP (protein-protein BLAST) against 8 databases,
- GPI anchor prediction: big-PI Predictor
- MitoProt (prediction of mitochondrial proteins)
- WoLF PSORT (prediction of subcellular localization sites)
- STRING
- InterPro
- Use the site search to navigate to the B9J08_000928 gene record page.

- Examine the evidence within the InterPro domains, which is located in the Protein Feature and Properties section.
- Determine the possible function of this unannotated gene in *Candida auris*.

▼ InterPro Domains [Download](#) [Data sets](#)

↓ Name	↓ Interpro ID	↓ Primary ID	↓ Secondary ID	↓ Description	↓ Start Min	↓ End Min	↓ E-value	↓ Transci
InterProScan	N/A	IPR034294	Aquaporin_transprt	Aquaporin transporter	43	285	N/A	B9J08_000
InterProScan	N/A	IPR023271	Aquaporin-like	Aquaporin-like	48	283	N/A	B9J08_000
InterProScan	N/A	IPR000425	MIP	Major intrinsic protein	51	70	N/A	B9J08_000
InterProScan	N/A	IPR000425	MIP	Major intrinsic protein	52	263	N/A	B9J08_000
InterProScan	N/A	IPR000425	MIP	Major intrinsic protein	55	266	N/A	B9J08_000
InterProScan	N/A	IPR022357	MIP_CS	Major intrinsic protein, conserved site	117	125	N/A	B9J08_000
PANTHER	IPR034294	PTHR19139	AQUAPORIN TRANSPORTER	Aquaporin transporter	43	285	3.9E-84	B9J08_000
PANTHER	N/A	PTHR19139:SF199	AQUAPORIN-LIKE PROTEIN 2	N/A	43	285	3.9E-84	B9J08_000
PFAM	IPR000425	PF00230	MIP	Major intrinsic protein	52	263	7.1E-42	B9J08_000

The **Function Prediction** section features Gene Ontology (GO) assignments that have been either downloaded from Gene Ontology databases and manually curated by FungiDB. GO Slim terms, Enzyme Commission (EC) numbers with links to EC number and GO terms description and relevant publications are available as well.

Gene ontology provides statements for describing the functions of genes along with three aspects: Molecular function, Biological process, and Cellular component, and it is organized in hierarchies. The GO terms table above provides GO IDs and terms associated with a particular gene and additional metadata that are available for these associations such as source, evidence code (e.g. IDA, IMP, etc.) and reference (PubMed ID).

There are three classes of GO terms in FungiDB:

1. Automatically assigned by InterPro2GO
2. Assigned by FungiDB curators
3. Obtained from external resources such as AspGD, MIPS, and others

- Continue on the gene record page for B9J08_000928.
 - Examine the GO terms (Inferred from Electronic annotation (IEA)) listed in the **Function prediction** section.
 - Determine if this data is consistent with the protein domain annotations of this protein possibly being a pore-forming membrane protein.
- Cross-reference your observations for B9J08_000928 with what is known in other model organisms.
 - Navigate to the **Orthology and Synteny** section

- Click on the **syntenic ortholog** in *C. albicans* SC5314 to be redirected to an ortholog gene record page.
- Navigate to the **Link outs** section and navigate to the CGD gene page

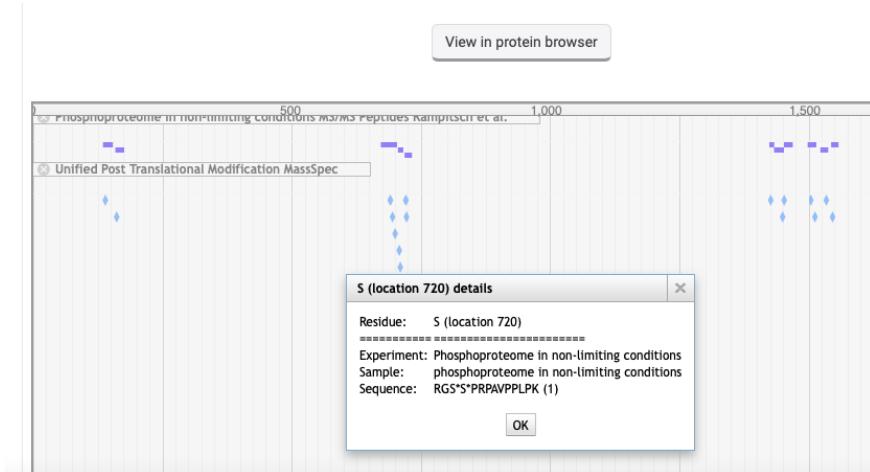
3 Link outs	
▼ External Links Download Data sets	
<input type="button"/> Database	<input type="button"/> External ID
CGD	CR_02920C_A
Entrez Gene	3642587
The Universal Protein Resource (UniProt)	Q5A1Z4

- Navigate to the **Phenotype** tab on the CGD record page for CR_02920C_A.
- What can you say about biofilm formation in the null mutants when cells are grown on RPMI medium?
 - Normal
 - Abnormal
 - Not determined

Pathways and interactions provide descriptions of metabolic pathways loaded from the KEGG and MetaCyc repositories. Genes are linked to individual pathways by EC numbers when this data is available and clicking on any of the links redirects to an interactive metabolic pathway viewer where the user can explore individual reactions or export all known data for a given pathway. EC numbers are inferred by the OrthoMCL pipeline automatically. As with any automated analysis, use caution when interpreting data.

The Proteomics section is populated when Mass Spec evidence data and phosphoproteomics datasets become available in FungiDB. You can view peptide alignments against the reference genome in JBrowse, which provides a graphic summary of proteomics evidence.

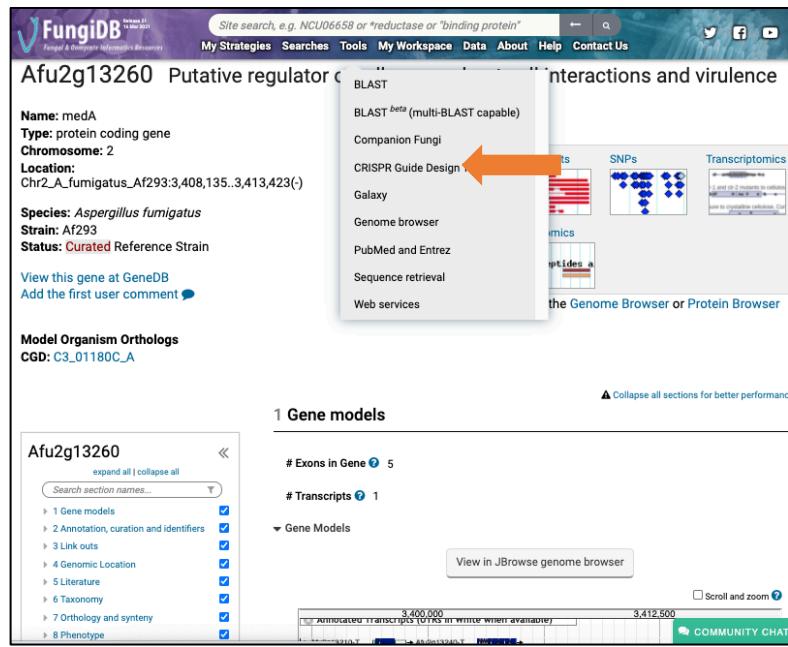
Here is an example of the proteomics section for FGRAMPH1_01G11133:



▼ Post Translational Modifications					
	Transcript ID(s)	Experiment	Sample	Modification Type	Modification Site
FGRAMPH1_01T11133	Phosphoproteome in non-limiting conditions	phosphoproteome in non-limiting conditions	phosphorylation site	139	S
FGRAMPH1_01T11133	Phosphoproteome in non-limiting conditions	phosphoproteome in non-limiting conditions	phosphorylation site	161	S
FGRAMPH1_01T11133	Phosphoproteome in non-limiting conditions	phosphoproteome in non-limiting conditions	phosphorylation site	691	S
FGRAMPH1_01T11133	Phosphoproteome in non-limiting conditions	phosphoproteome in non-limiting conditions	phosphorylation site	695	S
FGRAMPH1_01T11133	Phosphoproteome in non-limiting conditions	phosphoproteome in non-limiting conditions	phosphorylation site	708	S
FGRAMPH1_01T11133	Phosphoproteome in non-limiting conditions	phosphoproteome in non-limiting conditions	phosphorylation site	721	S

Accessing JBrowse

JBrowse can be accessed from the main menu and gene record pages



The screenshot shows the FungiDB gene record page for *Afu2g13260*. The page includes details about the gene, such as its name, type (protein coding gene), chromosome (2), location (Chr2_A_fumigatus_Af293:3,408,135..3,413,423(-)), species (*Aspergillus fumigatus*), strain (Af293), and status (Curated Reference Strain). It also links to GeneDB and allows users to add comments. A sidebar on the right provides links to various tools and databases, including BLAST, Companion Fungi, CRISPR Guide Design, Galaxy, Genome browser, PubMed and Entrez, Sequence retrieval, and Web services. An orange arrow points to the 'Genome browser' link in this sidebar.

Accessing JBrowse from gene record pages will pre-select the genome automatically. If navigating directly from the main page, the genome of choice can be chosen under the Genome tab.

- Navigate to JBrowse from the gene record page of [FGRAMPH1_01T12283](#) to learn the JBrowse environment.

Menu bar includes the Genome menu, Track menu, View menu, Help menu and the Sharing link.

Current genome is indicated above the tracks

Customised JBrowse views can be shared via a URL generated by clicking on the Share button

Select tracks

Annotated Transcripts (UTRs in White when available)

FGRAMPH1_01G12273 hypothetical protein

FGRAMPH1_01G12269 unnamed protein product

FGRAMPH1_01G12267

FGRAMPH1_01G12271 demethylmenaquinone methyltransferase

FGRAMPH1_01G12277

FGRAMPH1_01G12279 integral membrane

FGRAMPH1_01G12275 Isochoridomeric C-15 hydroxylase (cytochrome P-450 monooxygenase CYP65A1)

FGRAMPH1_01G12281 hypothetical protein

FGRAMPH1_01G12283 polygalacturonase 1 precursor

FGRAMPH1_01G12285 FGRAMPH1_01G12285 hypothetical protein

FGRAMPH1_01G12287

FGRAMPH1_01G12289 hypothetical protein

FGRAMPH1_01G12291

FGRAMPH1_01G12293 hypothetical protein FAVG1_04193

FGRAMPH1_01G12295 unnamed protein product

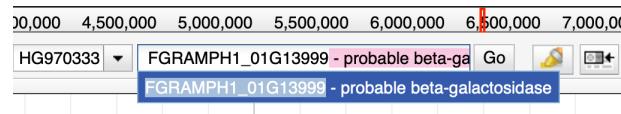
FGRAMPH1_01G12297 phenol hydroxylase

RNA-Seq Evidence for introns

Navigation bar contains zooming (magnifying glass icons), panning (left/right arrows) and highlighting (yellow highlighter) buttons, reference sequence selector (drop down with sequences from the selected genome sorted by length), a text box to search for features such as gene IDs and overview bar which shows the location of the region in view.

Genome view area

*Note: If you navigated away from the gene, you can type **FGRAMPH1_01T12283** directly in the location search box and select the highlighted match to return to your original position. You can also double click on the gene to re-centre your view.*



- Display more information about this gene and the coordinates for CDS.

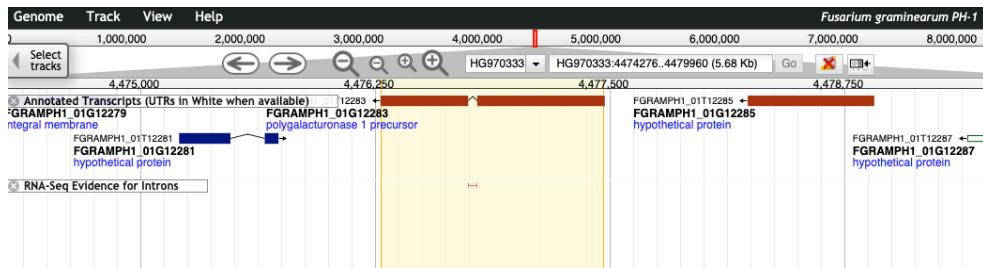
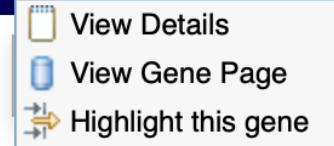
Gene Details	
Gene	FGRAMPH1_01G12283
Taxon	Fusarium graminearum PH-1
Type	protein_coding_gene
Description	polygalacturonase 1 precursor
Position	HG970333:4476280..4477469 (- strand)
OrthoMCL	OG6_102442
Links	JBrowse Gene Page

Transcript Details	
FGRAMPH1_01T12283	
Type	mRNA
Download	CDS protein
CDS	complement(4477469..4476795) complement(4476744..4476280)

Left-click on the gene and a pop-up window will display the coordinates of CDS, 3' and 5' UTRs (when available), etc. You can also export CDS and protein sequences or navigate to the gene record page.

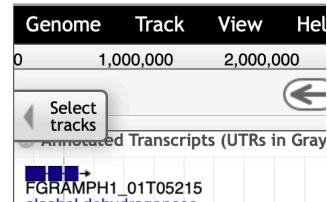
- Highlight this gene for easy tracking.

Right-click (or control click) on the gene feature to display the context menu which provides quick links to highlighting, navigation to the gene record page). You can also get the more details by selecting the View Details option, which will bring up the pop-up box shown above.



- Activate the following tracks to learn more about this gene (*hint: click on the Select tracks tab on the left*):
 - Intron Evidence (if not selected by default already)
 - RNA-Seq (mycelium and 6days post-infection of wheat with Fusarium (6dpi))
 - Chip-Seq tracks of chromatin marks in WT and kmt6 mutant (KMT6 is Histone H3 K27 Methyltransferase)
 - Syntenic Sequences and Genes (Shaded by Orthology)

To activate tracks, click on the **Select tracks** tab on the left of the screen.



- Next, select the Transcriptomics category and click on the “Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1” dataset and search for two tracks - **infected 6dpi** and **mycelia**, and then select **unique coverage** tracks only for both conditions/samples.

<input checked="" type="checkbox"/> Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1 - infected 6dpi (unique) Coverage	Transcriptomics	RNA-Seq	Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1	Coverage	unique	not strand specific
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<input checked="" type="checkbox"/> Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1 - mycelia (unique) Coverage	Transcriptomics	RNA-Seq	Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1	Coverage	unique	not strand specific
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- Clear your search by clicking on the “Clear All Filters” button and activate ChIP-Seq tracks to select H3K27me3 and H3K4me3 methylation marks in WT and kmt6 deletion mutant in low nitrogen growth conditions (low). Search for the following text in the “Contains text” filter to select the “unique coverage” tracks.

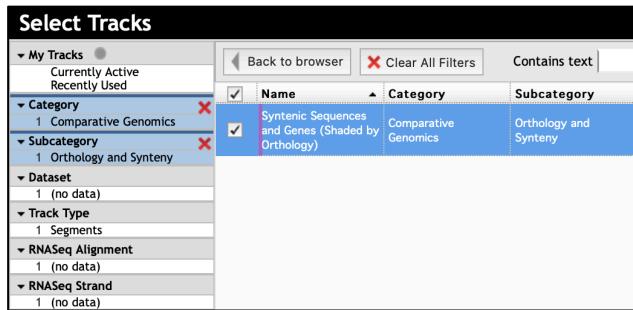
kmt6 mutant:

- H3K27me3_DELkmt6_neoR_low-R2
- H3K4me2_DELkmt6_neoR_low-R2

WT:

- H3K27me3_WT_low
- H3K4me2_WT_low

- Next, activate **the Syntenic Sequences and Genes (Shaded by Orthology)** track, which is located under the **Comparative Genomics** category, **Orthology and Synteny** subcategory but can be also searched for in the **Contains** text search window at the top (*hint: you can also use the filter*).



- Click on the **Back to browser** button
- Customise JBrowse view and organise tracks
- Customize the JBrowse syntenic view to display *Fusarium* species only.

*Hint: Click on the drop-down menu in the **Syntenic Sequences and Genes (Shaded by Orthology)** track, choose **Select Subtracks**, unselect current tracks, use the filter to identify “*Fusarium*” and then click on the “Save” button at the bottom.*

Label	Species	Kingdom	Genus	Phylum	Class	syntype	Taxon
fgrPH1-1 gene	<i>Fusarium</i> graminearum	Fungi	<i>Fusarium</i>	Ascomycota	Sordariomycetes	gene	<i>Fusarium</i> graminearum PH-1
fgrPH1-1 span	<i>Fusarium</i> graminearum	Fungi	<i>Fusarium</i>	Ascomycota	Sordariomycetes	span	<i>Fusarium</i> graminearum PH-1
fjuM58289 gene	<i>Fusarium</i> fujikuroi	Fungi	<i>Fusarium</i>	Ascomycota	Sordariomycetes	gene	<i>Fusarium</i> fujikuroi 58289
fjuM58289 span	<i>Fusarium</i> fujikuroi	Fungi	<i>Fusarium</i>	Ascomycota	Sordariomycetes	span	<i>Fusarium</i> fujikuroi 58289
fxyFo47 gene	<i>Fusarium</i> graminearum	Fungi	<i>Fusarium</i>	Ascomycota	Sordariomycetes	gene	<i>Fusarium</i> graminearum Fo47
fxyFo47 span	<i>Fusarium</i> graminearum	Fungi	<i>Fusarium</i>	Ascomycota	Sordariomycetes	span	<i>Fusarium</i> graminearum Fo47

- Pin the highlighted gene and gene model track to the top.

- Now, you can re-organise your tracks by drag and drop. Here is the order in which the tracks are shown below:
 - Gene model (pinned to top)

- RNA-Seq evidence: mycelia
- RNA-Seq evidence: 6dpi
- Intron Evidence 1
- Intron evidence 2
- ChiP-Seq H3K27 WT
- ChiP-Seq H3K4me2 WT H3K27
- ChiP-Seq H3K27 kmt6
- ChiP-Seq H3K4me2 kmt6

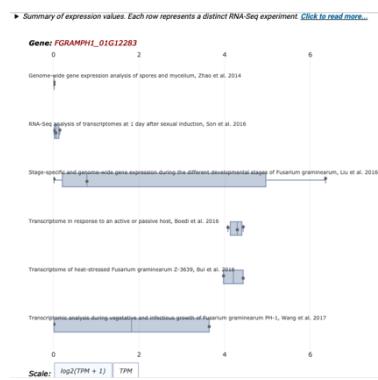
In *Fusarium* and other fungi, H3K4me2 and H3K27me3 are found in large, mutually exclusive, gene-rich blocks of the genome. About one-third of the *F. graminearum* genome is associated with H3K27me3 when the fungus is grown in a minimal medium with low nitrogen.

Kmt6 encodes a DNA methylase that deposits repressive chromatin mark H3K27me3. kmt6 mutants in *Fusarium* and other species demonstrate reorganization of chromatic and upregulation of genes that are normally suppressed.

Having this information in hand and using JBrowse track view, answer the following questions:

- Do you observe *FGRAMPH1_01T12283* expression in both samples (mycelia and 6 days post-infection)?
- Does this gene show de-regulation of repressive chromatin marks (H3K27me3) in the kmt6 mutant? Would you expect the expression of this gene to be up-regulated or down-regulated in the kmt6 mutant?
- Is this gene expressed in mycelia? How would you go about testing if it is not expressed in this stage of development or is an artefact?

Hint: take a look at the transcriptomics summary graph on the gene record page or other transcriptomic tracks



- Is there evidence of alternative splicing?
- Is this gene conserved in *Fusarium* species?
- Let's say you would like to share your JBrowse view with a colleague. How would you go about getting the link?

