

Exploring transcriptomics & proteomics datasets in FungiDB

Transcriptomics

Learning objectives:

- Query host-pathogen RNA-Seq data in HostDB and FungiDB, respectively.
- Create a proteomics query and save this strategy to your account.

Transcriptomics datasets can be analyzed using Fold Change (FC), Differential Expression (DE), Percentile (P), and Sense/Antisense searches (SA).

Percentile (P). For each Experiment and Sample, genes are ranked by expression level (e.g., search for low/high levels of gene expression).

Fold change (FC). Find genes with changes in gene expression when statistical analysis is not available (e.g. no replicates). After selecting samples, you have the option to take the average, minimum, or maximum expression value within each group. If choosing only one sample from a group, the selected 'operation' will not affect your results. Time-series experiments will offer an extra parameter called "Global min/max" which allows you to filter your results further. Finally, you can choose the directionality and the magnitude of the difference (e.g., up/down regulates, fold difference of 2, etc.)

Differential Expression (DE). This search uses DESeq2 analysis results. You can choose the directionality and the magnitude of the difference by setting both fold change and adjusted p values. For example, selecting up-regulated genes with a fold difference of 2 and an adjusted p-value cut off 0.1 will only show results where the comparator is twice that of the reference with an adjusted p-value of 0.1 or less.

Sense/antisense (SA). This search is applied to stranded datasets. You can find genes that exhibit simultaneous changes in sense and antisense transcripts in the Comparison sample relative to the Reference Sample. For example, you could look for genes showing increasing antisense transcripts and decreasing sense transcripts, as might occur when antisense transcription suppresses sense transcription. The search will perform all pairwise comparisons between the chosen Comparison samples and the chosen Reference samples.

MetaCycle. This search is applied to circadian datasets. For each study/experiment, you can choose either ARSER or JTK_Cycle method for detecting rhythmic signals. The search will return the corresponding period, amplitude and p-value.

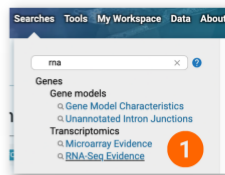
In this exercise we will query host (mouse) and pathogen (*Candida albicans*) RNA-Seq data generated by Kirchner et al. 2019. The authors used the experimental model of oropharyngeal candidiasis in mice to understand the interaction of *C. albicans* with the host at mucosal surfaces *in vivo*. Two *C. albicans* strains were used in this study – SC5314 (virulent lab strain) and the persistent strain 101.

Objectives:

1. Identify differentially expressed genes in the virulent SC5314 strain compared to strain 101 using FungiDB.
2. Identify genes upregulated in mouse in response to the infection with SC5314 but not strain 101.

1. The next block of exercises will be carried out in [FungiDB.org](https://fungi.db.org)

- **Identify genes that are up-regulated in SC5314 at 1d of infection.**
 1. Navigate to the RNA-Seq Evidence search and filter RNA-Seq datasets for “Kirch”.
 2. Click on the “DE” button.
 3. Choose to examine the sense strand.
 4. Select reference sample: SC5314_in vitro.
 5. Select comparator sample: SC5314_infected_1d.
 6. Look for up-regulated genes.
 7. Select magnitude of upregulation: 4 fold.



Identify Genes based on RNA-Seq Evidence

Legend: ☒ Coexpression ☒ Similarity ☒ Differential Expression ☒ Fold Change ☒ MetaCycle ☒ Percentile ☒ SenseAntisense

Filter Data Sets: kirch X 1 result (filtered from a total of 159)

Organism: Candida albicans SC5314

Data Set: Candida transcriptomes during oropharyngeal candidiasis infection in mouse (Kirchner, et al. 2019)

Choose a Search: ☒ DE ☐ FC ☐ P ☐ SA

3 ☒ Mouse transcriptomes during oropharyngeal candidiasis infection in mouse - Sense
☐ Mouse transcriptomes during oropharyngeal candidiasis infection in mouse - Antisense

Reference Sample

4 ☐ 101_in vitro
☐ 101_in vitro_hyphae
☐ 101_infected_1d
☐ 101_infected_3d
☐ 101_infected_7d
☒ SC5314_in vitro
☐ SC5314_in vitro_hyphae
☐ SC5314_infected_1d

Comparator Sample

5 ☐ 101_in vitro
☐ 101_in vitro_hyphae
☐ 101_infected_1d
☐ 101_infected_3d
☐ 101_infected_7d
☐ SC5314_in vitro
☒ SC5314_in vitro_hyphae
☐ SC5314_infected_1d

Direction

6 up-regulated

fold difference >=

7 4

adjusted P value less than or equal to

0.1

Get Answer

Calb_Kirchner_mouse (de)
589 Genes

+ Add a step

Step 1

- **Identify genes that are up-regulated in SC5314 but not 101 persistent strain at 1d of infection.**

1. Click on the “Add Step” button
2. Navigate to the RNA-Seq Evidence search, filter for “Kirch” to quickly identify the dataset and click on the “DE” button.
3. Choose to examine the sense strand.
4. Select reference sample: 101_in vitro.
5. Select comparator sample: 101_infected_1d.
6. Look for up-regulated genes.
7. Select magnitude of upregulation: 4 fold.

The screenshot displays the Gene Set Analysis tool interface, showing the workflow for identifying up-regulated genes in SC5314 compared to 101 persistent strain at 1d of infection. The workflow is divided into two main steps: Step 1 (Data Selection) and Step 2 (Analysis Parameters).

Step 1: Data Selection

- Combine with other Genes:** A box labeled "Calb_Kirchner_mouse (de)" is shown, with an "Add a step" button next to it.
- Transform into related records:** A box labeled "Calb_Kirchner_mouse (de)" is shown, with an "Add a step" button next to it.
- Use Genomic Colocation to:** A box labeled "Calb_Kirchner_mouse (de)" is shown, with an "Add a step" button next to it.
- Identify Genes based on RNA-Seq Evidence:** A search bar is shown with the text "Kirch" entered. The search results show "Calb_Kirchner_mouse (de)" as the top result.

Step 2: Analysis Parameters

- 3. Mouse transcriptomes during oropharyngeal candidiasis infection in mouse - Sense** (selected)
- Reference Sample:**
 - 4. 101_in vitro (selected)
 - 101_in vitro_hyphae
 - 101_infected_1d
 - 101_infected_3d
 - 101_infected_7d
 - SC5314_in vitro
 - SC5314_in vitro_hyphae
 - SC5314_infected_1d
- Comparator Sample:**
 - 5. 101_infected_1d (selected)
 - 101_in vitro
 - 101_in vitro_hyphae
 - 101_infected_3d
 - 101_infected_7d
 - SC5314_in vitro
 - SC5314_in vitro_hyphae
 - SC5314_infected_1d
- Direction:** 6. up-regulated (selected)
- fold difference >=** 7. 4 (selected)
- adjusted P value less than or equal to** 0.1 (selected)

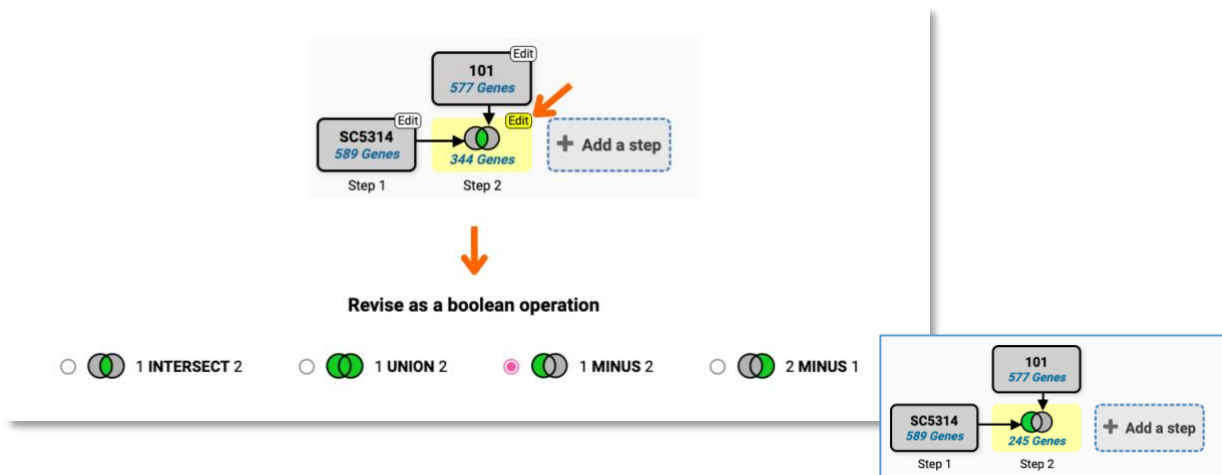
Run Step button is visible at the bottom right.

Summary of Results:

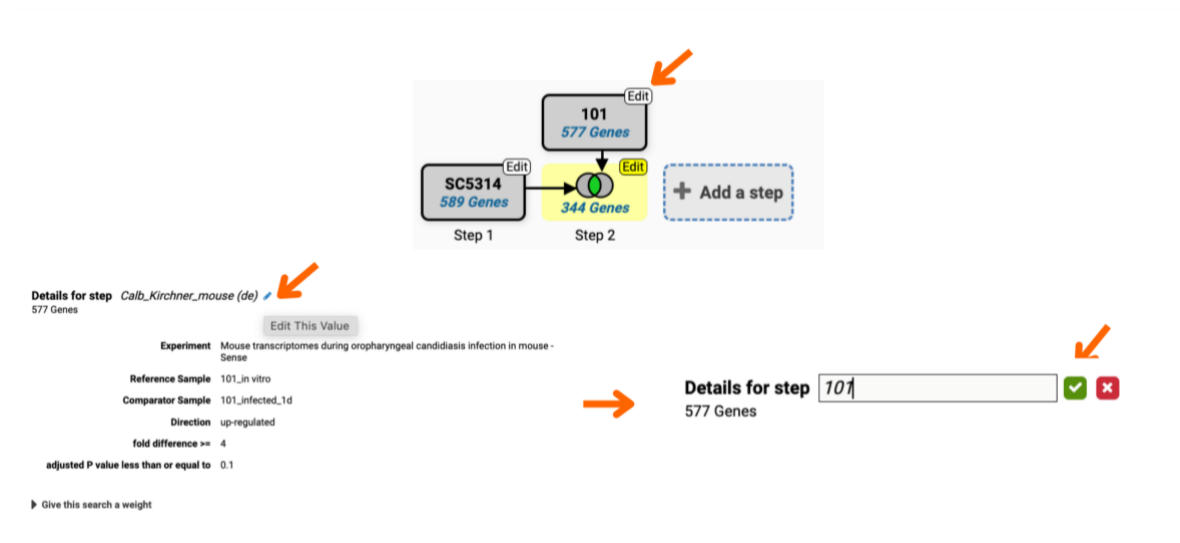
- Calb_Kirchner_mouse (de) 577 Genes
- Calb_Kirchner_mouse (de) 589 Genes
- 344 Genes (Intersection)

The default setting of the Boolean operators was set to the “intersect” option, which returns genes that are up-regulated by 4 fold in both strains.

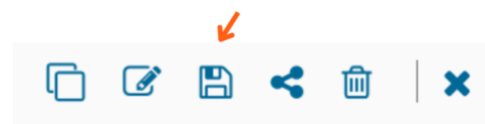
- **Change the search criteria to display genes upregulated in SC5314 only.**



Note: you can rename steps to keep track of the datasets/search results:



Save the strategy by clicking on the floppy disk icon on the right.

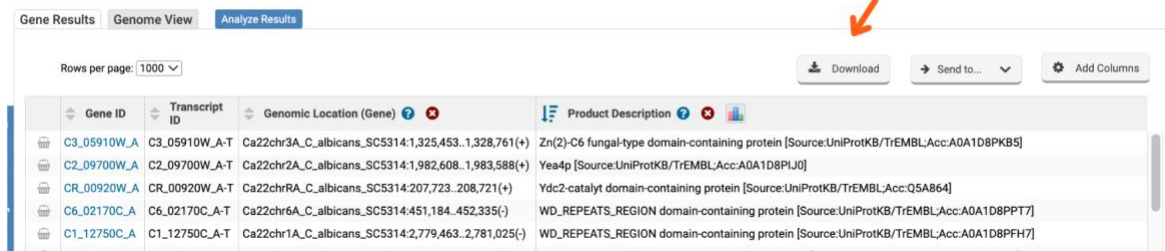


In summary, this strategy identified genes up-regulated in SC5314 when infecting mice at 1d while subtracting any genes that are also up-regulated in strain 101.

Strategy URL:

<https://fungidb.org/fungidb/app/workspace/strategies/import/802d9f2b606fc1fa>

Note: this data can be exported and FungiDB offers several download options that can be accessed by clicking on the Download button located above the results table.



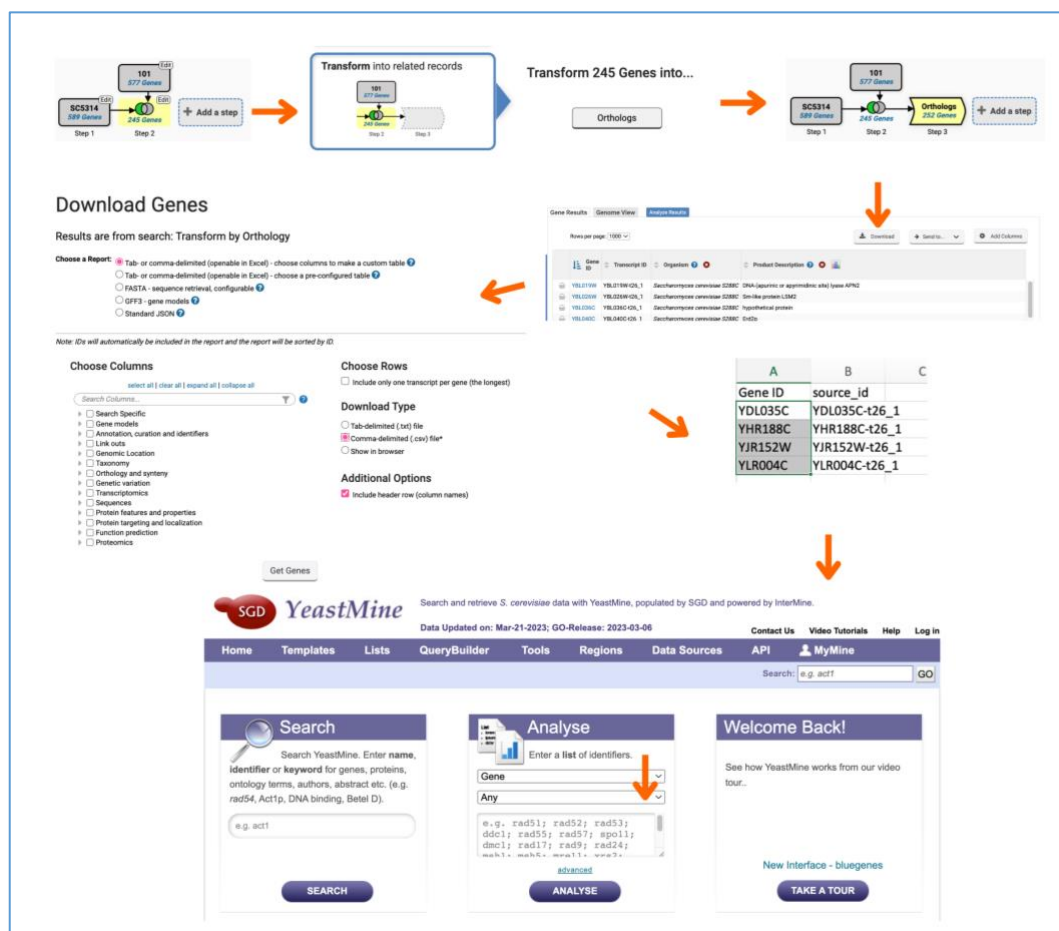
Gene ID	Transcript ID	Genomic Location (Gene)	Product Description
C3_05910W_A	C3_05910W-A-T	Ca22chr3A_C.albicans_SC5314:1,325,453..1,328,761(+)	Zn(2)-C6 fungal-type domain-containing protein [Source:UniProtKB/TrEMBL;Acc:A0A1D8PKB5]
C2_09700W_A	C2_09700W-A-T	Ca22chr2A_C.albicans_SC5314:1,982,608..1,983,588(+)	Yea4p [Source:UniProtKB/TrEMBL;Acc:A0A1D8PIJ0]
CR_00920W_A	CR_00920W-A-T	Ca22chrRA_C.albicans_SC5314:207,723..208,721(+)	Ydc2-catalyt domain-containing protein [Source:UniProtKB/TrEMBL;Acc:Q5A864]
C6_02170C_A	C6_02170C-A-T	Ca22chr6A_C.albicans_SC5314:451,184..452,335(-)	WD_REPEATS_REGION domain-containing protein [Source:UniProtKB/TrEMBL;Acc:A0A1D8PPT7]
C1_12750C_A	C1_12750C-A-T	Ca22chr1A_C.albicans_SC5314:2,779,463..2,781,025(-)	WD_REPEATS_REGION domain-containing protein [Source:UniProtKB/TrEMBL;Acc:A0A1D8PFH7]

Download Genes

Results are from search: Combine Gene results

Choose a Report: ☒ Tab- or comma-delimited (openable in Excel) - choose columns to make a custom table [?](#)
☐ Tab- or comma-delimited (openable in Excel) - choose a pre-configured table [?](#)
☐ FASTA - sequence retrieval, configurable [?](#)
☐ GFF3 - gene models [?](#)
☐ Standard JSON [?](#)

You can also export yeast orthologs of *C. albicans* genes into Yeast mine. YeastMine enables rapid retrieval and manipulation of curated biological data on yeast, which you can use to make predictions about orthologs in fungal pathogens. Here is an outline of the workflow extracting Gene IDs compatible with SGD searches:



Download Genes
Results are from search: Transform by Orthology

Choose a Report: ☒ Tab- or comma-delimited (openable in Excel) - choose columns to make a custom table [?](#)
☐ Tab- or comma-delimited (openable in Excel) - choose a pre-configured table [?](#)
☐ FASTA - sequence retrieval, configurable [?](#)
☐ GFF3 - gene models [?](#)
☐ Standard JSON [?](#)

Note: IDs will automatically be included in the report and the report will be sorted by ID

Choose Columns
select all | clear all | expand all | collapse all

Search Columns:

☐ Search Specific
☐ Gene models
☐ Annotation, curation and identifiers
☐ Link sets
☐ Genomic Location
☐ Taxonomy
☐ Orthology and synteny
☐ Genetic variation
☐ Transcriptionomics
☐ Sequences
☐ Protein features and properties
☐ Protein targeting and localization
☐ Function prediction
☐ Proteomics

Choose Rows
☐ Include only one transcript per gene (the longest)

Download Type
☐ Tab-delimited (.txt) file
☒ Comma-delimited (.csv) file*
☐ Show in browser

Additional Options
☒ Include header row (column names)

Get Genes

Gene ID	source_id
YDL035C	YDL035C-t26_1
YHR188C	YHR188C-t26_1
YJR152W	YJR152W-t26_1
YLR004C	YLR004C-t26_1

SGD **YeastMine** Search and retrieve S. cerevisiae data with YeastMine, populated by SGD and powered by InterMine.
Data Updated on: Mar-21-2023; GO-Release: 2023-03-06

Home Templates Lists QueryBuilder Tools Regions Data Sources Contact Us Video Tutorials Help Log In
API MyMine

Search: GO

Search
Search YeastMine. Enter name, identifier or keyword for genes, proteins, ontology terms, authors, abstract etc. (e.g. rad54, Act1p, DNA binding, Betel D).
 e.g. act1
SEARCH

Analyse
Enter a list of identifiers.
Gene
Any
 e.g. rad51; rad52; rad53;
ddcl; rad55; rad57; spo11;
dml1; rad17; rad9; rad24;
mch1; mch5; mch11; mch7;
advanced
ANALYSE

Welcome Back!
See how YeastMine works from our video tour...
New Interface - bluegenes
TAKE A TOUR

Next, we will identify gene up-regulated in mice when infected with SC5314 and 101 and select for SC5314-specific responses.

2. The next block of exercises will be carried out in [HostDB.org](https://hostdb.org)

- **Identify genes that are up-regulated in mice infected with SC5314 at 1d.**
 1. Navigate to the RNA-Seq Evidence search and filter RNA-Seq datasets for “Kirch”.
 2. Click on the “DE” button.
 3. Choose to examine the sense strand.
 4. Select reference sample: naïve.
 5. Select comparator sample: SC5314_infected_1d.
 6. Look for up-regulated genes.
 7. Select magnitude of upregulation: 4 fold.

The screenshot shows the HostDB.org RNA-Seq Evidence search interface. The top navigation bar includes 'Searches', 'Tools', 'My Workspace', 'Data', and 'About'. A search bar contains 'rna'. Below it, a sidebar lists 'Genes', 'Gene models', 'Transcriptomics', and 'RNA-Seq Evidence' (highlighted with a red circle 1). The main panel shows a legend with 'Similarity', 'Differential Expression', 'Fold Change', 'Percentile', and 'SenseAntisense'. The 'Filter Data Sets' section shows 'kirch' with 1 result. The 'Organism' is 'Mus musculus C57BL/6J' and the 'Data Set' is 'Mouse transcriptomes during oropharyngeal candidiasis infection (Kirchner, et al. 2019)'. The 'Choose a Search' section has buttons for 'DE', 'FC', 'P', and 'SA' (highlighted with a red circle 2). The 'Reference Sample' section has a red circle 3 next to the 'Mouse transcriptomes during oropharyngeal candidiasis infection - Sense' option. The 'Comparator Sample' section has a red circle 4 next to the 'naïve' option. The 'Direction' section has a red circle 5 next to the 'up-regulated' dropdown. The 'fold difference >=' section has a red circle 6 next to the '4' input field. The 'adjusted P value less than or equal to' section has a red circle 7 next to the '0.1' input field. At the bottom, there is a 'Revise' button and a summary box showing 'Calb_Galleria_mouse (de)' with '857 Genes' and 'Step 1'.

Searches Tools My Workspace Data About

rna

Genes

Gene models

Transcriptomics

RNA-Seq Evidence

Legend: Similarity Differential Expression Fold Change Percentile SenseAntisense

Filter Data Sets: kirch 1 result (filtered from a total of 44)

Organism: Mus musculus C57BL/6J

Data Set: Mouse transcriptomes during oropharyngeal candidiasis infection (Kirchner, et al. 2019)

Choose a Search: DE FC P SA

3 Mouse transcriptomes during oropharyngeal candidiasis infection - Sense

4 naïve

5 up-regulated

6 4

7 0.1

Revise

Calb_Galleria_mouse (de) 857 Genes Step 1

+ Add a step

- **Identify genes that are up-regulated in SC5314 but not 101 persistent strain at 1d of infection.**
 1. Click on the “Add Step” button.
 2. Navigate to the RNA-Seq Evidence search, select “1 minus 2” Boolean operator, filter for “Kirch” to quickly identify the dataset and click on the “DE” button.
 3. Choose to examine the sense strand.
 4. Select reference sample: naïve.
 5. Select comparator sample: 101_infected_1d.
 6. Look for up-regulated genes.
 7. Select magnitude of upregulation: 4 fold.

The screenshot illustrates the workflow for identifying up-regulated genes in SC5314 compared to 101 persistent strain at 1d of infection. The interface is divided into several sections, each with a numbered step indicator (1-7) in an orange circle.

Step 1: The initial state shows a search for "Calb_Galleria_mouse (de)" with 857 genes. A red arrow points to the "Add a step" button.

Step 2: The "Combine with other Genes" section is active. The "Choose how to combine with other Genes" dropdown is set to "1 MINUS 2". The "Choose which Genes to combine. From..." dropdown is set to "A new search". The "Search" button is highlighted.

Step 3: The "Reference Sample" section is active. The "naïve" sample is selected.

Step 4: The "Comparator Sample" section is active. The "101_infected_1d" sample is selected.

Step 5: The "Direction" section is active. The "up-regulated" dropdown is selected.

Step 6: The "fold difference >=" section is active. The value "4" is entered.

Step 7: The "adjusted P value less than or equal to" section is active. The value "0.1" is entered.

The "Run Step" button is highlighted with a red arrow.

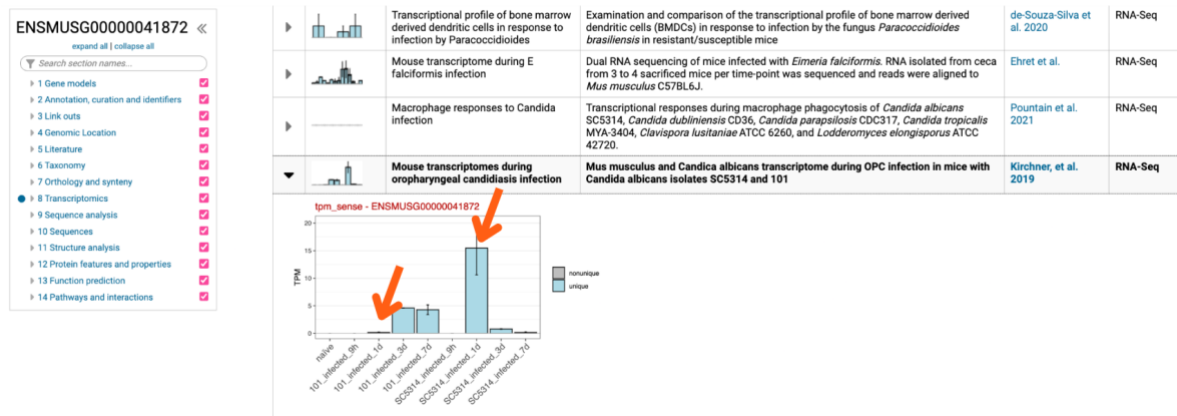
The final result shows a workflow diagram with two steps: Step 1 (Calb_Galleria_mouse (de) 857 Genes) and Step 2 (Calb_Galleria_mouse (de) 815 Genes). The "Add a step" button is also visible.

- **Examine the results in HostDB:**

1. Click on the [Gene ID](#) link for “interleukin 17F” and navigate to the transcriptomics expression section.

Gene ID	Transcript ID	Genomic Location (Gene)	Product Description	# Transcripts
ENSMUSG000000104379	ENSMUST000000194867	mmusCS7BL6J_chr1:15,853,331..15,856,499(+)	predicted gene, 37509 [Source:MGI Symbol;Acc:MGI:5610737]	1
ENSMUSG000000067780	ENSMUST000000088476	mmusCS7BL6J_chr1:17,601,901..17,630,939(+)	peptidase inhibitor 15 [Source:MGI Symbol;Acc:MGI:1934659]	1
ENSMUSG000000025929	ENSMUST000000027061	mmusCS7BL6J_chr1:20,730,905..20,734,494(+)	interleukin 17A [Source:MGI Symbol;Acc:MGI:107364]	1
ENSMUSG000000041872	ENSMUST000000039046	mmusCS7BL6J_chr1:20,777,146..20,790,617(-)	interleukin 17F [Source:MGI Symbol;Acc:MGI:2676631]	4
ENSMUSG000000041872	ENSMUST000000189301	mmusCS7BL6J_chr1:20,777,146..20,790,617(-)	interleukin 17F [Source:MGI Symbol;Acc:MGI:2676631]	4
ENSMUSG000000041872	ENSMUST000000190692	mmusCS7BL6J_chr1:20,777,146..20,790,617(-)	interleukin 17F [Source:MGI Symbol;Acc:MGI:2676631]	4
ENSMUSG000000041872	ENSMUST000000191111	mmusCS7BL6J_chr1:20,777,146..20,790,617(-)	interleukin 17F [Source:MGI Symbol;Acc:MGI:2676631]	4
ENSMUSG000000104358	ENSMUST000000192924	mmusCS7BL6J_chr1:34,823,525..34,826,560(+)	predicted gene, 37127 [Source:MGI Symbol;Acc:MGI:5610355]	1
ENSMUSG000000047180	ENSMUST000000056946	mmusCS7BL6J_chr1:36,264,597..36,274,679(+)	neutralized E3 ubiquitin protein ligase 3 [Source:MGI Symbol;Acc:MGI:2429944]	2
ENSMUSG000000047180	ENSMUST000000188666	mmusCS7BL6J_chr1:36,264,597..36,274,679(+)	neutralized E3 ubiquitin protein ligase 3 [Source:MGI Symbol;Acc:MGI:2429944]	2
ENSMUSG000000037447	ENSMUST000000097778	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115029	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115031	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115032	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000116629	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000124280	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000126413	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000137906	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000140218	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000141121	mmusCS7BL6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	15

In summary, we identified genes upregulated in response to SC5314 infection. Notice that the interleukin 17F response is much stronger at 1d in response SC5314 infection. This is consistent with mouse response to *C. albicans* strain 101 being delayed compared to strain SC5314. Now, you may want to go back and look at gene enrichment signatures in fungi to learn more about SC5314 and 101-driven responses.



Strategy URL: <https://hostdb.org/hostdb/app/workspace/strategies/import/de6763c0b7f9916c>

Dataset reference: Kirchner et al. 2019 DOI: 10.3389/fimmu.2019.00330

Proteomics

Learning objectives:

- Query proteomics data for *N. crassa* (e.g., genes upregulated between 40 and 46hr of incubation) and map results to *N. crassa* knockout phenotypes.

- **Identify proteins expressed in culture at 40 hr.**

1. Navigate to the “Quantitative Mass Spec. Evidence” search.
2. Click on the “DC” button for Hurley et al. 2019 dataset.
3. Select delta-csp1 mutant.
4. Choose to look for up-regulated genes.
5. Set Comparison to 40hr.
6. Leave the fold difference parameter at default.

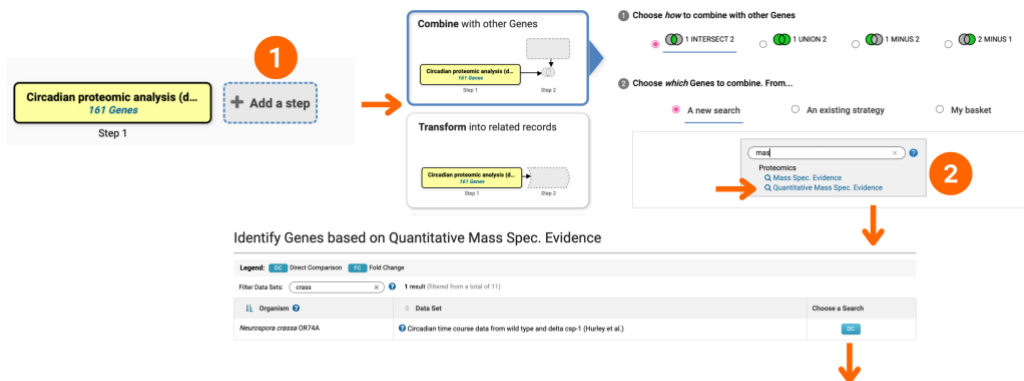
The screenshot shows the Proteomics search interface with the following steps highlighted:

- 1**: Click on the "proteo" search bar in the "Searches" tab.
- 2**: Click on the "DC" button for the Hurley et al. 2019 dataset.
- 3**: Select the "delta-csp1" mutant under the "Organism" filter.
- 4**: Select "up-regulated" under the "Direction" filter.
- 5**: Select "40 hr" under the "Comparison" filter.
- 6**: The "Fold difference >=" filter is set to 1.5.

The results show 198 genes identified at 40 hr. A button labeled "+ Add a step" is visible at the bottom right.

- Identify proteins expressed in culture at 46 hr.

1. Click on the “Add step”.
2. Select the “Combine with other Genes” search and navigate to the Quantitative Mass. Spec Evidence search.
3. Click on the “DC” button for Hurley et al. 2019 dataset.
4. Select WT sample.
5. Choose to look for up-regulated genes.
6. Set Comparison to 46hr.



3. ☒ Circadian proteomic analysis - delta csp-1
☐ Circadian proteomic analysis - Wild Type

Direction

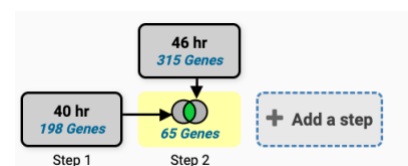
4.

Comparison

5. ☐ 2 hr
☐ 4 hr
☐ 6 hr
☐ 8 hr
☐ 10 hr
☐ 12 hr
☐ 14 hr
☐ 16 hr
☐ 18 hr
☐ 20 hr
☐ 22 hr
☐ 24 hr
☐ 26 hr
☐ 28 hr
☐ 30 hr
☐ 32 hr
☐ 34 hr
☐ 36 hr
☐ 38 hr
☐ 40 hr
☐ 42 hr
☒ 46 hr
☐ 48 hr

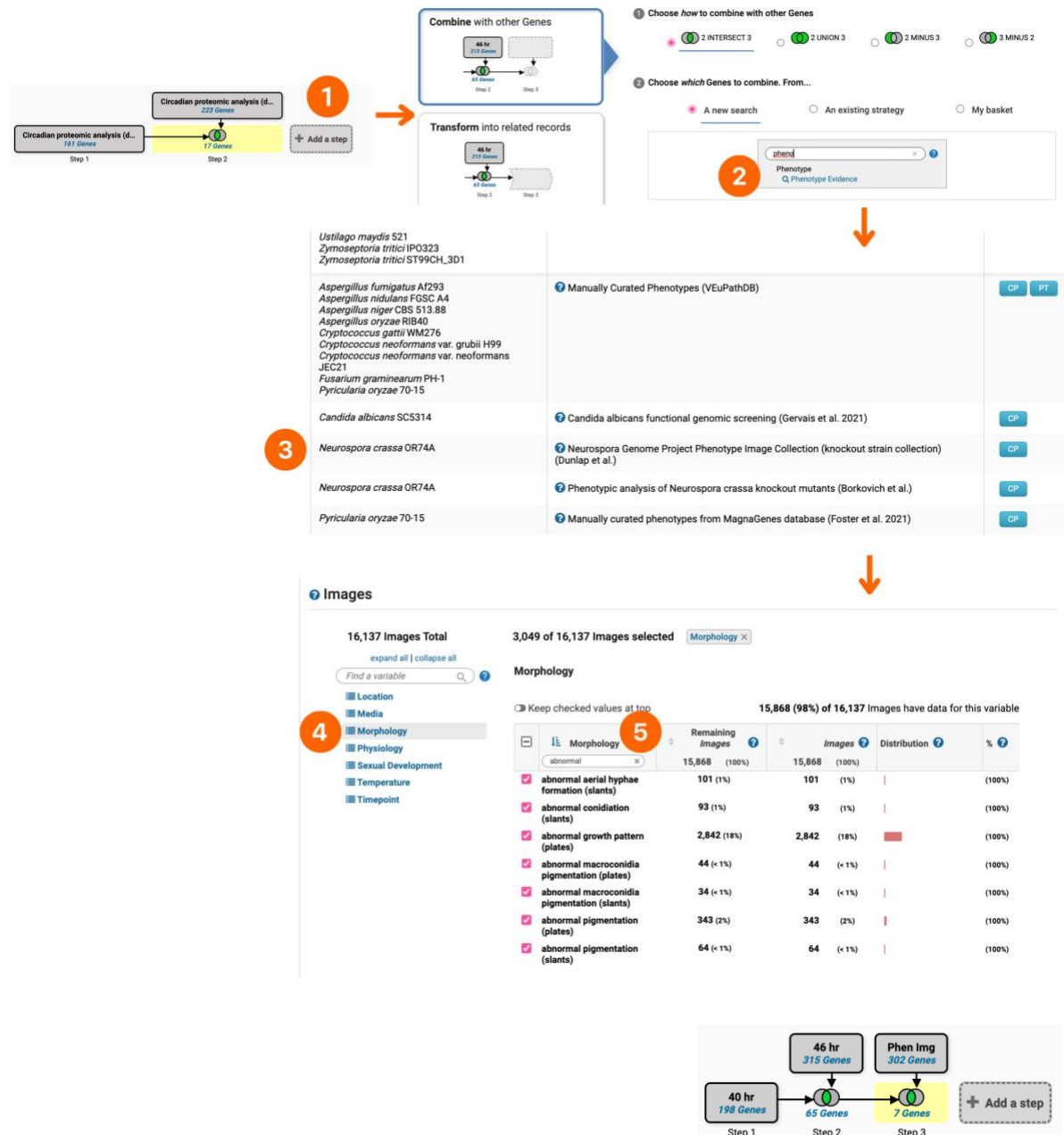
Fold difference >=

6.



- Identify genes required for normal growth morphology in *N. crassa*.

- Click on the “Add step”.
- Select the “Combine with other Genes” search and navigate to the Phenotype Evidence search.
- Click on the curated phenotypes (CP) button to investigate records from Neurospora Genome Project Phenotype Image Collection (Dunlap et al.).
- Navigate to the “Morphology” section.
- Filter on “abnormal” and select all annotated abnormal phenotypes.



Step 1: Circadian proteomic analysis (d...)
167 Genes

Step 2: Combine with other Genes
46 hr 214 Genes

Step 3: Phenotype Evidence
46 hr 315 Genes

Manually Curated Phenotypes (VeuPathDB)

Gene	Phenotype	CP	PT
<i>Ustilago maydis</i> 521			
<i>Zymoseptoria tritici</i> IPO323			
<i>Zymoseptoria tritici</i> ST99CH_3D1			
<i>Aspergillus fumigatus</i> Af293			
<i>Aspergillus nidulans</i> FGSC A4			
<i>Aspergillus niger</i> CBS 513.88			
<i>Aspergillus oryzae</i> RIB40			
<i>Cryptococcus gattii</i> WM276			
<i>Cryptococcus neoformans</i> var. <i>grubii</i> H99			
<i>Cryptococcus neoformans</i> var. <i>neoformans</i> JEC21			
<i>Fusarium graminearum</i> PH-1			
<i>Pyricularia oryzae</i> 70-15			
<i>Candida albicans</i> SC5314			
<i>Neurospora crassa</i> OR74A			
<i>Neurospora crassa</i> OR74A			
<i>Pyricularia oryzae</i> 70-15			

Images
16,137 Images Total
3,049 of 16,137 Images selected Morphology

Morphology
Keep checked values at top
15,868 (98%) of 16,137 Images have data for this variable

Remaining Images	Images	Distribution	%
15,868 (100%)	15,868 (100%)		
101 (1%)	101 (1%)		(100%)
93 (1%)	93 (1%)		(100%)
2,842 (18%)	2,842 (18%)		(100%)
44 (< 1%)	44 (< 1%)		(100%)
34 (< 1%)	34 (< 1%)		(100%)
343 (2%)	343 (2%)		(100%)
64 (< 1%)	64 (< 1%)		(100%)

Abnormal Phenotypes

- abnormal aerial hyphae formation (slants)
- abnormal conidiation (slants)
- abnormal growth pattern (plates)
- abnormal macroconidia pigmentation (plates)
- abnormal macroconidia pigmentation (slants)
- abnormal pigmentation (plates)
- abnormal pigmentation (slants)

Step 1: 40 hr 198 Genes
Step 2: 46 hr 315 Genes
Step 3: Phen Img 302 Genes

Strategy URL:

<https://fungidb.org/fungidb/app/workspace/strategies/import/0cae335cef282483>

Reference: Hurley et al. 2018 DOI: 10.1016/j.cels.2018.10.014