

Optional: Examining host-pathogen datasets.

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

- **Identify genes up-regulated in mice infected with SC5314 at 1d.**
 1. Navigate to the RNA-Seq Evidence search and filter RNA-Seq datasets for “Kirch” to examine the dataset by Kirchner et al. 2019.
 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 illustrates the HostDB.org RNA-Seq Evidence search interface, showing the steps to identify up-regulated genes in mice infected with SC5314 at 1d.

Step 1: The search bar contains "ma". The "RNA-Seq Evidence" link is highlighted.

Step 2: The "DE" (Differential Expression) button is selected in the "Choose a Search" section.

Step 3: The "Experiment" section shows the selected dataset: "Mouse transcriptomes during oropharyngeal candidiasis infection - Sense".

Step 4: The "naive" sample is selected as the reference sample.

Step 5: The "SC5314_infected_1d" sample is selected as the comparator sample.

Step 6: The "Direction" is set to "up-regulated".

Step 7: The "fold difference >=" is set to 4.

The "adjusted P value less than or equal to" is set to 0.1.

Result: The search results show 857 genes up-regulated in Calb_Galleria_mouse (de).

- **Identify genes up-regulated in response to 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.

Step 1: Click on the “Add Step” button.

Step 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.

Step 3: Choose to examine the sense strand.

Step 4: Select reference sample: naïve.

Step 5: Select comparator sample: 101_infected_1d.

Step 6: Look for up-regulated genes.

Step 7: Select magnitude of upregulation: 4 fold.

Legend: Similarity Differential Expression Fold Change Percentile Sense/Antisense

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

Organism: Mus musculus C37BL/6J

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

Choose a Search: [Go] [Cancel] [Reset]

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

4 **Reference Sample**

☒ naïve
☐ 101_infected_9h
☐ 101_infected_1d
☐ 101_infected_3d
☐ 101_infected_7d
☐ SC5314_infected_9h
☐ SC5314_infected_1d
☐ SC5314_infected_3d
☐ SC5314_infected_7d

5 **Comparator Sample**

☐ naïve
☐ 101_infected_9h
☒ 101_infected_1d
☐ 101_infected_3d
☐ 101_infected_7d
☐ SC5314_infected_9h
☐ SC5314_infected_1d
☐ SC5314_infected_3d
☐ SC5314_infected_7d

6 **Direction**

up-regulated

7 **fold difference >=**

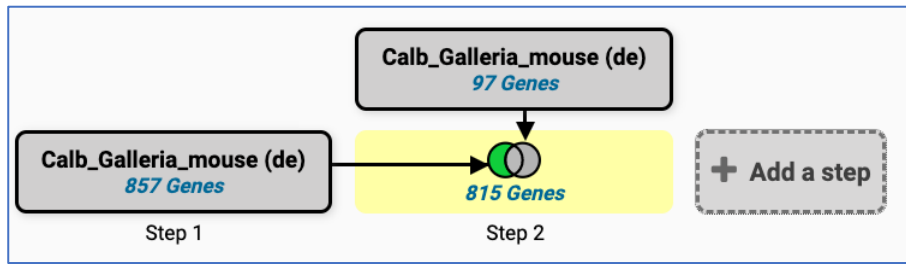
4

adjusted P value less than or equal to

0.1

Get Answer

- Modify the Boolean operator to determine genes that are upregulated in response to SC5314 but not 101 strain.

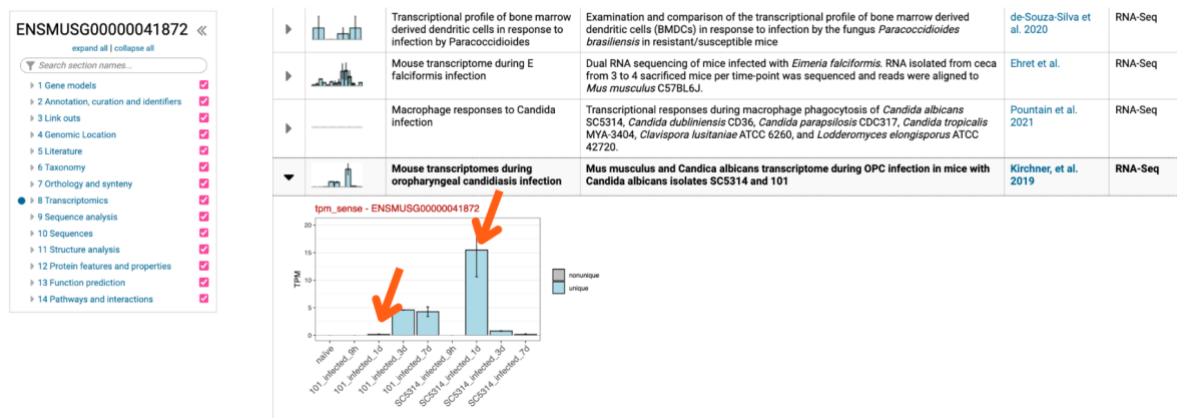


- Examine the results in HostDB:

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	mmusCS78L6J_chr1:15,853,331..15,856,499(+)	predicted gene, 37509 [Source: MGI Symbol; Acc: MGI:5610737]	1
ENSMUSG000000067780	ENSMUST000000088476	mmusCS78L6J_chr1:17,601,901..17,630,939(+)	peptidase inhibitor 15 [Source: MGI Symbol; Acc: MGI:1934659]	1
ENSMUSG000000025929	ENSMUST000000027061	mmusCS78L6J_chr1:20,730,905..20,734,496(+)	interleukin 17A [Source: MGI Symbol; Acc: MGI:107364]	1
ENSMUSG000000041872	ENSMUST000000039046	mmusCS78L6J_chr1:20,777,146..20,790,617(+)	interleukin 17F [Source: MGI Symbol; Acc: MGI:2676631]	4
ENSMUSG000000041872	ENSMUST000000189301	mmusCS78L6J_chr1:20,777,146..20,790,617(+)	interleukin 17F [Source: MGI Symbol; Acc: MGI:2676631]	4
ENSMUSG000000041872	ENSMUST000000190692	mmusCS78L6J_chr1:20,777,146..20,790,617(+)	interleukin 17F [Source: MGI Symbol; Acc: MGI:2676631]	4
ENSMUSG000000041872	ENSMUST000000191111	mmusCS78L6J_chr1:20,777,146..20,790,617(+)	interleukin 17F [Source: MGI Symbol; Acc: MGI:2676631]	4
ENSMUSG000000104358	ENSMUST000000192924	mmusCS78L6J_chr1:34,823,525..34,826,560(+)	predicted gene, 37127 [Source: MGI Symbol; Acc: MGI:5610355]	1
ENSMUSG000000047180	ENSMUST000000056946	mmusCS78L6J_chr1:36,264,597..36,274,679(+)	neuralized E3 ubiquitin protein ligase 3 [Source: MGI Symbol; Acc: MGI:2429944]	2
ENSMUSG000000047180	ENSMUST000000188666	mmusCS78L6J_chr1:36,264,597..36,274,679(+)	neuralized E3 ubiquitin protein ligase 3 [Source: MGI Symbol; Acc: MGI:2429944]	2
ENSMUSG000000037447	ENSMUST000000097778	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115029	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115031	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115032	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115033	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000115034	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000124280	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000126413	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000137906	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000140218	mmusCS78L6J_chr1:36,307,733..36,324,029(+)	AT rich interactive domain 5A (MRF1-like) [Source: MGI Symbol; Acc: MGI:2443039]	15
ENSMUSG000000037447	ENSMUST000000141121	mmusCS78L6J_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.



Search strategy links:

FGC2024 advanced search strategy 2:

<https://hostdb.org/hostdb/app/workspace/strategies/import/ec36d02df763b3d5>