Advanced search strategies (optional)

SC5314 induces rapid transcriptional response in the host, while 101 has slower kinetic. The commensal 101 strain has also reduced filamentation when compared to SC5314.

- **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.

- **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.

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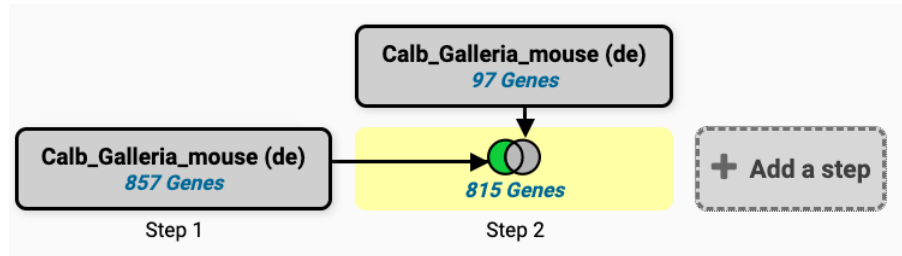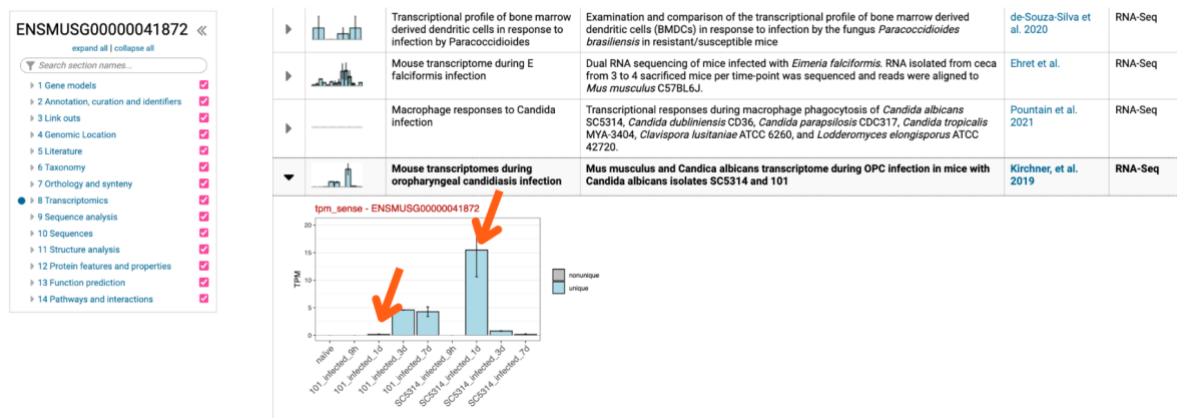

- **Examine the results in HostDB:**

  1. Click on the Gene ID link for "interleukin 17F" and navigate to the transcriptomics expression section.

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