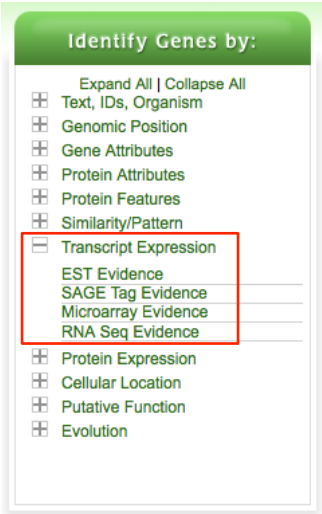
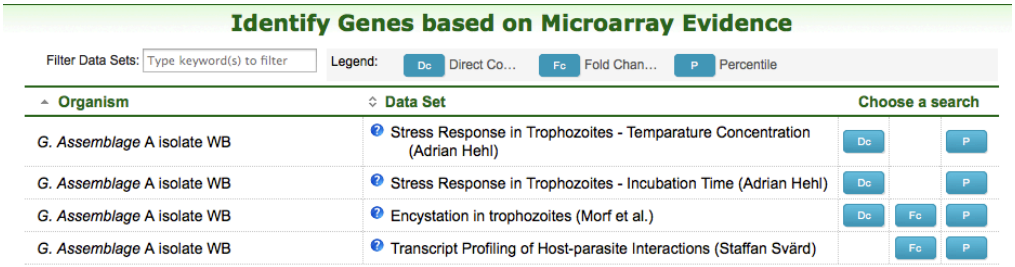
# Exploring Proteomics Data
# (Exercise 5)

1. **Find *Giardia* genes that are differentially regulated (up or down) at 6 and 18 hours post interaction with host cells. (http://giardiadb.org)**

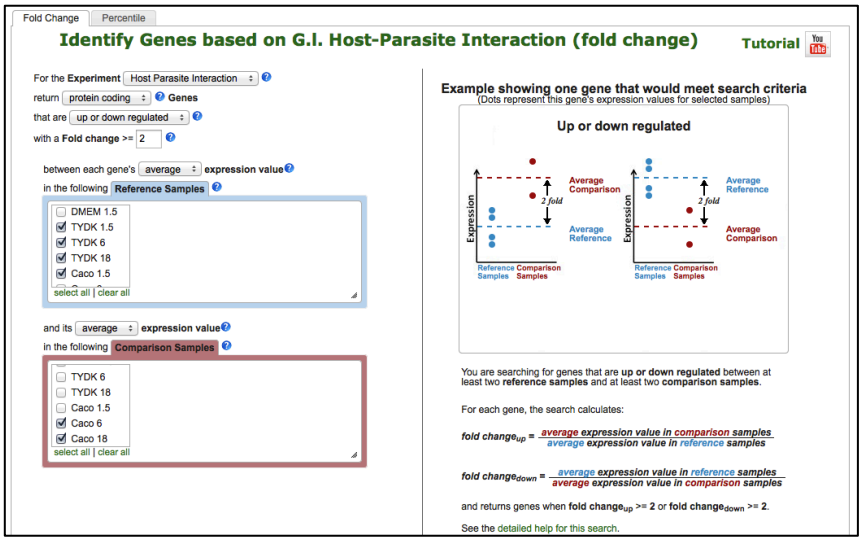
   - What types of data are available in GiardiaDB that provide information about transcript expression? Explore the various categories of transcription data.



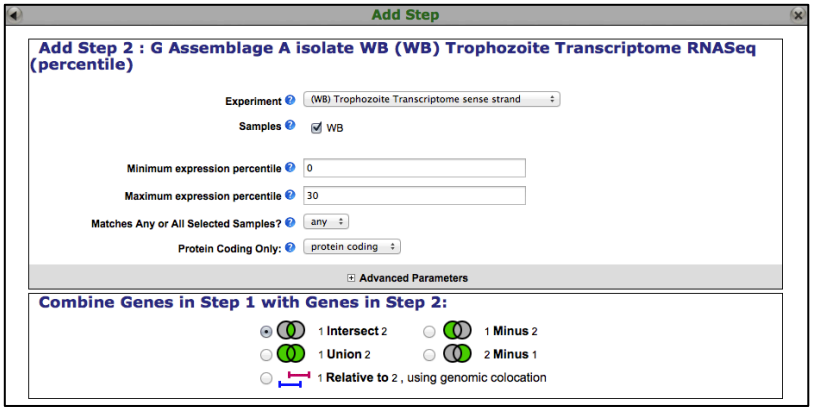

   - For host interaction, GiaridaDB currently has a microarray dataset from Staffan Svard's group called: "Transcript Profiling of Host-parasite Interactions". You can find this search by selecting "Microarray Evidence" under the "Transcript Expression" section.



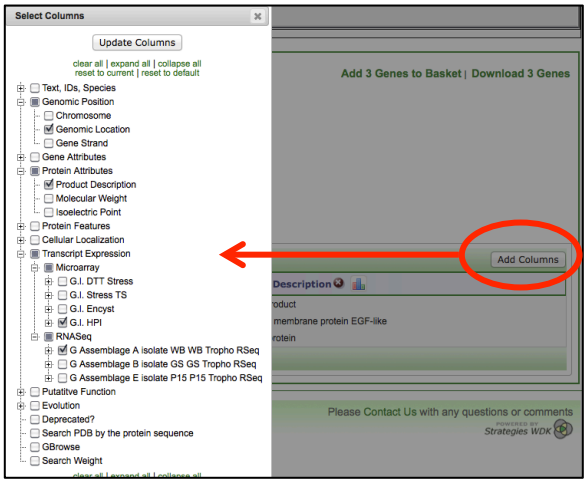

   - Note that if you want to find genes that are changing in expression select the fold change (Fc) query.
   - The configurable search page allows you to define the type of expression profile you are interested in. In this case, we are interested in genes that are differentially regulated between the Caco 6 and 18 samples (comparison samples) compared to the Caco 1.5, TYDK 1.5, TYDK 6 and TYDK 18 samples (reference).




- How many genes did you identify?
- What do the expression profile graphs look like? Do they agree with your search parameters?
- How many of these genes are expressed in the lower 30% percentile from the trophozoite RNAseq experiment available in GiardiaDB? (hint: add a step and go to the RNAseq section – configure the percentile query for "(WB) Trophozoite Transcriptome sense strand" to return genes expressed between 0 and 30 percentile).



Look at your results and add the columns for expression graphs from the experiments you searched. Do the graphs coincide with what you searched?

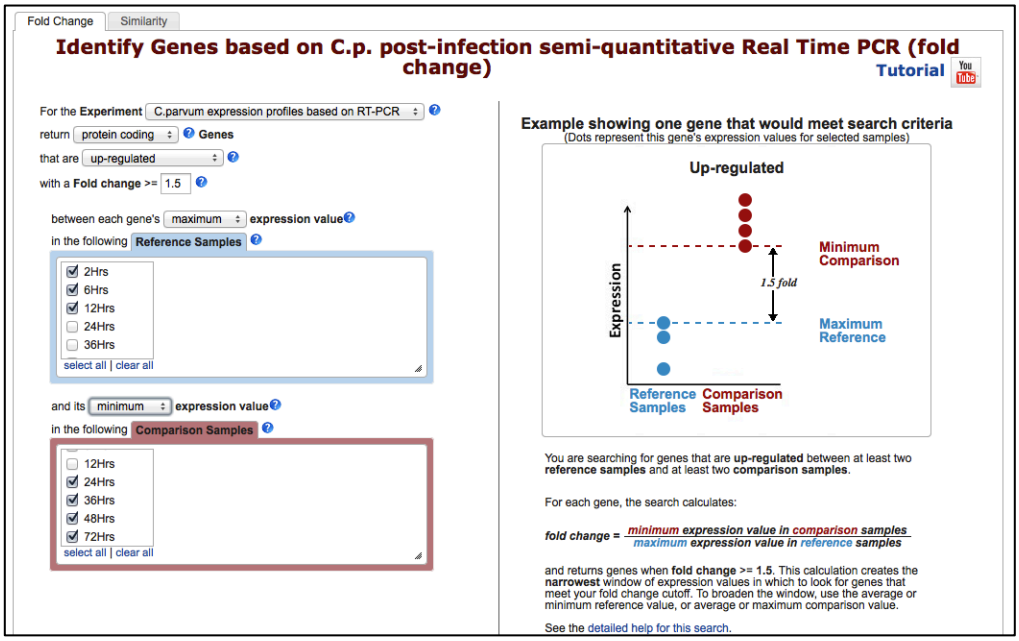




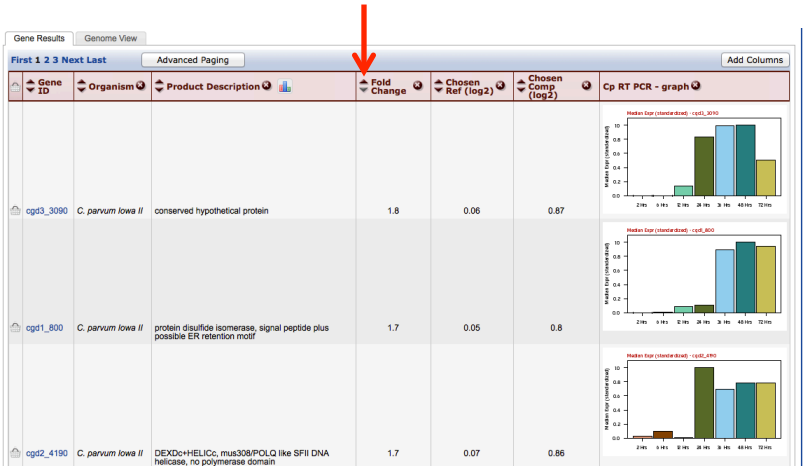
- Notice that one of the genes has a high level of antisense transcription. Could this be indicating something interesting about how this gene is regulated?

2. **Find *Cryptosporidium* genes that are upregulated during exystation based on RT PCR evidence. (http://cryptodb.org)**

   - Configure the fold change search of the *Cryptosporidium parvum* RT-PCR data to identify genes that are upregulated by at least 1.5 fold between the minimal expression level at time points 24-72 hrs compared to the maximal expression level at time points 2-12hrs.
   - How many genes did you get? What happens if you revise this search to




     compare the average expression values between the selected time points.
   - Which gene has the highest fold difference in expression? You can sort the columns by clicking on the up or down arrow in the fold change column.




   - Can you find out anything about the function of this gene? (hint: you can add additional columns from the "putative function" section, of you can visit the gene page and explore it further).