

Host Response

- Find host genes that are upregulated in infected mouse cells compared to uninfected ones.

For this exercise use <http://hostdb.org>

- Navigate to the “Transcript Expression” section then select “RNA Seq Evidence”. Select the fold change query for the “Transcriptome during infection with 25 strains of *T. gondii* (Minot et al.)” experiment.

The screenshot shows the HostDB interface for identifying genes based on RNA Seq Evidence. On the left, a sidebar titled 'Identify Genes by:' lists various criteria, with 'Transcript Expression RNA Seq Evidence' selected. The main panel is titled 'Identify Genes based on M musculus C57BL6J Transcriptome during infection with 25 strains of T. gondii RNASeq (fold change)'. It shows search parameters: Organism: M. musculus C57BL6J, Data Set: Transcriptome during infection with 25 strains of T. gondii (Minot et al.), and a search filter for 'FC' (Fold Change) with a value of 10. A graph on the right, titled 'Example showing one gene that would meet search criteria', shows a plot of Expression vs. Reference Samples. The graph indicates an up-regulated gene with a fold change of 10, comparing the average expression value of comparison samples to the reference samples.

- Configure the query so that you are comparing all infected samples to the uninfected control. Make sure to select upregulated. In the example above a fold change of 10 was selected and the “average” operation was applied on the comparison samples. Feel free

The screenshot shows the HostDB interface displaying a list of 200 genes from Step 1. The table has columns for Gene ID, Organism, Product Description, Fold Change, Chosen Ref (log2), and Chosen Comp (log2). A gene with a fold change of 456.4 is highlighted. A graph on the right shows the expression profile for the selected gene across different samples.

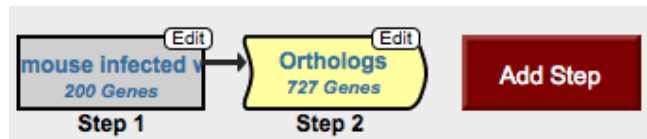
Gene ID	Organism	Product Description	Fold Change	Chosen Ref (log2)	Chosen Comp (log2)
ENSMUSG00000031779_1	M. musculus C57BL6J	chemokine (C-C motif) ligand 22 (Ccl22)	456.4	0.84	9.68

to run the query exactly as above.

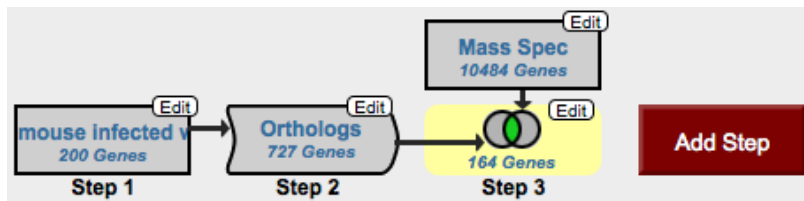
- c. What kinds of GO terms are enriched in this result set? *Hint:* click on the “Analyze Results” tab and select the GO enrichment analysis.

GO ID	GO Term	Genes in the bkgd with this term	Genes in your result with this term	Percent of bkgd Genes in your result	Fold enrichment	Odds ratio	P-value	Benjamini	Bonferroni
GO:0009611	response to wounding	1017	38	3.7	8.79	10.7	3.31e-24	4.18e-21	4.18e-21
GO:0001817	regulation of cytokine production	640	29	4.5	10.66	12.36	9.28e-21	4.76e-18	1.17e-17
GO:0006950	response to stress	4086	64	1.6	3.68	5.01	1.13e-20	4.76e-18	1.43e-17
GO:0010033	response to organic substance	2918	54	1.9	4.35	5.65	2.19e-20	6.92e-18	2.77e-17
GO:0006952	defense response	1184	36	3.0	7.15	8.56	4.18e-20	1.06e-17	5.28e-17
GO:0051240	positive regulation of multicellular organismal process	908	32	3.5	8.29	9.74	1.01e-19	2.12e-17	1.27e-16
GO:0070206	protein trimerization	63	14	22.2	52.26	56.27	2.45e-19	4.43e-17	3.10e-16
GO:0032496	response to lipopolysaccharide	387	23	5.9	13.98	15.73	4.27e-19	6.74e-17	5.39e-16
GO:0002237	response to molecule of bacterial origin	411	23	5.6	13.16	14.81	1.50e-18	2.11e-16	1.90e-15
GO:0051704	multi-organism process	1445	37	2.6	6.02	7.21	2.85e-18	3.60e-16	3.60e-15
GO:0042127	regulation of cell proliferation	2165	44	2.0	4.78	5.9	5.39e-18	6.19e-16	6.81e-15
GO:0050710	negative regulation of cytokine secretion	44	12	27.3	64.14	68.32	1.11e-17	1.14e-15	1.41e-14
GO:0016477	cell migration	1076	32	3.0	6.99	8.19	1.17e-17	1.14e-15	1.48e-14
GO:0032879	regulation of localization	2555	47	1.8	4.33	5.4	1.44e-17	1.26e-15	1.82e-14
GO:0050707	regulation of cytokine secretion	145	16	11.0	25.95	28.2	1.50e-17	1.26e-15	1.89e-14

- d. Can you identify the human orthologs of these genes? *Hint:* add a “Transform by Orthology” step.

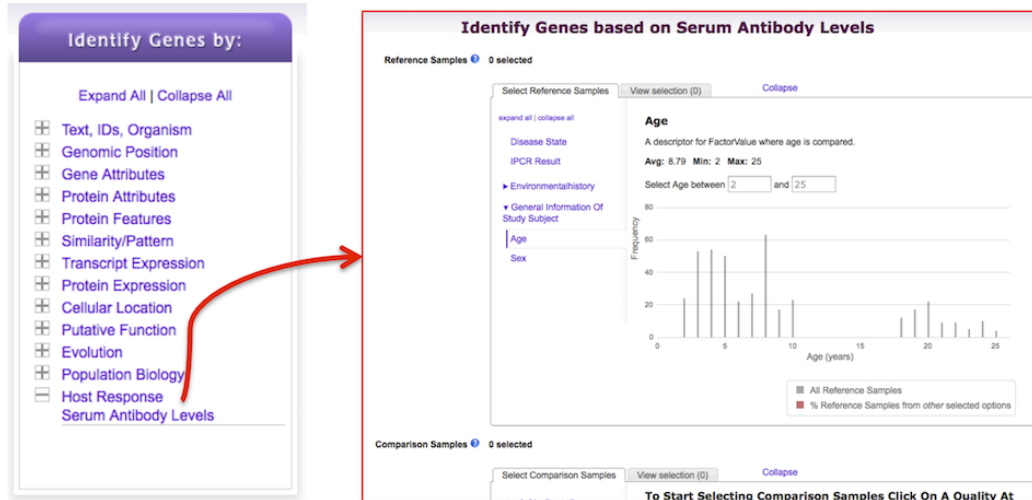


- e. Do any of these human genes also have peptide evidence for their expression during infection? *Hint:* add a step and explore the “Mass Spec Evidence” data in the protein expression section. Run the search using the default parameters.



2. Find *Plasmodium falciparum* antigens that are immunogenic. For this exercise use <http://plasmodb.org>

- a. Identify antigens (genes) that exhibited an increased immunogenicity in children (ages 0-18) with no disease (normal) compared to children with disease (infected). *Hint:* the “Serum Antibody Levels” search is available in the “Host Response” menu item in the “Identify Genes By” section of the home page.



Note that you will be comparing “comparison” samples to “reference” samples. So in this example, your comparison samples will be normal children and your reference samples will be infected children. You can configure the samples by making a selection from left. What do your results look like? Could these represent potential protective antigens?

