

# Functional Genomics II

## 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.

**Identify Genes based on RNA Seq Evidence**

Filter Data Sets: Type keyword(s) to filter

Legend: FC Fold Change, FQv Fold Change..., P Percentile, S Similarity

Organism: *M. musculus* C57BL6J

Data Set: Transcriptome during infection with 25 strains of *T. gondii* (Minot et al.)

Choose a search: FC, FQv, P, S

**Identify Genes based on *M. musculus* C57BL6J Transcriptome during infection with 25 strains of *T. gondii* RNaseq (fold change)**

For the Experiment: Transcriptome during infection with 25 strains of *T. gondii* Murine macrophages

return protein coding Genes

that are up-regulated

with a Fold change >= 10

between each gene's expression value in the following Reference Samples

- TgCATB5 infected
- VAND infected
- VEG infected
- WTD3 infected
- not infected

and its average expression value in the following Comparison Samples

- TgCATB5 infected
- VAND infected
- VEG infected
- WTD3 infected
- not infected

**Example showing one gene that would meet search criteria**

(Dots represent this gene's expression values for selected samples)

Up-regulated

Expression

Average Comparison

Reference

Reference Samples

Comparison Samples

A maximum of four samples are shown when more than four are selected.

You are searching for genes that are up-regulated between one reference sample and at least two comparison samples.

For each gene, the search calculates:

$$\text{fold change} = \frac{\text{average expression value in comparison samples}}{\text{reference expression value}}$$

and returns genes when fold change >= 10. To narrow the window, use the minimum comparison value. To broaden the window, use the maximum

- 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 to run the query exactly as above.

**My Strategies:** New, Opened (1), All (1), Basket, Public Strategies (1), Help

(Genes) Strategy: mouse infected with 25 Tg strains (fc) \*

mouse infected 200 Genes Add Step Step 1

200 Genes from Step 1 Strategy: mouse infected with 25 Tg strains (fc) Add 200 Genes to Basket | Download 200 Genes

Filter results by species

Gene Results Genome View Analyze Results **BETA**

First 1 2 3 4 5 Next Last Advanced Paging Add Columns

Gene ID	Organism	Product Description	Fold Change	Chosen Ref (log2)	Chosen Comp (log2)	mouse infected with 25 Tg strains - fpkm Graph
ENSMUSG00000031779_1	<i>M. musculus</i> C57BL6J	chemokine (C-C motif) ligand 22 (Ccl22)	456.4	0.84	9.68	

c. What kinds of GO terms are enriched in this result set? *Hint:* click on the

Gene Results | Genome View | Gene Ontology Enrichment | **Analyze Results** BETA | [Rename This Analysis] | Copy These Parameter Values ]

### Gene Ontology Enrichment

Find Gene Ontology terms that are enriched in your gene result. [Read More](#)

**Parameters**

**Analysis Results** [Download Analysis Results](#)  
This analysis result may be lost if you change your gene result.  
To save this analysis result, please download.

Got a total of 1,263 results Filter:

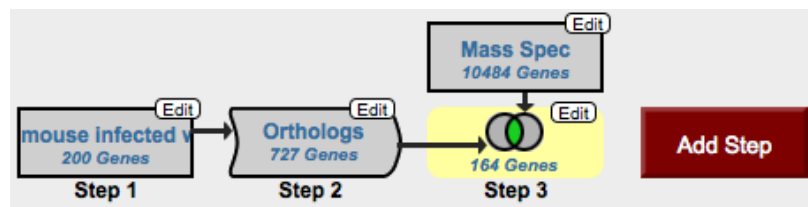
GO ID	GO Term	Genes in the bkgd with this term	Genes in your result with this term	Percent of bkgd Genes in your result	Fold enrichment	Odds ratio	P-value	Benjamini	Bonferroni
GO:0009611	response to wounding	1017	38	3.7	8.79	10.7	3.31e-24	4.18e-21	4.18e-21
GO:0001817	regulation of cytokine production	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

“Analyze Results” tab and select the GO enrichment analysis.

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

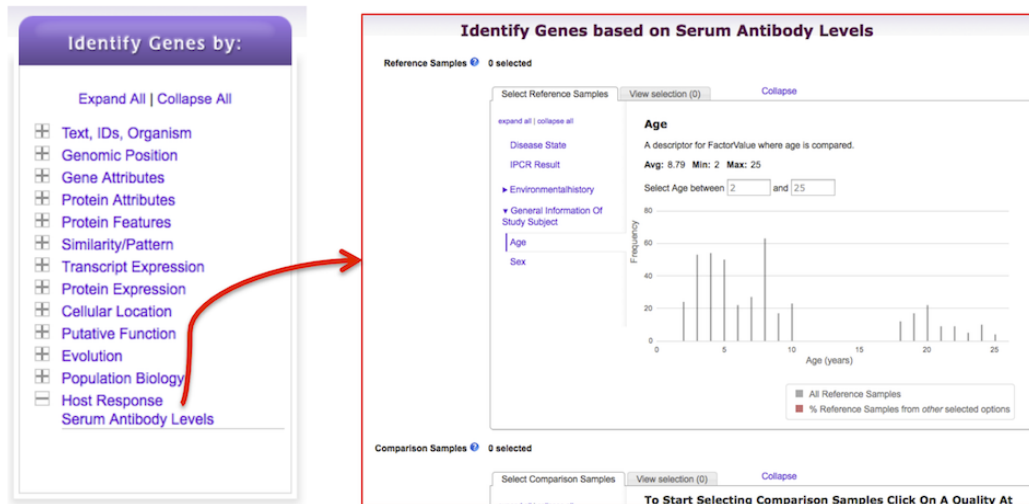


e. Do any of these human genes also have peptide evidence for their expression during infection? *Hint:* add a step and explore the “Mass Spec Evidence” data in the protein expression section. Run the search using the default parameters.



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 selection from left. What do your results look like? Could these represent potential protective antigens?

