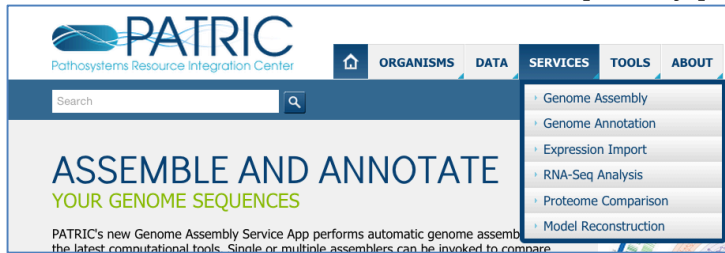
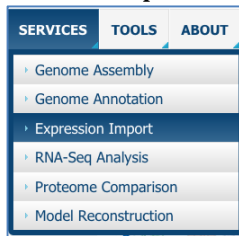


## Uploading an experiment using the Differential Expression service

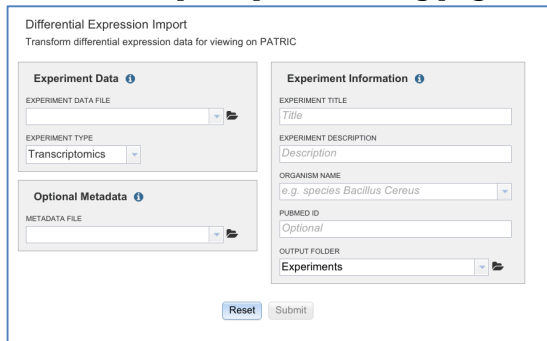
1. You must be logged in to use the PATRIC services. Once you are logged in, click on the Services tab that can be found at the top of any page in PATRIC.



2. Click Experiment Import.



3. This will open up the landing page for the Differential Expression Import service.

A screenshot of the 'Differential Expression Import' landing page. The page title is 'Differential Expression Import' with a subtitle 'Transform differential expression data for viewing on PATRIC'. The form is divided into three main sections: 'Experiment Data', 'Optional Metadata', and 'Experiment Information'. 'Experiment Data' includes fields for 'EXPERIMENT DATA FILE' and 'EXPERIMENT TYPE' (set to 'Transcriptomics'). 'Optional Metadata' includes a 'METADATA FILE' field. 'Experiment Information' includes fields for 'EXPERIMENT TITLE' (with a placeholder 'Title'), 'EXPERIMENT DESCRIPTION' (with a placeholder 'Description'), 'ORGANISM NAME' (with a dropdown menu showing 'e.g. species Bacillus Cereus'), 'PUBMED ID' (with a placeholder 'Optional'), and 'OUTPUT FOLDER' (with a dropdown menu showing 'Experiments'). At the bottom of the form are 'Reset' and 'Submit' buttons.

4. First you must upload the experiment data. If you are unsure as to what data, or what format you need, click on the “i” next to the words Experimental Data and this will open up a screen showing you all the information.

**Experiment Data** i

EXPERIMENT DATA FILE

EXPERIMENT TYPE

Transcriptomics

**What is this?**  
At PATRIC, you can upload your own pre-processed differential expression datasets generated by microarray, RNA-Seq, or proteomic technologies to your workspace and analyze them using annotations and analysis tools. Currently, PATRIC only supports differential gene expression data in the form of log ratios, generated by comparing samples/conditions/time points. You may also compare your data with other transcriptomics datasets available at PATRIC. Data uploaded in your workspace is private and protected.

**Experiment Data**  
Upload a data file containing differential gene expression values in the form of log ratios. The file should be in one of the supported formats described below. Optionally, you may also upload metadata related to sample comparisons in the prescribed format to help later in the data analysis.

**Supported IDs**

1. RefSeq Locus Tag
2. PATRIC Feature ID
3. NCBI GI Number
4. NCBI Protein ID
5. SEED ID
6. PATRIC Legacy ID

**File Format**  
Currently, PATRIC allows you to upload your transcriptomics datasets in the form of differential gene expression measured as log ratios. Data can be uploaded in multiple file formats: comma separated values (.csv), tab delimited values (.txt), or Excel (.xls or .xlsx). Click to download [Sample Data template](#) in Gene Matrix Format. Files should contain data in one of the following formats:

**1. Gene Matrix:**

Gene ID	Comparison1	Comparison2
b0002	0.767	-1.316
b0003	0.815	-1.841
b0004	0.856	-1.643

**2. Gene List:**

Data is presented in three columns: Gene ID, Sample ID, and expression value. Expression value should be in the form of log ratio (i.e. log2 (test/control)). Below is an example of transcriptomics data in Gene List format:

Gene ID	Comparison ID	Log Ratio
b0002	Comparison1	0.767
b0003	Comparison1	0.815
b0002	Comparison2	-1.316

**Experiment Type**  
This field specifies the the experiment type Transcriptomics, Proteomics, or Phenomics.

**ID Type**  
In order to take full advantage of PATRIC data, gene IDs provided in the experiment data are mapped to PATRIC. Due to differences in annotation that may exist some genes may go unmapped. Unmapped genes will be excluded from subsequent analysis.

**File Type**  
This field specifies whether the uploaded Experiment Data File is tab/comma delimited or an excel file.

The data that you upload must be in a specific format, either for a Gene Matrix or Gene list. The first column **MUST** be called Gene ID. For the Gene Matrix, the format must match the format below, but can have multiple comparisons:

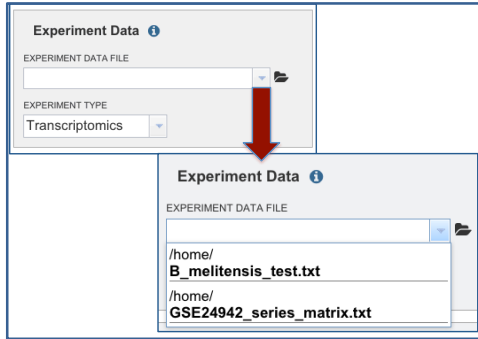
**1. Gene Matrix:**

Gene ID	Comparison1	Comparison2
b0002	0.767	-1.316
b0003	0.815	-1.841
b0004	0.856	-1.643

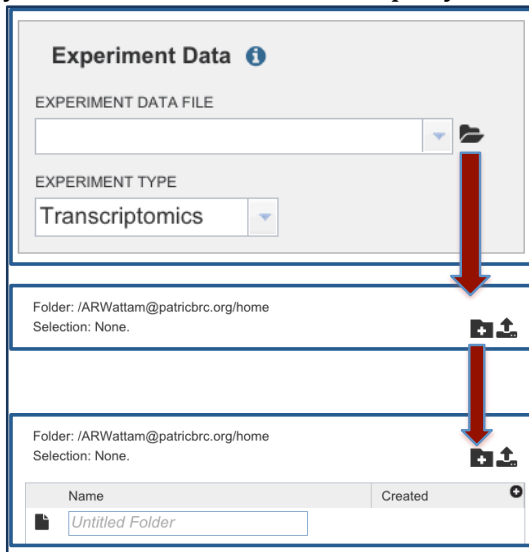
For the Gene list, the data must match the format below:

Gene ID	Comparison ID	Log Ratio
b0002	Comparison1	0.767
b0003	Comparison1	0.815
b0002	Comparison2	-1.316

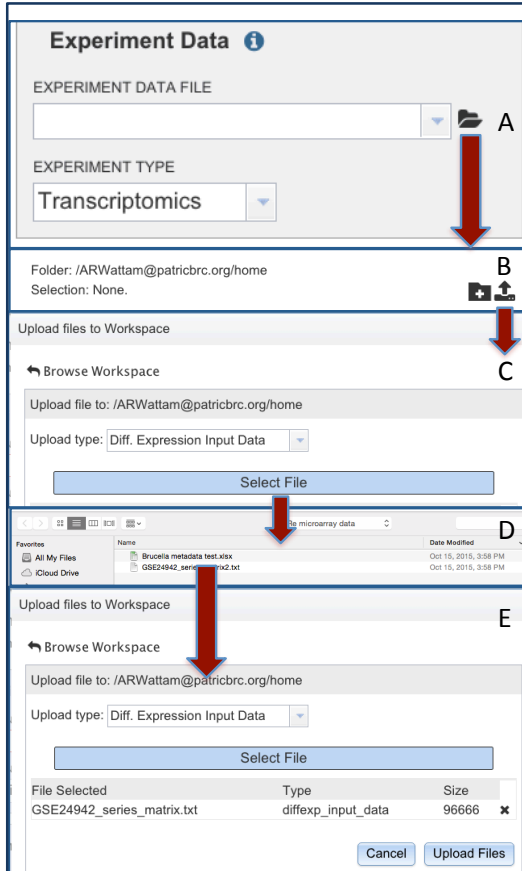
5. If you click on the down arrow next to the text box under the words “Experimental Data/File”, you will be able to see data that you have previously loaded.



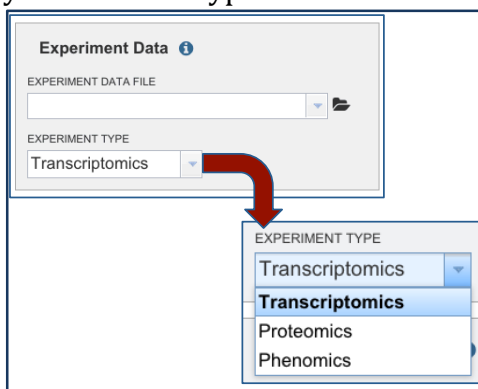
6. If you click on the icon that looks like a folder next to that text box, a window will pop up that shows a folder icon and a icon representing the upload button next to it. If you click on the folder icon in that window, that will open up a text box that allows you to name a new folder to put your data into.



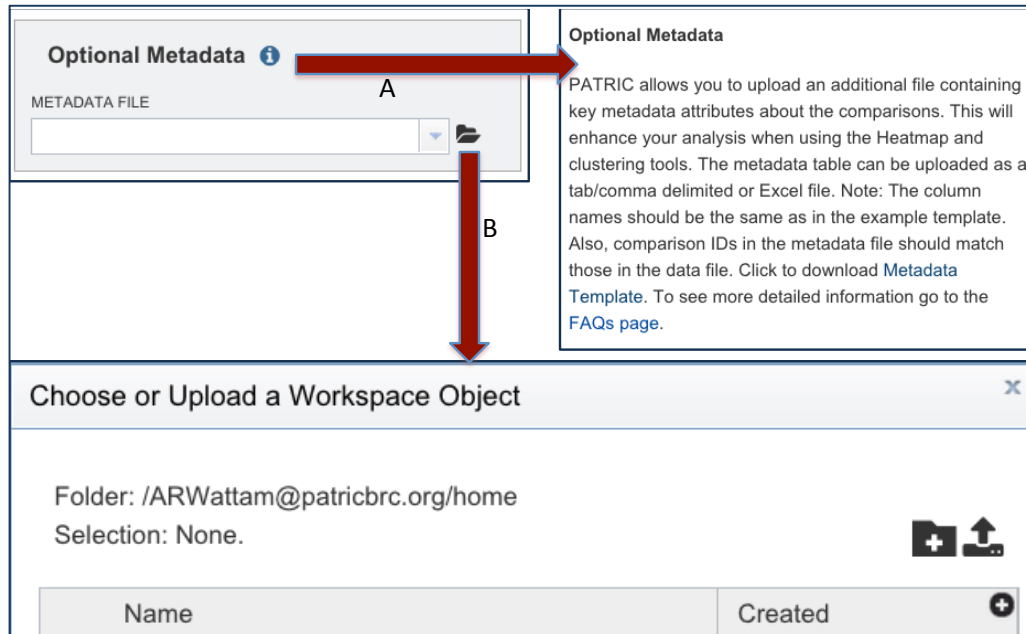
7. To upload the data, click on the folder next to the Experiment Data/File folder (A) that opens up the new window with the folder icon and icon to upload data next to it(B). Click on the data upload icon. This will open up a new window (C) that allows you to select data that is on your computer. Clicking the blue "Select File" button will open up the window on your computer that allow you to select the file you want to upload (D). Once you have selected that file, it will appear in the grey bar on the upload page (E). Then click on the blue "Upload File" button at the bottom of the page.



8. Now you need to define the type of experiment you have uploaded. Clicking on the arrow next to the text box that contains the word “Transcriptomics” will allow you select the type of data that matches what you just uploaded.

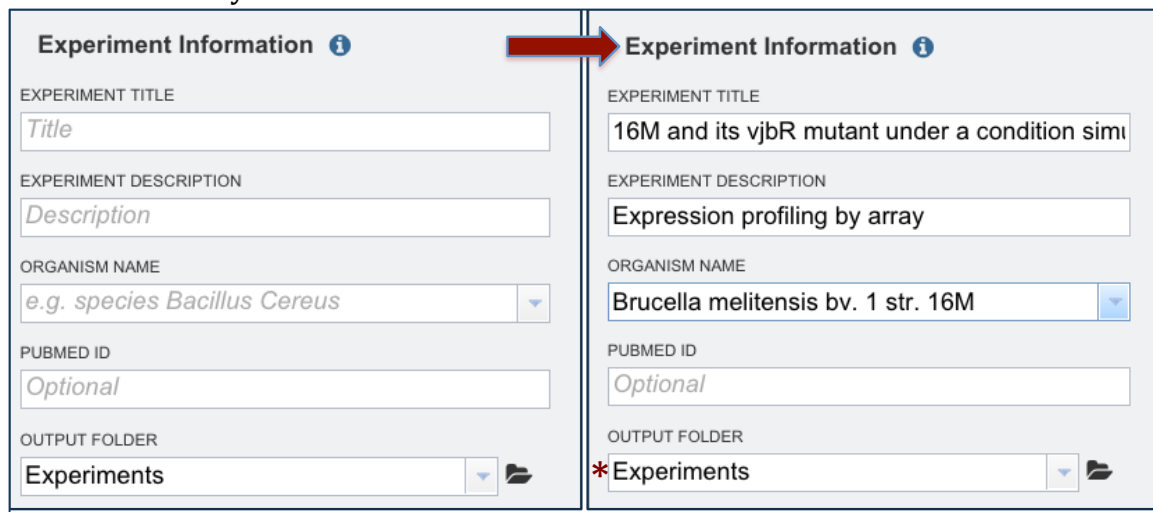


9. Now you can take the opportunity to upload metadata that is associated with your experimental data. This will help you identify the data associated with each experimental condition once your data is uploaded and you are using the PATRIC transcriptomic tools. On the landing page for the Differential Expression Import service, in the section labeled Optional Metadata, you can click on the “I” icon (A) to find out what the parameters are, and the folder icon (B) to upload that data, following the same steps as described above (7A-E).



When you click on the information icon, the box that pops up will have a hyperlink for a Metadata Template. Clicking of this will download an excel file that you will need to fill in with your metadata, and then upload it. You DON'T need to fill in all the parameters, but the Comparison IDs and the Title (experimental conditions) are particularly useful.

10. Now you need to provide the experiment information. As you type in the text box under the words "Organism Name" it will attempt to autofill the information that matches your query. Choose to put the data in the Experiments folder, or in whatever folder you created to hold it.



11. Once you've uploaded your data, any metadata you're interested in, and the experimental information, Click the submit button.

### Experiment Data i

EXPERIMENT DATA FILE  
 📎

EXPERIMENT TYPE

### Experiment Information i

EXPERIMENT TITLE

EXPERIMENT DESCRIPTION

ORGANISM NAME

PUBMED ID

OUTPUT FOLDER  
 📁

←

11. At the very bottom of the page, you will see a box called “Jobs” that is followed by four sets of numbers. Mousing over this box (A) will show you what each of those numbers mean. When you double click on the word “Jobs” (B) a page will upload that will show you the status of the job you just submitted.

📁 Uploads
0·0

📁 Jobs
43·0·1·7

Completed · In progress · Queued · Suspended

↓ A B

Status	Submit	App	Output Name	Start	Completed
● completed	10/18/15, 8:26 AM	DifferentialExpression	16M and its vjbR mutant under a condition simulating environments of macrophage	10/18/15, 8:27 AM	10/18/15, 8:27 AM

12. To see the results, you must go to your workspace by clicking on the words “WORKSPACE: HOME” in the blue ribbon at the top of the page.



13. You workspace, with all of your jobs will appear. You must scroll down until you find the folder where you put the data (I put mine in Experiments). Double click on that folder.



14. This will open up a page with all the experiments that you have run through the Differential Expression Import service. Find the title that you gave your experiment and double click on it.

Name	Size	Owner	Created
Parent Folder			
16M and its vjbR mutant under a condition simulating environments of macrophag	3.4 kB	ARWattam	10/18/15, 8:27 AM

15. You will see all the experimental conditions from the metadata that you uploaded. To see all those genes and manipulate them using the PATRIC's transcriptomics tools, select them all (they will be highlighted blue once you have selected them).

ARWattam / home / Experiments / 16M and its vjbR mutant under a condition simulating environments of macrophage

Platform Organism: Brucella melitensis bv. 1 str. 16M Pubmed ID: Undefined  
Genes Mapped/Genes Total: 2963/3048 Samples: 4

Title	Genes	Significant Genes (Log Ratio)	Significant Genes (Z Score)	Strain	Gene Modification	Experiment Condition	Time Point
Brucella-16M delta vjbR-GEM 4.0	2798	82	117	Brucella melitensis	vjbR	mutant vs wild type	
Brucella-16M-GEM 4.0	2899	45	107	Brucella melitensis	vjbR	mutant vs wild type	
Brucella-16M delta vjbR-GEM 4.0	2873	197	126	Brucella melitensis	vjbR	mutant vs wild type	
Brucella-16M-GEM 4.0	2686	94	110	Brucella melitensis	vjbR	mutant vs wild type	

16. In the workspace, you can also see a vertical green band. One you have selected the experimental conditions you want to compare, you will need to go to that green band. There is an icon called GENES. Mousing over that (A) will pop up the words that say "View Experiment Gene list. Double click on that icon, and the genes experimental conditions and genes will be loaded into PATRIC's Transcriptomics tool.

The image shows a two-step process. Step A: A red arrow labeled 'A' points from the 'GENES' icon in a left-hand menu to the 'View Experiment Gene List' page. Step B: A red arrow labeled 'B' points from the 'DETAIL' icon in the same menu to a detailed view of a gene list.

**Transcriptomics Gene List**

The gene list below provides details about gene regulation across a given set of experiments and comparisons. The gene list can be filtered based on regulation within each comparison as well as by locus tag and keyword. To learn more, see our [Transcriptomics Gene List User Guide](#).

**Filter By** Table Heatmap

**4 comparison(s)**

Source	Title	Strain
me	Brucella-16M de...	16M
me	Brucella-16M-G...	16M
me	Brucella-16M de...	16M
me	Brucella-16M-G...	16M

**2963 genes found**

Workspace View Download Tools Columns Help

Add Feature(s) FASTA DNA FASTA Protein Pathway Summary Multiple Seq Alignment MAP IDs to...

Show/Hide Default User Guide

RefSeq Locus	Gene Symbol	Product Description	Comparisons	Up	Down
BMEI1697		virulence-associated protein E	4	2	2
BMEI1221		transposition protein, putative	3	2	1
BMEI1222		transposition protein, putative	4	3	1
BMEI1758		transcriptional regulator, LuxR autoinducer regulated fam...	4	3	1
BMEI1300	smpB	tmRNA-binding protein SmpB	3	2	1
BMEI0329		thiamine-phosphate pyrophosphorylase, putative	4	2	2
BMEI1040		tRNA-specific adenosine-34 deaminase (EC 3.5.4.33)	4	1	3
BMEI0428	mmmA	tRNA-specific 2-thiouridylylase MmmA	4	3	1
BMEI1976		tRNA-(6)A37 methyltransferase (EC 2.8.4.3)	4	3	1

Filter by Genome: [dropdown]

Filter by one or more keywords or locus tags [input field]