



Data Visualization Portal Tutorial

Authors: Justin Davis and Ana Uriarte-Acuna

Link to Data Visualization Portal

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About OSDR

GeneLab is an open-access resource that enables scientists to upload, store, share, and analyze omics data from spaceflight experiments. It facilitates information sharing, fosters innovation, and accelerates scientific discovery in space biology. By studying the effects of microgravity and space environment on DNA, RNA, proteins, and metabolites, GeneLab contributes to our understanding of biology, and advances in genomics. It provides coordinated data sets and metadata, allowing users to gain comprehensive insights and make novel discoveries. GeneLab's impact lies in its ability to facilitate information sharing, drive innovation, and ultimately expand our knowledge of how space conditions affect the fundamental building blocks of life.

About Data Visualization

OSDR has a Data Visualization portal that currently provides users the ability to interact with the processed RNA sequencing data from the OSDR database. The portal encompasses various visualization types, including Gene Expression query tables, Dendrograms, Heatmaps, Gene Set Enrichment Analysis and a range of interactive plots including Principal Component Analysis (PCA) plots, Pair plots, and Volcano plots. Each tool offers researchers flexibility to adjust parameters and explore specific aspects of the data effectively.

Metadata Dashboard

Link to Metadata Dashboard

Filters

The metadata dashboard is designed to help users narrow search results for experimental data. It provides various tools for filtering and displaying results. The main tools for filtering the studies table's results are the pie charts and the filters on the left side of the dashboard. Each section of the pie chart acts as a separate section of filters, and when a filter from the pie chart is selected the results containing that category will automatically populate in the studies table below. A user can make one selection on each pie chart to narrow results in the studies table further.



In addition to the pie charts, there are specific filters on the left side of the dashboard that can be selected to narrow down results. When selecting filters on the pie charts, both sections will be updated to show the selected filters and the studies table will be updated to show the relevant studies. When selecting filters on the sidebar, sections will be updated after clicking on the "Apply filters" button, this allows the user to select multiple filters.

By default, the "Show only studies with processed data" filter is selected. Studies with processed data have the necessary data to display the visualization plots or combine multiple studies. The user can remove this filter to display information about all available



studies in the repository.

Another tool that is provided with each individual pie chart is the crosshair located on the bottomleft of the chart. When you select the crosshair a bar graph displaying the different categories listed within the Pie chart will appear.

Filter				DETA
Apply filters		Factors	×	BETA
Clear all filters	Gr			
Show only studies with processed data		Click on a bar to select and use Apply filter button to filter studies		
Factors				
spaceflight 102		100		Tissue
ionizing radiation 36				
🗌 time 26		<u>80</u>		
genotype 25		15 60		
altered gravity 22		o La		
^				
Assay Technology Type				
rna sequencing (rna-seq) 102		مى م		
microarray 69		sand all all all all all all all all all al		
Organism	*	with all all a set and a set and a set a s		
rodent 92	Co	×		Search:
plant 34				Factor
🗌 human 19			Apply filter Close	
fruit fly 11		OSD-1 Expression data nom drosophila melanogaster Drive microarray	melanogaster	infection,spaceflight
worm 4				
^		OSD-3 Drosophila melanogaster gene expression DNA microarray changes after spaceflight.	Drosophila nan melanogaster	developmental stage,spaceflight
Tissue	C	OSO-4 Microarray Analysis of Space-flown Murine DNA microarray Thymus Tissue	Mus musculus thymus	spaceflight
other 36		Transcription profiling of rat keratinopytes		
liver 14		OSD-6 DNA microarray	Rattus norvegicus nan	ionizing radiation
seedlings 12		sualize Study		
spleen 9		abidopsis spacetlight transcriptome: a		

The bar graph is an additional way to display the number of results each category has, and when a bar is selected from the bar graph a new graph will be displayed with the subcategories included in the selected value. The below example shows the breakdown of choosing "Time" from the bar graph selection.



After selecting the desired filter from the bar graph, the user can press the "Apply filter" button to update the results within the studies table.

When a filter is selected, a red "X" will also appear next to the crosshair of the associated pie chart. Pressing the red "X" button will clear the selected filters.



The "Clear all filters" button at the top left can be used to remove all selected filters at once.

Studies Table

Below the pie charts is a table that lists the studies resulting from the selected filters from above. The table includes the following information for each study: OSD, Title, Assay, Organism, Tissue, and Factor.

Show	w 10 v entries									
•	OSD 🕴	Title	Assay	Organism 🗧	Tissue	Factor				
0	OSD-1	Expression data from drosophila melanogaster	DNA microarray	Drosophila melanogaster	whole organism	infection.infection.term accession number,infection.term source ref.spaceflight.spaceflight.term accession number.spaceflight.term source ref,				
	OSD-3	Drosophila melanogaster gene expression changes after spaceflight.	DNA microarray	Drosophila melanogaster		developmental stage.developmental stage.term accession number.spaceflight.spaceflight.term accession number.spaceflight.term source ref,				
	OSD-4	Microarray Analysis of Space-flown Murine Thymus Tissue	DNA microarray	Mus musculus	thymus	spaceflight.spaceflight.term accession number,spaceflight.term source ref,				
Ο	OSD-6	Transcription profiling of rat keratinocytes exposed to a 56Fe ion beam	DNA microarray	Rattus norvegicus		ionizing radiation,				
0	OSD-7	The Arabidopsis spaceflight transcriptome: a comparison of whole plants to discrete root. hypocotyl and shoot responses to the orbital environment	DNA microarray	Arabidopsis thaliana		organism part.organism part.term accession number.organism part.term source ref.spaceflight.spaceflight.term accession number.spaceflight.term source ref,				
0	OSD-14	Response of Pseudomonas aeruginosa PAO1 to low shear modeled microgravity	DNA microarray	Pseudomonas aeruginosa		microgravity simulation,				
O Vi	OSD-15	Transcriptional and proteomic response of Pseudomonas aeruginosa PAO1 to spaceflight conditions involves Hfq regulation and reveals a role for oxygen	DNA microarray	Pseudomonas aeruginosa		spaceflight.spaceflight.term accession number,spaceflight.term source ref,				
-0						organism part.organism part.term				

By default, the studies will be listed in order of OSD-# from smallest to largest, but the order can be flipped based on each information category by clicking the title of the category twice.

Show	10 👻 entr	ies				Search:
	OSD 🔻	Title	Assay	Organism	Tissue	Factor
0	OSD- 580	Transcriptional profiling of heart tissue from mice flown on the RRRM-2 mission	RNA Sequencing (RNA-Seq)	Mus musculus	Heart.heart right ventricle	age,euthanasia location.spaceflight.spaceflight.term accession number.spaceflight.term source ref,
0	OSD- 548	Balancing apelin and angiotensin-II signaling to reduce heart injury during weightlessness	DNA microarray	Mus musculus	cardiac muscle tissue	hindlimb unloading,
0	OSD- 547	Whole gene expression data from osteocyte-like cell line MLO-Y4 under large gradient high magnetic field (LG-HMF)	DNA microarray	Mus musculus	Cells	altered gravity,
0	OSD- 546	SCD – Stem Cell Differentiation Toward Osteoblast Onboard the International Space Station	DNA microarray	Homo sapiens	Cells	spaceflight.spaceflight.term accession number.spaceflight.term source ref,treatment,
	OSD- 542	Effects of 14 days of confinement on blood gene expression profiles in men	DNA microarray	Homo sapiens	Whole Blood	time,
D	OSD- 539	Transcriptomic response of bioengineered human cartilage to parabolic flight microgravity is sex-dependent	RNA Sequencing (RNA-Seq)	Homo sapiens	human engineered cartilage	sex.sex.term accession number.treatment,
0	OSD- 519	PUCHI represses early meristem formation in developing lateral roots of Arabidopsis thaliana	RNA Sequencing (RNA-Seq)	Arabidopsis thaliana		genotype.genotype.term accession number.genotype.term source ref.organism part.time.time.term accession number.time.term source ref.time.unit.treatment.
Vi	OSD- 514	Artificial gravity partially protects space-induced neurological deficits in Drosophila melanogaster	RNA Sequencing (RNA-Seq)	Drosophila melanogaster	head	altered gravity.sex.sex.term accession number.spaceflight.spaceflight.term accession number.spaceflight.term source ref,
						spaceflight.spaceflight.term

Finally, once a user has selected a study or multiple studies, they can press the "Visualize Study" button to be directed to the data visualization tools. A user may also select multiple studies to visualize simultaneously in which case a user will be directed to a Multi-Study preview page before being directed to the data visualization tools.

Single Study Visualization Portal

When a user has selected one study to visualize, they will be directed to the data visualization portal. The following plots are available for each study:

- PCA plot
- Pair plots
- Volcano plot
- Heatmap
- Interactive Differential Gene Expression (DGE) table
- Gene Set Enrichment Analysis (GSEA) plots:
 - Normalized Enrichment Score (NES) Table
 - Enrichment Score Plot
 - o Normalized Enrichment Score (NES) Plot
 - o Dot Plot
 - o Ridge Plot
 - Network Plot



Sidebar Functions

A sidebar of helpful tools is provided on the left side of the screen.

GeneLab Visualization						
OSD-173						
Study details						
K						
Home						
PCA						
Volcano						
Pair plot Group 1						
Pair plot Group 2						
Heatmap						
DGE						
GSEA						

The "Study details" button is located at the top of the sidebar. This button pulls up a display with the study information including a small description.

GeneLab Visualization	Open Science for Life in Space Home About - Data & Tools - Research & Resources - Working Groups - Help - EETA
OSD-173 Study details Home PCA Volcano Pair plot Group 1 Pair plot Group 2	OSD-173 PCA Samples 2D O 3D X: PC1 v y: PC2 v z: PC3 v Color by factor: all v Update Mmus_C57-6CR_LVR_GC_Rej v Mmus_C57-6CR_LVR_GC_Rej v Mmus_C57-6CR_LVR_GC_Rej v % Difference Color Threshold: 20 Update
Heatmap DGE GSEA Group Selection Group 1: Ground Control Group 2: Space Flight	Studies Samples PC3 STS-135: Mouse Liver Transcriptomics using RNA-Sea Organism Assay Type Release Description OSD-173 Organism Assay Type Release Description OSD-173 Organism Assay Type Release Description OSD-173 Organism Assay Type Release Description Max_musculus (RNA-Sea) Old Harper Female C578L/RCR mice were flown onboard 5T5-135 for 13 Old Harper OSM 1M 1.5M Metuae C57-6CB_LVR_GC_Rep1_G40
Modify groups	OSD-173 Volcano C) OSD-173 Pair plot Group 2 C) Y axis: -Log10(Adj P val) × Adj P val threshold: 0.05 ILog2 FC] threshold: 100 Update Mmus_C67-6CR_LVR_FLT_Re × Mmus_C67-6CR_LVR_FLT_Re × % 25 • Log20 t. 41 and -Log10 Adj P > 1.30 20

The display also includes a tab labeled "Samples" that a user can press to see the individual samples and additional information for the study.

GeneLab Visualization	GeneLab Open Science for Life	in Space Home About - Data & Tools -	Research & Resources	 Working Groups 	+ Help + BETA
OSD-173 Study details		OSD-173 PCA	~ E	3	OSD-173 Pair plot Group 1 ^ []
Home PCA Volcano Pair plot Group 1	O 2D O 3D X: PC1 ✓	Y: PC2 V Z: PC3 V Color by factor: all Studies Samples	Vpdate	Sampl	C_Rej V Mmus_C57-6CR_LVR_6C_Rej V eshold: 20 Update
Pair plot Group 2 Heatmap DGE GSEA		Factors: spaceflight, all Number of samples: 6 Number of genes:	Data normalization and t using DESeq2	DGE analysis were done	z ² = 0.9760
Group Selection		Sample name	spaceflight	all	_
Group 1: Ground Control	PC3	Mmus_C57-6CR_LVR_FLT_Rep1_F58 Mmus_C57-6CR_LVR_FLT_Rep2_F64	Space Flight	Space Flight	•
Group 2: Space Flight		Mmus_C57-6CR_LVR_GC_Rep1_G40	Ground Control	Ground Control	:
		Mmus_C57-6CR_LVR_GC_Rep2_G44	Ground Control	Ground Control	0.5M 1M 1.5M
		Mmus_C57-6CR_LVR_VIV_Rep1_V14 Mmus_C57-6CR_LVR_VIV_Rep2_V9	Vivarium Control	Vivarium Control	C57-6CR_LVR_GC_Rep1_G40
					-173 Pair plot Group 2 ^ []
	Y axis: -Log10(Adj P val)	Adj P val threshold: 0.05 [Log2 FC	threshold: 1.00	Samp Mmus_C57-6C % Difference C	California Contraction Contrac
Modify groups	(146 25	 Log2fc < -1 and -L 	og10 Adj P > 1.30	264	





Below the study details button is a label for each individual plot provided for a user within the data visualization tool. Clicking these labels will automatically direct the user to the plot associated with the label.

At the bottom of the sidebar is the default Group selection that is utilized for each plot. This groups represent the factor values used on the pairwise comparisons displayed on, or used to filter the Volcano plot, Pair plots, Heatmap, DGE table and GSEA.

For example, if Group 1 is Ground Control and Group 2 is Space Flight:

- Volcano plot will display the Log2 Fold Change and P value between Ground Control samples and Space Flight samples.
- Pair Plot Group 1 will only display Ground Control samples.
- Pair Plot Group 2 will only display Space Flight samples.
- Heatmap will use Log2 Fold Change and Adjusted P value between Ground Control samples and Space Flight samples to filter genes.

• DGE table will display Log2 Fold Change, P value and

Adjusted P value between Ground Control samples and Space Flight samples.

- GSEA will be performed using only Ground Control and Space Flight samples.
- PCA will not change based on group selection because it is calculated using data from all samples.

A user can modify the groups that are selected by pressing the "Modify Groups" button. This button will open a modal displaying the options for the first group.

GeneLab Visualization	Cpen Science for Life in Space Home About - Data & Tools - Research & Resources - Working Grou	ps + Help + BETA
OSD-173 Study details Home PCA Volcano	OSD-173 PCA	OSD-173 Pair plot Group 1 ^ [1] nples
Pair plot Group 1 Pair plot Group 2 Heatmap DGE GSEA Group Selection Group 1: Ground Control Group 2: Space Flight	Group Selection To display valid group comparisons, select an option for the first group. Group 1 # spaceflight © Ground Control © Space Flight © Vivarium Control	× === 0.3763
Modify groups	Close Update group se OSD-173 Volcano ^ [3] Y axis: -Log10(Adj P val) ~ Adj P val threshold: 0.05 Log2 FC threshold: 1.00 Mmus_C57 % Difference	0.5M 2M 1.5M
would groups	25 Log2fc < -1 and -Log10 Adj P > 1.30	

After the user has selected an option, valid options for the second group will be displayed.

GeneLab Visualization	Open Science for Life in Space Home About - Data & Tools - Research & Resources - Working Groups - Help - EBETA
OSD-173 Study details	OSD-173 PCA ACC OSD-173 Pair plot Group 1 ACC
Home	2D • 3D x; PC1 ··· y; PC2 ··· z; PC3 ··· Color by factor; all ··· Update Samples
PCA Volcano Pair plot Group 1	Group Selection X Teshold: 20 Update
Pair plot Group 2 Heatmap DGE	Only valid group comparisons are displayed, to modify please undo your Group 1 selection.
GSEA	# spaceflight
Group Selection	PC3 Group 2
Group 2: Space Flight	# spaceflight O Vivarium Control
	O Ground Control 0.5M 1M 1.5M C 57-6CR LVR SC Rep1 640
	Close Update group selection -173 Pair plot Group 2
	Y axis: -Log10(Adj P val) Adj P val threshold: 0.05 ILog2 FCj threshold: 1.00 Samples Update Mmus_C57-6CR_LVR_FLT_Re Mmus_C57-6CR_LVR_FLT_Re Mmus_C57-6CR_LVR_FLT_Re % Difference Color Threshold: 20 Update
Modify groups	25 • • Log2fc < -1 and -Log10 Adj P > 1.30

Once the user has selected an option for both groups, the Update group selection button can be used to update the plots.

GeneLab Visualization	Open Science for Life in Space Home About + Data & Tools + Research & Resources + Working Groups + Help + [BETA]
OSD-173 Study details	OSD-173 PCA AC OSD-173 Pair plot Group 1 AC
Home PCA Volcano	Subject Subject
Pair plot Group 1 Pair plot Group 2 Heatmap	Group Selection ×
DGE GSEA	Group 1 # spaceflight
Group Selection Group 1: Ground Control	PC3 Space Flight Group 2
Group 2: Space Flight	# spaceflight Image: Ground Control 0.5M
	Close Update group selection
	USD-173 Volcano USD-173 Pair plot Group 2 CI Y axis: -Log10(Adj P val) Adj P val threshold: 0.05 [Log2 FC] threshold: 100 Samples
	Update Mmus_C57-6CR_LVR_FLT_Re V Mmus_C57-6CR_LVR_FLT_Re V % Difference Color Threshold: 20 Update
Modify groups	25 • Log2fr < -1 and -Log10 Adj P > 1.30

A feature exclusive to multi-study visualization is the option to download the combined Differential Gene Expression table.

DGE stands for Differential Gene Expression and represents the number of sequence reads that originated from a particular gene. The higher the number of counts, the more reads associated with that gene, and the assumption that there was a higher level of expression of that gene in the sample.

Plotly

Plotly is a third-party software that is using data provided by GeneLab to create the interactive visualizations displayed. At the top-right corner of each plot will be options to help a user better visualize the data.



The house icon within the options will reset the axes of the plots back to default. Users are also provided the option to zoom in/out on each plot as well as auto-scale the graphic. There are two tools provided for data point selection, which are the lasso tool and box tool. Each of these tools provides a shape that will select any data points that fall within them. Lastly, there is a download button in the shape of a camera that will let you download the plot as a PNG file.



PCA Plots

Link to read about PCA plots

PCA stands for Principal Component Analysis, and this type of plot is used to reduce the dimensionality of large sets of data to simplify the process of analyzing the data points.



Each PCA plot will include options for a 2D and 3D representation of the data. The default selection is a 3D representation on an "X", "Y", and "Z" axis.

• In the upper left corner of the plot area select the "2D" button and then press "Update." The graph will update to display the data on an "X", and "Y" axis only.



The "Color by Factor" feature allows users to select a specific factor from the study for representation on the graph to allow for an easier comparison between differences in the data.

- Select the "Color by Factor" drop down menu.
- Within the drop-down menu select one factor, then press the "Update" button. In this example, the "spaceflight" factor was selected from the drop down.



The results will now be represented by colors matching the factor that was selected.

In this example, (OSD-321) the colors are representing the different spaceflight conditions from the experiment and clearly shows how it could be a factor in the differences between the data points.

Another feature within the PCA plot tool allows users to hide factors by selecting the label located on the right side of the plot.

The labels provided represent the factor values corresponding to each sample. Click on the label "Space Flight & Wild Type" and the data points will be hidden as shown below:



• Click on the label a second time and the data will return.

Pair Plots

Link to read about Pair Plots

Pair plots are used for Exploratory Data Analysis, where the plot visualizes the data in order to find a relationship between variables that can be continuous or categorical. A Pair plot is used to understand the best set of features to explain a relationship between two variables or to form the most separated clusters. It also helps to form some simple classification models by drawing some simple lines or make linear separation in a dataset.

The default display for the pair plot will be the comparison between two sets of data with a % difference color threshold of 20%. Two plots will be displayed on the dashboard for the ability to compare multiple sets of data simultaneously.



Within the plot, users have the ability to change the % difference color threshold. Below is an example of the color threshold being altered to 37%.



Clicking each of the drop-down menus will allow user to change the samples displayed. By default, the pair of samples with the lowest correlation coefficient is displayed.



Users also have the capability to view different data correlations by clicking the green "Samples" button at the top of the plot. Clicking this button will change the dropdown to show multiple correlation coefficients for a set of data. When clicking "Update" the plot will show the pair of samples with the selected correlation coefficient.



Volcano Plots

Link to read about Volcano Plots

A volcano plot is useful for identifying events that differ significantly between two groups of experimental subjects. The name volcano plot comes from its resemblance to a volcanic eruption with the most significant points at the top, like spewed pieces of molten lava. Each point on the graph represents a gene. The log2-fold differences between the groups are plotted on the x-axis and the -log10 P value differences are plotted on the y-axis. The horizontal dashed line represents the significance threshold specified in the analysis, usually derived using a multiple testing correction.

The default display for Volcano Plots will have the -Log10(Adj P Value) with and Adj P Value threshold of 0.05 and a Log2 FC threshold of 1.00 as shown below.



Users have the ability to change the type of data displayed on the Y axis, and the options from the dropdown menu include "P Value, Adjusted P Value, and -Log10(P Value)". Below is an example of the "P value" display for a volcano plot.



The ability to change the P value threshold is available and the image below shows a P value threshold increase to 0.5.



Heatmap

Link to read about Heatmaps

Heatmaps allow researchers to quickly and easily identify patterns of gene expression that are associated with specific conditions or treatments and uses color coding to indicate the magnitude of values. By measuring the number of RNA molecules produced by genes in a particular sample, researchers can determine the level of gene expression. The default settings for the heat map are shown in the image below. The heatmap links genes depending on how alike they are based on the conditions set in the experiment.



- **Choosing Clustering Method:** Users can select a clustering method to display results. The default is set to UPGMA (Unweighted Pair Group Method with Arithmetic Mean). Clustering helps group genes with similar expression profiles, making patterns more apparent.
- **Toggling Rows and Columns:** Users can toggle off rows or columns of genes. This affects how the heatmap links genes based on similarity. Toggling off rows or columns can help focus on specific groups of genes and their expression patterns. The following example shows the heatmap with clustered columns but not rows.



- **Log2 Transformation:** The Log2 transformation is available to enhance the display of genes with more pronounced differences. Applying Log2 transformation can reveal subtler variations in gene expression between conditions.
- **Filtering by Significance:** Users can filter the genes displayed on the heatmap based on their significance. By default the heatmap shows only the genes with an Adjusted P Value < 0.05 for the selected group. This filtering helps highlight genes with statistically significant expression changes. If the study has no genes with an Adjusted P Value smaller than the value entered, an error message will be displayed saying "No genes passed through the filtering condition". The user can modify the value and Update the plot.

DGE Table

Each study will have an associated Differential Gene Expression (DGE) table available that includes information on each individual sample from the study.

OSD-4 [DGE			0
			Maximum p-value:	
		Maxi	mum adjusted p-value: 0.0	5
Copy CSV Excel PDF Print			Search:	
ENSEMBL	Symbol	LOG2FC	PVAL	ADJP
Search ENSEMBL	Search Symbol	Search LOG2FC	Search PVAL	Search ADJP
ENSMUSG0000066245[ENSMUSG0000081857 ENSMUSG0000031167 ENSMUSG00000114277 ENSMUSG00000099875	nan	-1.3838068496	2.6290334586299503e-08	0.0008068807918803
ENSMUSG00000066245[ENSMUSG00000081857 ENSMUSG00000031167 ENSMUSG00000114277 ENSMUSG00000099875	nan	-1.3046175841	4.5386477212306204e-08	0.0008068807918803
ENSMUSG00000066245[ENSMUSG00000081857 ENSMUSG00000031167 ENSMUSG00000099875	nan	-1.4090674464	9.732537739171061e-08	0.0011535003728465
ENSMUSG0000029657	Hsph1	1.8926726769	7.76553908509728e-07	0.0069027876927429
ENSMUSG00000021270[ENSMUSG00000083899[ENSMUSG00000082896	nan	1.018205293	1.41949943664704e-06	0.0100943443938844
ENSMUSG00000021270[ENSMUSG00000083899[ENSMUSG00000082896	nan	0.8799615852	3.25203368654189e-06	0.0192715516264473
ENSMUSG00000035126	Dnai4	0.9467218001	4.20228761165586e-06	0.0213452197600051
ENSMUSG00000021270[ENSMUSG00000083899]ENSMUSG00000082896	nan	0.8510760275	5.4094536827111705e-06	0.0214875220088584
ENSMUSG00000020917	Acly	1.2295847543	5.4389610214795095e-06	0.0214875220088584
ENSMUSG00000034855	Cxcl10	1.4988720017	6.81805846185027e-06	0.0242422886669548
		100000	BVAL	+
ENSEMBL Showing 1 to 10 of 11 entries (filtered from 35,556 total entries)	зутво	LUGZPC	Previous	1 2 Next

To export a Differential Gene Expression (DGE) table from the study visualization page, follow these steps:

- Locate the DGE Table: Scroll down to the bottom of the study visualization page. There, you'll find the Differential Gene Expression table containing valuable data.
- **Copy the Table to Clipboard:** Identify the "Copy" button within the DGE table. It should be prominently displayed. Click the "Copy" button. This action will copy the entire table, including all data, headers, and values, to your device's clipboard.
- Save as CSV, Excel, PDF, or Print: To save the data in various file formats, look for the corresponding buttons.
 - *For a CSV file:* Locate and click the "CSV" button. This will prompt a download of the DGE table data in CSV format to your device.
 - For an Excel file: Look for the "Excel" button. Click it to initiate the download of the DGE table data in Excel format (XLSX) to your device.
 - *For a PDF file:* Find and select the "PDF" button. This action will convert the DGE table into a PDF file that you can save to your device.
 - *For Printing:* Spot the "Print" button. Clicking this will open a new window displaying a printer-friendly version of the DGE table. You can then use your browser's print functionality to print the table directly.

By following these steps, you can export the Differential Gene Expression table data from the study visualization page in a variety of formats. Choose the method that best suits your needs to access and analyze the DGE data efficiently.

GSEA

Link to read about GSEA

GSEA stands for gene set enrichment analysis, a method to identify gene groups that are overrepresented in a large gene set. It uses statistics to pinpoint significantly enriched or depleted gene classes.



On the Gene Lab Visualization Portal, you'll find a dedicated GSEA section for each study. Within this GSEA section, there are various parameters you can customize:

- **Choose Gene Sets:** Opt for the gene sets to filter from. The default is "KEGG 2019".
- **Permutations:** Decide on the number of permutations you desire and whether they're based on phenotypes or gene sets. The default is 300.
- **Gene Number Range**: Adjust the minimum and maximum gene sizes. Increasing the minimum size omits genes with fewer than 15 data points, same for the maximum size.

- Weighted Score Type: Defaults to one, representing the t-test. Alternatively, choose signal-to-noise, fold change, or log2 fold change.
- **Statistical Method:** Select your preferred statistical method. The default is the t-test.

To update the plot with your changes, simply click "Update." A range of plot types is available:

• **NES Table:** View different gene sets in a table format. Export this table using the options at the top. The table includes the Enrichment Score (ES), Normalized Enrichment Score (NES), P value (PVAL), False Discovery Rate (FDR), Gene set size, Matched size and genes for each resulting gene set.

	OSD-173 GSEA ^ 🖸																
Gene sets:	MSigDB_Halln	nark_2	020		Ƴ Permu	tations: 300	Permuta	tion type: Ge	ene set	✓ Min size: 15							
Max size:	500	Weigl	hted score type:	1 ~ N	lethod: T test	~	Update										
Plot type:			Copy	Excel PDF	Print					Search:							
Enrichme NES Plot	ment Score Plot ot		TERM	ES	NES	PVAL	FDR 0	GENESET SIZE	MATCHED SIZE	GENES							
 Dot Plot Ridge Plot 	ot		Adipogenesis	-0.5374929471	-1.9959665689	0	0.0040045767	200	192	COL15A1;STOM;ATP1B3;ESYT1;TALDO1;TKT;PTG							
NetworkGSEA Inf	EA Info	Network Plot		Allograft Rejection	0.4889066332	1.7143450447	0	0.034965035	200	133	ITGB2;CD86;STAT1;MMP9;FLNA;IL16;EGFR;ITK;(
			Bile Acid Metabolism	-0.5693107907	-2.0060311559	0	0.0042906178	112	103	NR0B2;ABCA2;ALDH8A1;SLC29A1;ABCA3;ABCD							
				Fatty Acid Metabolism	-0.6922610371	-2.4173214531	0	0	158	136	SMS;NTHL1;FASN;HSPH1;ERP29;KMT5A;GLUL;E						
								Interferon Alpha Response	0.6803133399	2.2187139719	0	0	97	87	TRIM14;MOV10;DHX58;LY6E;TMEM140;IRF9;IRF		
				Interferon Gamma Response	0.5697208182	2.0420931068	0	0.0018731269	200	171	TRIM14;CSF2RB;RNF213;CIITA;IL10RA;CD86;ST/						
					Myc Targets V2	-0.6703000137	-2.0467858467	0.0062893082	0.0047673532	58	56	MCM5;RABEPK;TCOF1;RRP9;AIMP2;DUSP2;PRM					
										Oxidative Phosphorylation	-0.5962237175	-2.1113286881	0	0	200	179	MRPL34;CYB5R3;MRPS12;RHOT2;BAX;NQO2;M
								Pperoxisome	-0.5642496456	-1.8356085691	0.0136986301	0.0100114416	104	86	IDE;ABCB9;ABCD1;ABCC5;ERCC1;DHRS3;PEX6;		
			Xenobiotic Metabolism	-0.4425480191	-1.5979653154	0.0071942446	0.0453579601	200	176	DHRS1;GCNT2;ACP2;CRP;COMT;CNDP2;BCAR1;							
			TERM	ES	NES	PVAL	FDR	GENESET SIZE	MATCHED	GENES							

• **NES Plot:** The default plot displays normalized enrichment scores based on gene sets. The number of gene sets displayed can be modified by adjusting the number under "Number of gene sets" under the plot options. By default, the gene sets with an FDR bigger or equal to 0.25 are displayed in red while the gene sets with an FDR smaller than 0.25 are displayed in blue. FDR indicates the likelihood that a result is valid, e.g., FDR of 0.25 means a 25% chance of validity. This threshold can also be modified.

In the example below the plot has been modified to show only the first 10 gene sets ordered by ascending NES and gene sets with an FDR smaller than 0.50 are displayed in blue.



• **Dot Plot:** Similar to NES Plot, it showcases the top gene sets sorted by NES and filtered by FDR. The FDR threshold for gene sets to be displayed can be modified by adjusting the number under "Maximum FDR". The size of each dot represents the gene ratio. The color of each dot represents its FDR, blue being the lowest value and red being the highest.



• **Enrichment Plot:** This reveals the fold change distribution of the top gene sets with an FDR of under 0.25. As with previous plots, the number of gene sets displayed, and FDR threshold can be modified. The color of each plot represents

the FDR value for the gene set, blue being the lowest value and red being the highest value.



 Network Plot: Allows you to visualize relationships between gene sets using a network plot. The size of each dot represents the gene set size, while the color of each dot represents the adjusted p value for the gene set (blue being the lowest value and red being the highest). As with previous plots, the number of gene sets displayed, and FDR threshold can be modified. Hover overing one dot will highlight the gene sets it is connected to.



• **GSEA Info:** For in-depth details about GSEA creation, statistics, and plot documentation.



With these steps, you can effectively navigate and utilize the GSEA section, gaining insights into gene set enrichment analysis for your study.

Multi-Study



Multi-Study analysis is an advanced tool designed for analyzing and visualizing multiple RNA sequencing studies concurrently. The multi-study page is used to initialize the parameters for data visualization of the multiple studies. Researchers can uncover intricate patterns of gene expression associated with specific conditions or treatments across a variety of experiments.

To combine studies, there are two main steps: selecting the samples and factors you wish to use and running the Differential Gene Expression (DGE) analysis. Factors are used as the groups between which differential expression is calculated.

To help you select the samples and variables to be used as factors, you will be redirected to a page containing the PCA plot for the combined studies, a table to add variables to be used as factors and a table to select samples. This page has the following components:

- Information about how studies were combined and normalized.
- PCA plot of normalized counts.
- PCA plot of unnormalized counts.
- Factor selection table: Displays each studies' values for the variables added to the table.
- Sample selection table
- Option to normalize data using a subset of samples and specific variables as factors.

Below are detailed instructions on how to effectively navigate and utilize the Multi-Study Page:

- Selecting studies for Multi-Study analysis:
 - For your initial test, let's use rodent studies as an example.
 - Start by selecting "rodent" as the organism of interest.
 - Since combining DNA microarray assays is not yet supported, ensure to filter by both "rodent" and "RNA sequencing" in the assay technology type.
 - Choose multiple different rodent studies that encompass various tissue types. For this example, OSD-101, OSD-102 and OSD-103 were selected.
 - Mark the checkboxes beside the selected studies in the studies table.
 - Click the "Visualize Study" button to proceed.

Filter	Copy	CSV E	acel PDF Print			Search	hi
Apply filters	0	SD	Title	Assay	Organism	Tissue	Factor
Clear all filters Show only studies with	OSI 47	iD- M	Rodent Research-1 (RR1) National Lab Validation Flight: Mouse liver transcriptomic, proteomic, epigenomic and histology data	mass spectrometry, Microscopy, RNA Sequencing (RNA- Seq), Whole Genome Bisulfite Sequencing	Mus musculus	Liver	spaceflight
Factors	O 48	iD- II	Rodent Research-1 (RR1) NASA Validation Flight: Mouse iver transcriptomic, proteomic, epigenomic and histology data	Microscopy,RNA Sequencing (RNA-Seq),Whole Genome Bisulfite Sequencing,Whole Transcriptome Bisulfite Sequencing,mass spectrometry	Mus musculus	Liver	dissection condition,spacefligh
spaceflight 51 dissection condition 13 preservation method 12 duration 9	OSI 49	iD- N	Multi-omic investigations of mouse liver subjected to simulated spaceflight freezing and storage protocols	mass spectrometry,RNA Sequencing (RNA-Seq),nucleotide sequencing	Mus musculus	Liver	sample preservation method,sample storage time,time o sample collection after treatment
weightlessness simulation 9	© OSI 98	iD- a	Rodent Research-1 (RR1) NASA Validation Flight: Mouse adrenal gland transcriptomic, proteomic, and epigenomic data	mass spectrometry,RNA Sequencing (RNA-Seq),nucleotide sequencing	Mus musculus,Not Applicable	Not Applicable,Adrenal glands- both sides	spaceflight
rna sequencing (ma-seq) 67	0 os	iD- e	Rodent Research-1 (RR1) NASA Validation Flight: Mouse extensor digitorum longus muscle transcriptomic and epigenomic data	RNA Sequencing (RNA-Seq),nucleotide sequencing	Mus musculus	Extensor digitorum longus- both sides	spaceflight
Organism	O OS	iD- F	Rodent Research-1 (RR1) NASA Validation Flight: Mouse eye transcriptomic and epigenomic data	RNA Sequencing (RNA-Seq),Whole Genome Bisulfite Sequencing	Mus musculus	left eye	spaceflight
rodent 67 mus musculus 64 rattus norvegicus 3	♥ OSI 101	iD- F 1 k	Rodent Research-1 (RR1) NASA Validation Flight: Mouse eft gastrocremius muscle transcriptomic, proteomic, and opigenomic data	mass spectrometry,RNA Sequencing (RNA-Seq),nucleotide sequencing	Mus musculus	NaN,Gastrocnemius-left	spaceflight
Tissue	♥ OS 102	1D- F 2 k	Rodent Research-1 (RR1) NASA Validation Flight: Mouse cidney transcriptomic, proteomic, and epigenomic data	mass spectrometry,RNA Sequencing (RNA-Seq),nucleotide sequencing	Mus musculus,Not Applicable	Not Applicable,Left kidney	spaceflight
other 16 liver 12	♥ OSI 103	iD- F 3 6	Rodent Research-1 (RR1) NASA Validation Flight: Mouse quadriceps muscle transcriptomic, proteomic, and spigenomic data	Whole Transcriptome Bisulfite Sequencing,mass spectrometry,RNA Sequencing (RNA-Seq),Whole Genome Bisulfite Sequencing	Mus musculus	Not Applicable,Quadriceps- left	spaceflight
spieen 9 skin 5 thymus 6	O OS 104	iD- F 4 8	Rodent Research-1 (RR1) NASA Validation Flight: Mouse soleus muscle transcriptomic and epigenomic data	RNA Sequencing (RNA-Seq), nucleotide sequencing	Mus musculus	Soleus-both sides	spaceflight
	Visual	lize Sti	rs selected	Assay	Organism	Tissue Previous 1 2 3 4	Factor

- Data Normalization:
 - A dialog box will appear to prompt you for data normalization options.
 - The default selection is "DESeq2" for normalization, but you can also choose "No Normalization". If normalization is chosen, the studies will be normalized by their accession number.
 - If desired, you can enter your email address to receive a notification when the studies have been combined. The email will contain a URL you can use to access the combined studies.
 - Alternatively, proceed without entering an email address.

Filtor	Cop	y CSV	Excel PDF Print					Search	h:
Apply filters		OSD	Title	Multiple RNA Se	quencing (RNA-Seq) studies	6	Organism	Tissue	Factor
Clear all filters	0	OSD-	Rodent Research-1 (RR1) National Mouse liver transcriptomic, protect	selected		ng (RNA-	Mus musculus	Liver	spaceflight
Show only studies with processed data		47	histology data	You have selected s	tudies with assay technology RNA	0			
Factors	U	OSD- 48	liver transcriptomic, proteomic, epi data	Sequencing (RNA-Seq). Would you like to normalize? Normalize using DESeq2 No normalization Combining and normalizing the data for multiple studies might take a while. If you would like to receive an email once this process is done, please enter your email address below. You can enter multiple email addresses separated by ; Instructional addresses separated by ; Instructional addresses separated by ; Instructional addresses reparated by ; Instructional reparate repa		Bisulfite	Mus musculus	Liver	dissection condition,spaceflight
spaceflight 51 dissection condition 13 preservation method 12 duration 9	0	OSD- 49	Multi-omic investigations of mou simulated spaceflight freezing and t			,nucleotide ,nucleotide	Mus musculus	Liver	sample preservation method,sample storage time,time of sample collection after treatment
weightlessness simulation	0	OSD- 98	Rodent Research-1 (RR1) NASA Vi adrenal gland transcriptomic, prote data				Mus musculus,Not Applicable	Not Applicable,Adrenal glands- both sides	spaceflight
Assay Technology Type arran sequencing (ma-seq) 67	0	OSD- 99	Rodent Research-1 (RR1) NASA V. extensor digitorum longus musc epigenomic data			-1	Mus musculus	Extensor digitorum longus- both sides	spaceflight
Organism	0	OSD- 100	Rodent Research-1 (RR1) NASA Vi eye transcriptomic and epigenomic of	data	Sequencing	Bisulfite	Mus musculus	left eye	spaceflight
rodent from the second	Q	OSD- 101	Rodent Research-1 (RR1) NASA Va left gastrocnemius muscle transcrip epigenomic data	lidation Flight: Mouse tomic, proteomic, and	mass spectrometry,RNA Sequencing (RNA-Seq) sequencing),nucleotide	Mus musculus	NaN,Gastrocnemius-left	spaceflight
Tissue	Q	OSD- 102	Rodent Research-1 (RR1) NASA Va kidney transcriptomic, proteomic, ar	lidation Flight: Mouse d epigenomic data	mass spectrometry,RNA Sequencing (RNA-Seq) sequencing),nucleotide	Mus musculus,Not Applicable	Not Applicable,Left kidney	spaceflight
other 16 liver 12	♥	OSD- 103	Rodent Research-1 (RR1) NASA Va quadriceps muscle transcriptom epigenomic data	lidation Flight: Mouse lic, proteomic, and	Whole Transcriptome Bisulfite Seque spectrometry,RNA Sequencing (RNA-Seq),Whol Bisulfite Sequencing	encing,mass le Genome	Mus musculus	Not Applicable,Quadriceps- left	spaceflight
spleen 9 skin 5	0	OSD- 104	Rodent Research-1 (RR1) NASA Va soleus muscle transcriptomic and ep	lidation Flight: Mouse	RNA Sequencing (RNA-Seq),nucleotide sequencing	9	Mus musculus	Soleus-both sides	spaceflight
5	V	isualize S	Study 3 rows selected		Assay		Organism	Tissue Previous 1 2 3 4	Factor 5 6 7 Next

Exploring the Multi-Study Page

Information about how the studies were combined and normalized and the resulting number of samples, genes and discarded genes can be displayed by clicking on the information icon next to the label "Counts were normalized using DESeq2".

OSD-101&OSD-102&OSD-103	
Multi-Study PCA Counts were normalized using DESeq2 Change normalized Counts PCA O 2D 3D X: PCI V Y: PCZ Color: dataset accession V Shape: V Size: V Undate To add more options to Color, Shape, and Size, you can add more variables to the Factor table on the right. Normalized Counts PCA Plot	Factor selection Select variables and click 'Add' to add variables to the factors table. The variables selected will be as used as factors for Differential Gene Expression Analysis. If no variables are added as factors, OSD will be used as a factor. Adding a variable to the table will automatically add it as a color option on the PCA. Factors
0 -0.1 0 0.05 0.1 0.15 0.2 0.25 0.25 PCI 97.48% FOLLOW US FOLLOW US R ⁰ Visualize Studies	CONTACTS OTHER RESOURCES NASA Official: Sylvain Costes • NASA Space Biology Program • NASA Ames Space Biosciences Division



Multi-Study PCA Plot

A PCA plot for data visualization will be included on the multi-study page. If the data was normalized, the PCA plot for normalized counts will be displayed at the top. You can use the drop-down menus to change the color, shape and size on each dot based on each sample's condition. The variables available on each drop-down menu are dynamically added when you add variables to the Factors table.



The PCA plot can be displayed as a 2D or 3D plot



You can display the PCA plot of the Unnormalized counts by clicking on the checkbox next to "Show Unnormalized Counts PCA". The unnormalized counts PCA plot has the same features as the normalized counts PCA, it can be displayed as a 2D or 3D plot and the color, shape and size of the dots can be customized.



Factor Selection for Gene Expression Analysis

The variables selected as factors will be used to group samples and calculate differential expression. The counts table will also be normalized based on these groups. For example, on the image below the user has added material type to the factors table. If the user choses to use material type as a factor, all samples with material type "Gastrocnemius-left" will be treated as one group, samples with material type "Left kidney" will be treated as a second group and samples with material type "Quadriceps-left" will be treated as a third group. DGE Analysis will then show comparisons (Fold Change, P value, Adjusted P value) between Gastrocnemius-left & Left kidney, Gastrocnemius-left & Quadriceps-left, Left kidney & Quadriceps-left.

Any characteristic, parameter or factor on the studies' metadata can be added to the table. Adding a variable to the table will also add it as an option to change the color,

size, and shape of the PCA plots. Under "Factor Selection," choose variables to generate a factors table for differential gene analysis.

Select parameters, characteristics, or factors from the dropdown list to add to the table. The factors, characteristics and parameters are retrieved from the studies metadata ISA files. More information about the ISA model and what defines a parameter, characteristic or factor can be found here <u>https://isa-specs.readthedocs.io/en/latest/isamodel.html</u>.

Factor selection Select variables and click 'Add' to add variables to the factors table. The variables selected will be as used as factors for Differential Gene Expression Analysis. If no variables are added as factors, OSD will be used as a factor. Adding a variable to the table will automatically add it as a color option on the PCA. Parameters Carcass preservation method 							
OSD	spaceflight 🗍		material type 🗍	sample preservation method $\overline{\Box}$			
OSD-101	Ground Control,Space F	light	Gastrocnemius-left	Liquid Nitrogen			
OSD-102	Ground Control,Space F	light	Left kidney	RNALater			
OSD-103	Ground Control,Space F	light	Quadriceps-left	Liquid Nitrogen			
Normalize using only selected samples and/or factors Expand table The expanded table will allow you to select the samples you want to use for the Differential Gene Expression							
Analysis. All samples are selected by default.							

The table will display the values each study contains for the added variables. If a variable is not common between studies and the information is not available on one of the studies' metadata, the table will display an empty value and it will be filled with NA for the next steps.

Factor selection Select variables and click 'Add' to add variables to the factors table. The variables selected will be as used as factors for Differential Gene Expression Analysis. If no variables are added as factors, OSD will be used as a factor.							
Adding a variable to the table will automatically add it as a color option on the PCA. Parameters Carcass preservation method. Add 							
OSD	spaceflight	material type 🗍	sample preservation method 🗍	carcass preservation method 🗍			
OSD- 101	Ground Control,Space Flight	Gastrocnemius- left	Liquid Nitrogen	Mini Cold Bag to -80C freezer			
OSD- 102	Ground Control,Space Flight	Left kidney	RNALater	Mini Cold Bag to -80C freezer			
OSD- 103	Ground Control,Space Flight	Quadriceps-left	Liquid Nitrogen				

Variables can be deleted from the table by clicking on the trash icon next to each column header.



Sample Selection for Gene Expression Analysis

Select specific samples by clicking the "Expand table" button. This will display a table with all the samples and their values for the variables added to the factors table.

OSD	Sample	spaceflight	material type	sample preservation method
Search	Search	Search	Search	Search
OSD-101	Mmus_C57- 6J_GST_FLT_Rep1_M23	Space Flight	Gastrocnemius-left	Liquid Nitrogen
OSD-101	Mmus_C57- 6J_GST_FLT_Rep2_M24	Space Flight	Gastrocnemius-left	Liquid Nitrogen
OSD-101	Mmus_C57- 6J_GST_FLT_Rep3_M25	Space Flight	Gastrocnemius-left	Liquid Nitrogen
OSD-101	Mmus_C57- 6J_GST_FLT_Rep4_M26	Space Flight	Gastrocnemius-left	Liquid Nitrogen
OSD-101	Mmus_C57- 6J_GST_FLT_Rep5_M27	Space Flight	Gastrocnemius-left	Liquid Nitrogen
OSD-101	Mmus_C57- 6J_GST_FLT_Rep6_M28	Space Flight	Gastrocnemius-left	Liquid Nitrogen
OSD-101	Mmus_C57- 6J_GST_GC_Rep1_M33	Ground Control	Gastrocnemius-left	Liquid Nitrogen
OSD-101	✓ Mmus_C57- 6J_GST_GC_Rep2_M34	Ground Control	Gastrocnemius-left	Liquid Nitrogen
OSD-101	✓ Mmus_C57- 6J_GST_GC_Rep3_M35	Ground Control	Gastrocnemius-left	Liquid Nitrogen
OSD-101	Mmus_C57- 6J_GST_GC_Rep4_M36	Ground Control	Gastrocnemius-left	Liquid Nitrogen

You can use the checkbox next the Samples table header to select all samples. The search boxes underneath each column header can be helpful to filter samples with a specific value.

OSD	Sample	spaceflight	material type	sample preservation method
Search	Search	Search	kidney	Search
OSD-102	Mmus_C57- 6J_KDN_FLT_Rep1_M23	Space Flight	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_FLT_Rep2_M24	Space Flight	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_FLT_Rep3_M25	Space Flight	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_FLT_Rep4_M26	Space Flight	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_FLT_Rep5_M27	Space Flight	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_FLT_Rep6_M28	Space Flight	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_GC_Rep1_M33	Ground Control	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_GC_Rep2_M34	Ground Control	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_GC_Rep3_M35	Ground Control	Left kidney	RNALater
OSD-102	Mmus_C57- 6J_KDN_GC_Rep4_M36	Ground Control	Left kidney	RNALater
OSD-102	✓ Mmus_C57- 6J_KDN_GC_Rep5_M37	Ground Control	Left kidney	RNALater
OSD-102	Mmus_C57-	Ground Control	Left kidney	RNALater

Use the checkbox next to each sample name to select the samples you wish to use on the next steps.

Normalize using only selected samples and/or factors:

You can choose to normalize the combined counts table using only a subset of samples and any factor (or factors) added to the factors table. The PCA plot will be updated, and this can help you make a better decision on which variables to use as factors for DGE analysis.

• Click on the Normalize using only selected samples and/or factors button. This will display a modal with the different options for normalization.

O 3D X: PC1 → Y: PC2 → Z: PC3 → Color: dataset acces		Parameters		~ carcass	preservation method	✓ Add	
Size: Size:	and/or factors	ny selected san	npies		material type 📋	sample preserv	vation method 📋
lized Counts PCA Plot	Unnormalized counts will be normalized using only the samples			pace Flight	Gastrocnemius-left	Liquid Nitrogen	
	selected in the expanded table a	nd the results will	be refelected	pace Flight	Left kidney	RNALater	
	In the PCA IDA If you haven't selected any samples in the expanded table, all samples will be used What factors do you want to use to re-normalize the counts table? (Multiple factors can be selected) © OSD (Default) © osaportlight material type = sample preservation method			pace Flight	Quadriceps-left	Liquid Nitrogen	
				ples and/or factors			
1411							
PC003				u to select the sa d by default.	e samples you want to use for the Differential Gene Expression		
to rene at the set					spaceflight	material type	sample preservation method
,		Close	Normalize		Search	kidney	Search
• 3D X: PC1 • Y: PC2 • Z: PC3 • Color: dataset access	ion Y Shape:	OSD-102	Mmus_C57 6J_KDN_FLT_	Rep1_M23	Space Flight	Left kidney	RNALater
Size: Update malized Counts PCA Plot		OSD-102	Mmus_C57 6J_KDN_FLT_	Rep2_M24	Space Flight	Left kidney	RNALater
	© OSD-101	OSD-102	Mmus_C57 6J_KDN_FLT_	'- Rep3_M25	Space Flight	Left kidney	RNALater
	 OSD-102 OSD-103 	OSD-102	Mmus_C57 6J_KDN_FLT_		Space Flight	Left kidney	RNALater
		OSD-102	Mmus_C57 6J_KDN_FLT_	Rep5_M27	Space Flight	Left kidney	RNALater
		OSD-102	Mmus_C57	-	Space Flight	Left kidney	RNALater

• Use the checkboxes to select the factor or factors you want to use to normalize. Only the samples selected on the samples table will be used.

Visualizing and Downloading Results:

Click "Visualize Studies" to proceed to visualization plots or download the counts table. A modal will be displayed with the options to continue. You can choose to download the unnormalized counts table, download the normalized counts table, or navigate to visualization plots.



If you wish to navigate to visualization plots you can choose which variables you would like to use as factors. Only samples selected on the samples table will be used. You will have the option to enter your email to be notified when the DGE analysis is ready. The email sent will contain a URL you can use to access the visualization plots resulting of the DGE analysis

• Click the continue button to perform the selected action.

Exploring Visualization Plots:

Upon completion, the page will direct you to a range of visualization plots and graphs for your data analysis.



The visualization portal will have the same plots and capabilities as the single study visualization portal.



With these comprehensive instructions, you are well-equipped to navigate the Multi-Study Page efficiently. This tool empowers you to analyze multiple RNA sequencing studies simultaneously, uncovering complex gene expression patterns and gaining valuable insights into your experimental data.

