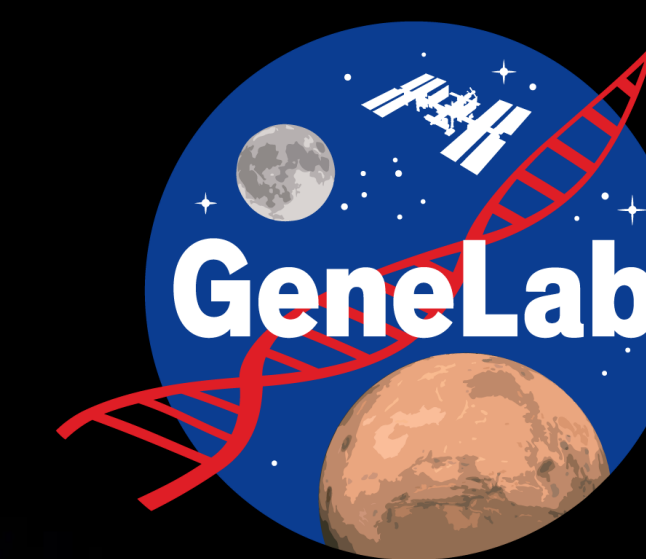




GeneLab: The NASA Systems Biology Platform for Space Omics Repository, Analysis, and Visualization



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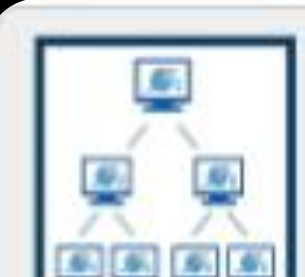
GeneLab Data and Tools

genelab.nasa.gov

- Data repository** features well-curated spaceflight and space-relevant omics datasets
 - ✓ Rich metadata
 - ✓ Unique Identifier, DOIs
 - ✓ Open, publicly available
 - ✓ Ontologies, controlled vocabulary, community standards
 - ✓ Searchable
- Environmental data** from spaceflight environments including radiation, temperature and humidity, used to support data analysis
- A data system with tools to **share, store, analyze**, and **visualize** spaceflight data
- Coming soon!** Web-based submission portal with a step-by-step workflow, defined fields and ontologies, and fast data transfer.

**Data Repository**
Search and upload spaceflight datasets

**Environmental Data**
Radiation data collected during experiments conducted in space

**Collaborative Workspace**
Share, organize and store files

**Analyze Data**
Perform large-scale analysis of biological omics data

**Visualize Data**
Interact with GeneLab processed data

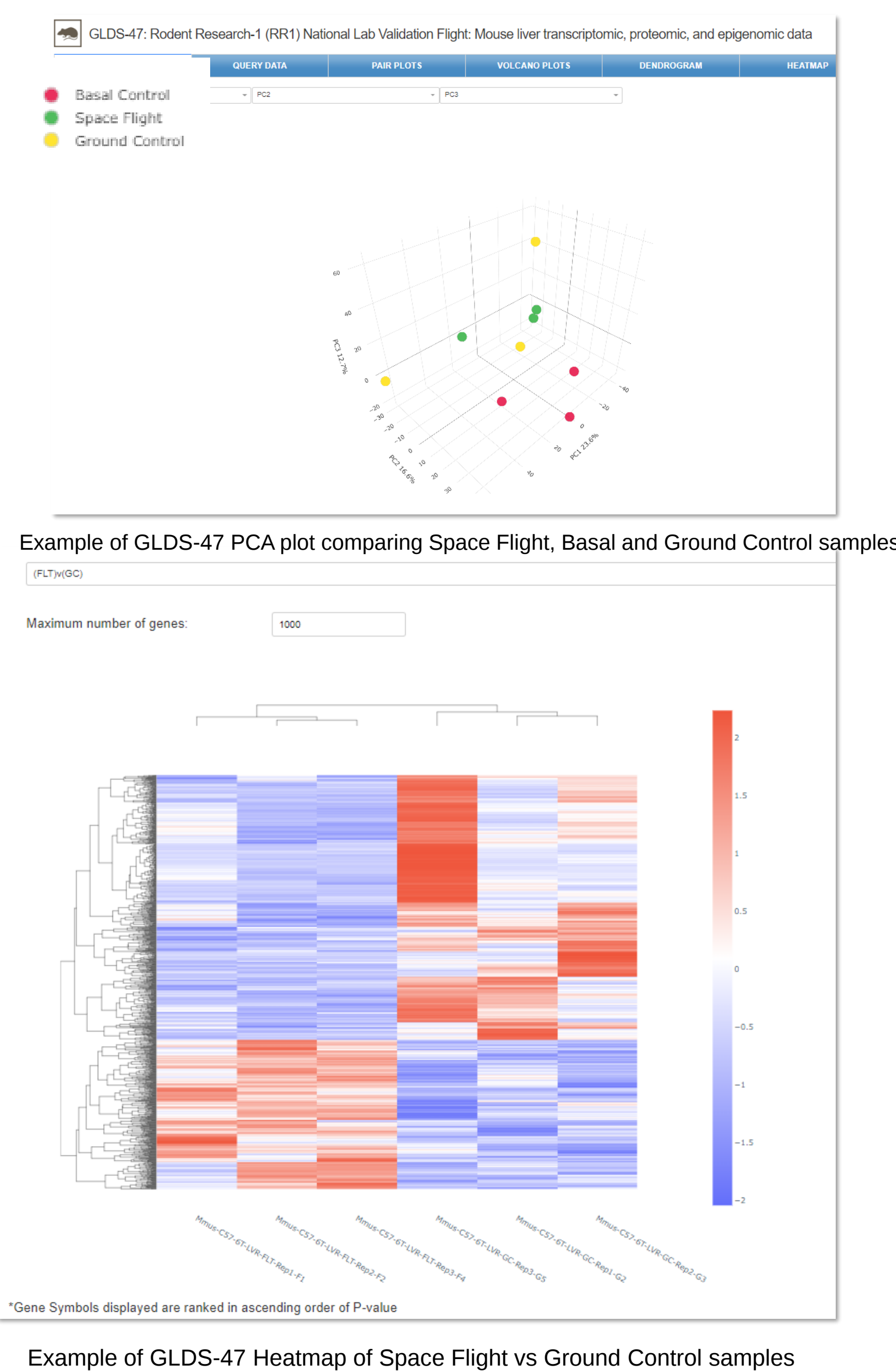
**Submit Data**
Have space-relevant data to submit to GeneLab?

Visualizing the Data

Using standardized pipelines, GeneLab provides processed data for 94 transcriptomics studies in the Data Repository. All levels of processed data are available for download in the 'Study Files' panel of the Data Repository. For transcriptomics studies, GeneLab's visualization portal pulls data from the differential gene expression tables to create interactive plots and tools to visualize the data.

Types of data visualization provided:

- PCA, Pair, and Volcano plots** used to view general similarities and differences in gene expression data between samples
- Data Query** to select and view specific gene symbols and group comparisons
- Dendrogram** shows how individual genes and samples cluster
- Heatmap** displays up- and down-regulated genes for the selected group comparison
- S-plot** used to visualize fold change differences in expression of individual genes associated with selected gene ontology terms between selected groups



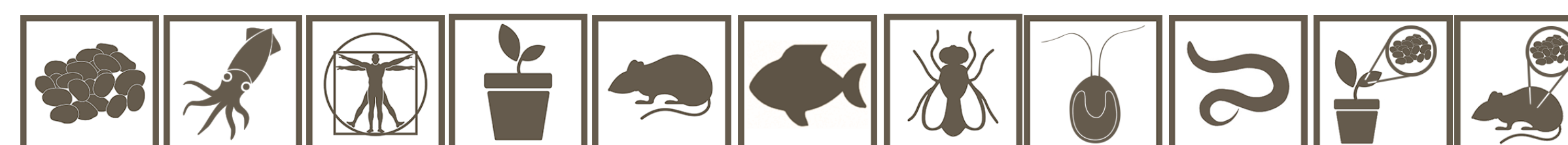
Space Omics Data Repository

<https://genelab-data.ndc.nasa.gov/genelab/projects>

240+ studies
45 species
10+ assays
115 TB

First comprehensive database for spaceflight and space-relevant experiments.

All data are publicly available and include transcriptomic, proteomic, metabolomic, epigenomic, and metagenomic studies from model organisms ranging from plants and animals to microbes.



Enter keywords in the search bar or use filters to search for data. To search across several federated databases, select NCBI GEO, EBI PRIDE, MG-RAST, or all.

☐ All ☒ GeneLab ☐ NIH GEO ☐ EBI PRIDE ☐ ANL MG-RAST

Search Filters (GeneLab Only)

Project Type

Factors

Organisms

Assay Type

Clear

☐ Ground
☒ Spaceflight
☐ Parabolic Flight Study

ions

Search results for: using filter(s): [('Project Type = Flight Study' OR 'Project Type = Flight' OR 'Project Type = Spaceflight Project' OR 'Project Type = Spaceflight Study' OR 'Project Type = Spaceflight')] Total Search Results Found: 135

Sort by Relevance 25

1 2 3 4 Next >>

Microgravity effect on C. elegans N2/VC (CERISE 8days)
<https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-41>



Microgravity effect on C. elegans gene expression was analysed by whole genome microarray. The worms were cultivated under microgravity for 8 days in the Japanese Module of the International Space Station. The samples of this study were divided three experimental groups: 1. microgravity for 8 days 2. artificial 1G control for 8 days on orbit 3. ground 1G control for 8 days This study was repeated with three biological and two technical replicates.

Organism: Caenorhabditis elegans Factor: gravity Assay Type: transcription profiling Accession: GLDS-41 PI/Contact: Akira Higashihata, To Release/Publication Date: 28-Jun-2012

Filter match(es): Project Type=Spaceflight Study, Project Type=Spaceflight, Project Type=Flight Study, Project Type=Flight.

Gene Expression Profile Changes due to Bleomycin-Induced DNA Damage in Human Fibroblasts in Space
<https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-114>



To understand gene expression responses in confluent human fibroblast in microgravity conditions to bleomycin treatment. Confluent human fibroblasts AG01522 were flown to the International Space Station (ISS). After three day on ISS the cells were treated with bleomycin at 1.0 microg/ml for 3 hours. The cells were washed and fixed with RNALater. Total RNA were isolated after the samples were returned to earth and subject to microarray analysis.

Each study contains detailed metadata, raw, and processed data files. Unique to GeneLab, spaceflight studies contain environmental data, including radiation dosimetry data, from the spacecraft.

**GLDS-243**
Version 6

DESCRIPTION

PROTOCOLS

SAMPLES

ASSAYS/MEASUREMENTS

PUBLICATIONS

STUDY FILES

VISUALIZATION

To view files, click on the folder of interest.

- All Files
- RNA-Seq
- GeneLab Processed RNA-Seq Files
- Aligned sequence data/Alignment logs
- Trimmed sequence data/FASTQ reports
- Differential expression analysis data
- Aligned sequence data
- Raw counts data
- Trimmed sequence data/FASTQ report
- Normalized counts data
- Trimmed sequence data
- Trimmed sequence data/Trimming reports
- Study Metadata Files

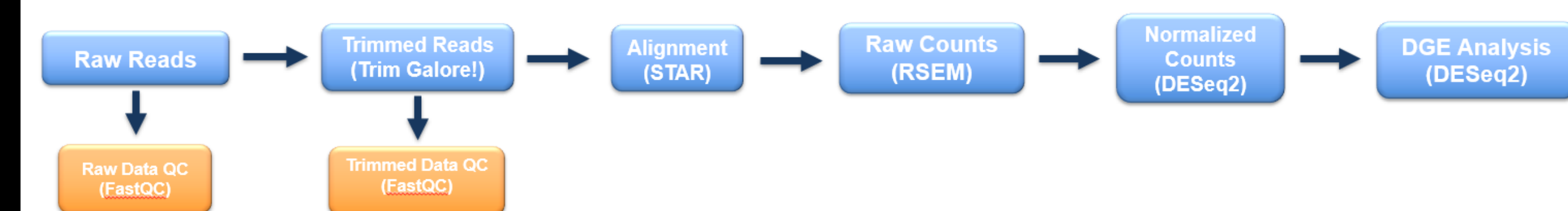
0 files selected Download Selected Files

FILES	FILE SIZE	RESOURCE CATEGORY	RESOURCE DESCRIPTION
GLDS-243_rna_seq_MRNA_C57-6T_200M_RNA_SEQ_T_1000_01_01_1000.fastq.gz	601.73 KB	Raw sequence data/FASTQ Reports	RNA-Seq

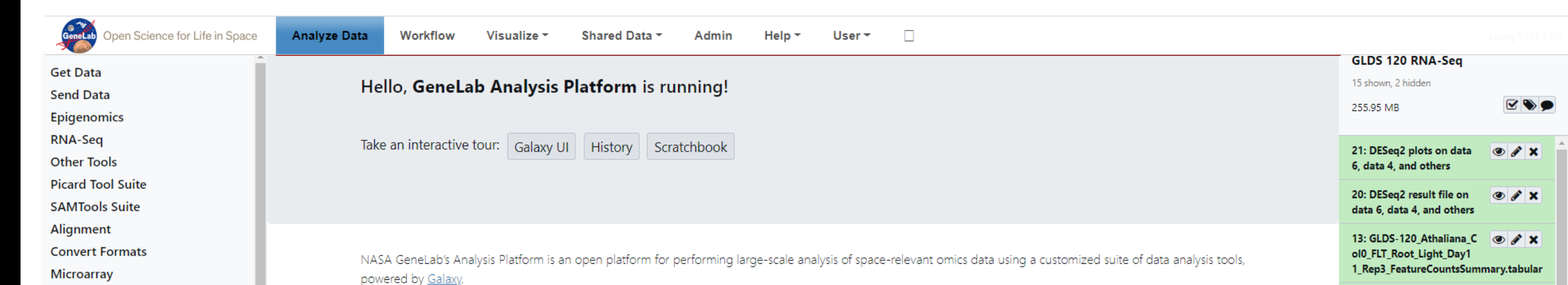
Analysis Platform

The GeneLab Analysis platform provides users with resources to analyze space-relevant omics data, including RNA-seq data.

GeneLab's RNA-seq analysis pipeline used to generate processed data:

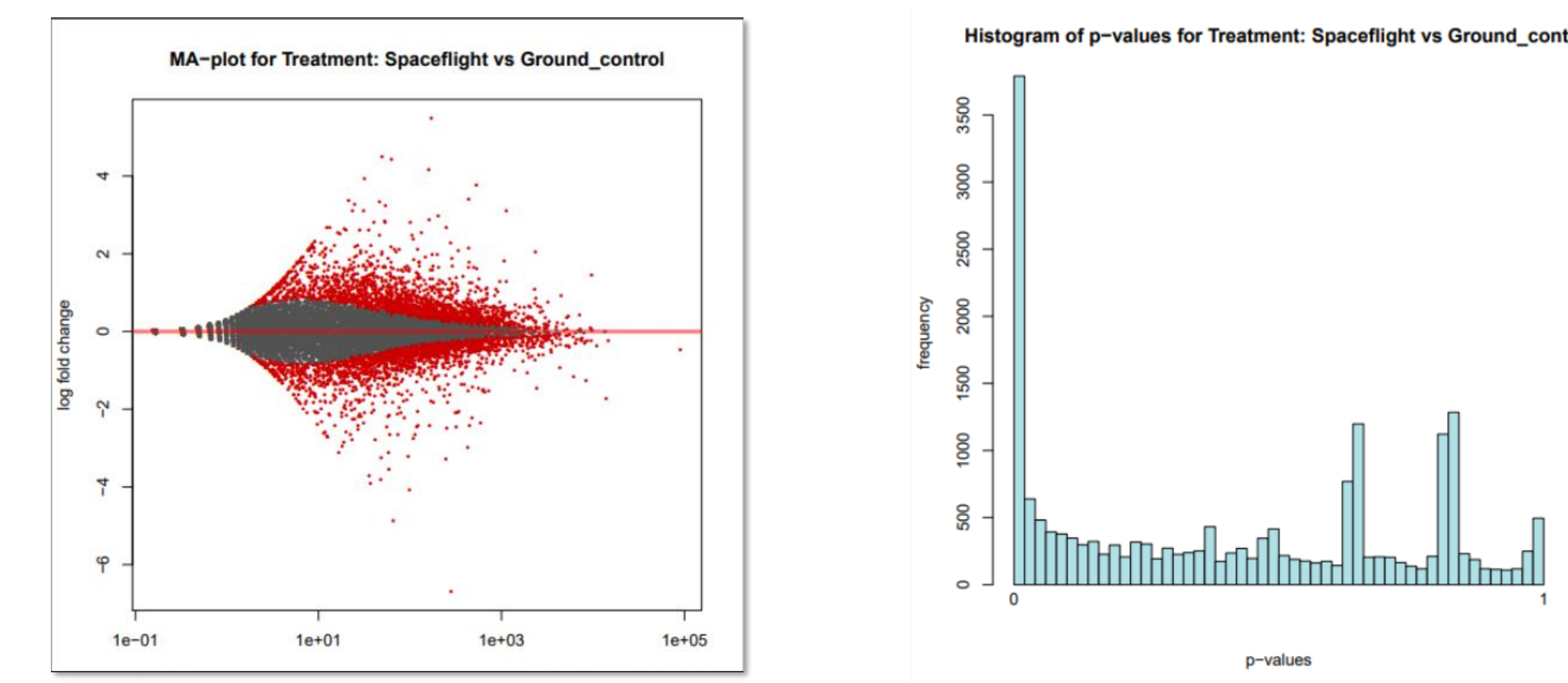


GeneLab has integrated a customized Galaxy platform, equipped with data and tools used to process omics data hosted on GeneLab. Login and follow GeneLab's tutorial to learn how to analyze RNA-Seq data from spaceflight studies.



This platform allows users to select tools, execute jobs, create custom workflows, and save all pipelines and data generated.

Example output plots from differential expression analysis of Arabidopsis samples flown in space compared to ground controls using DESeq2:



Participate in Data Analysis

Join GeneLab's Analysis Working Groups (AWGs):

- 120+ scientists** worldwide analyzing spaceflight and space-relevant omics data
- Four scientific groups: **Animals** (Mammals and Non-mammals), **Plants, Microbes, and Multi-omics**
- Open to all scientific investigators, bioinformaticians, graduate students, and postdocs interested in investigating the impacts of the space environment on living organisms
- Email:** arc-dl-genelab-awg@mail.nasa.gov

Acknowledgements

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