

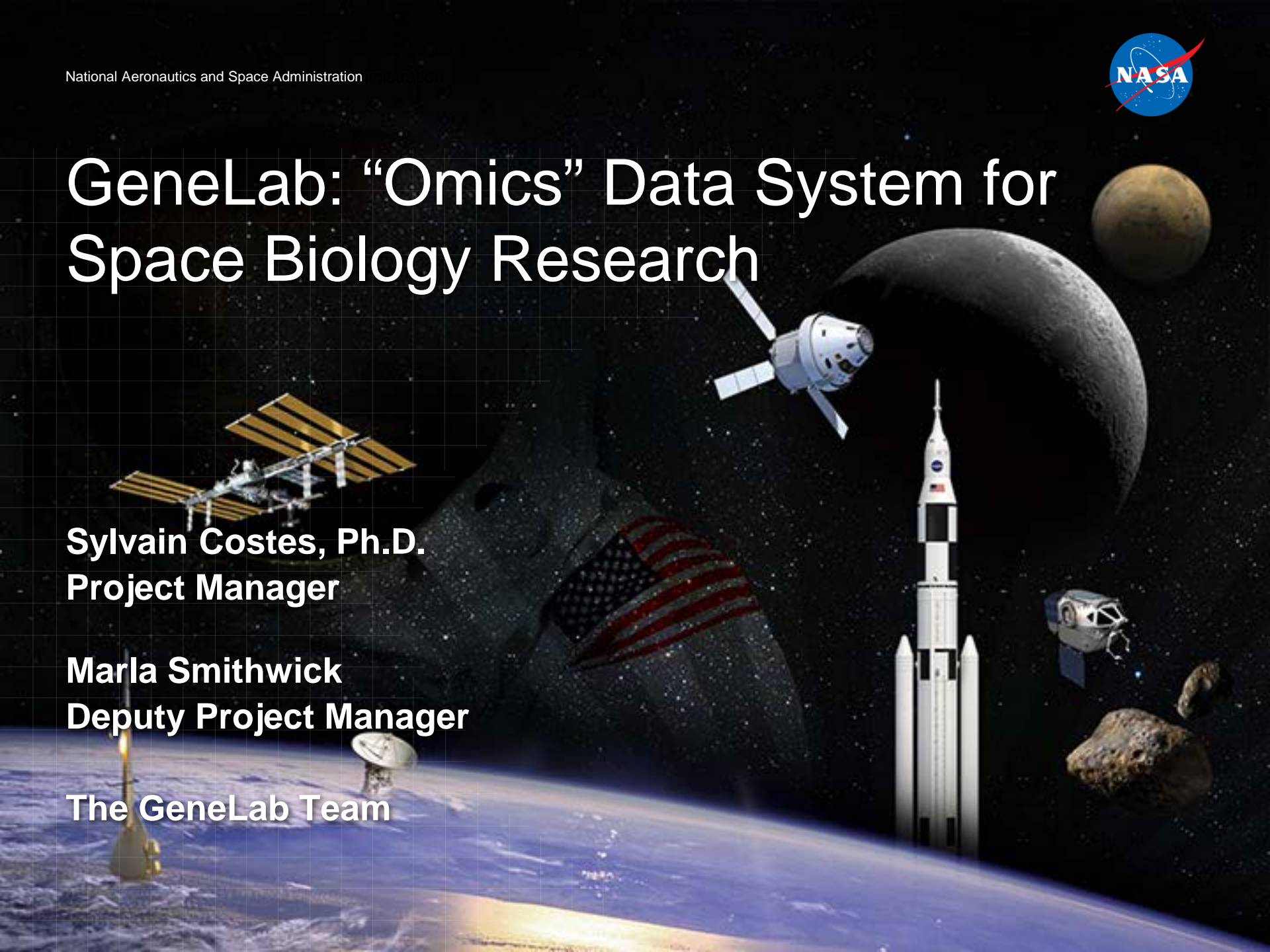


# GeneLab: “Omics” Data System for Space Biology Research

**Sylvain Costes, Ph.D.**  
**Project Manager**

**Marla Smithwick**  
**Deputy Project Manager**

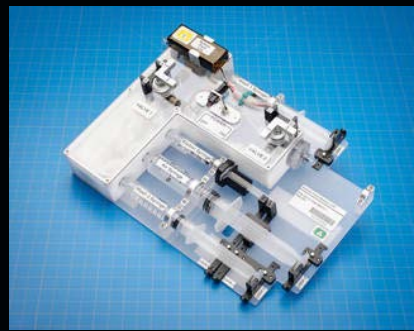
**The GeneLab Team**





# Omics Acquisition in Space is Now a Reality

This is truly an exciting time for cellular and molecular biology, omics and biomedicine research on ISS with these amazing additions to the suite of ISS Laboratory capabilities.



Sample Preparation Module

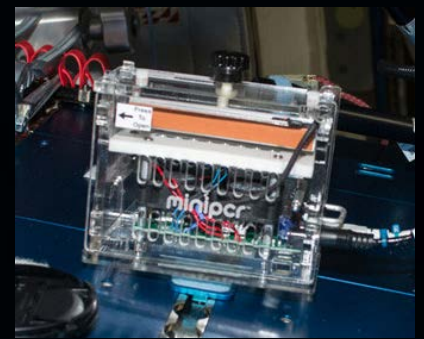


Oxford Nanopore MinION Gene Sequencer

Cepheid Smart Cycler qRT-PCR



Reaction tube containing lyophilized chemical assay bead (proprietary)



Mini-PCR

- New technologies to produce high-quality Omics data from research missions aboard the ISS
- Limited access and high demand for the ISS platform
- Facilitate systems biology to predict and/or mitigate changes due to microgravity

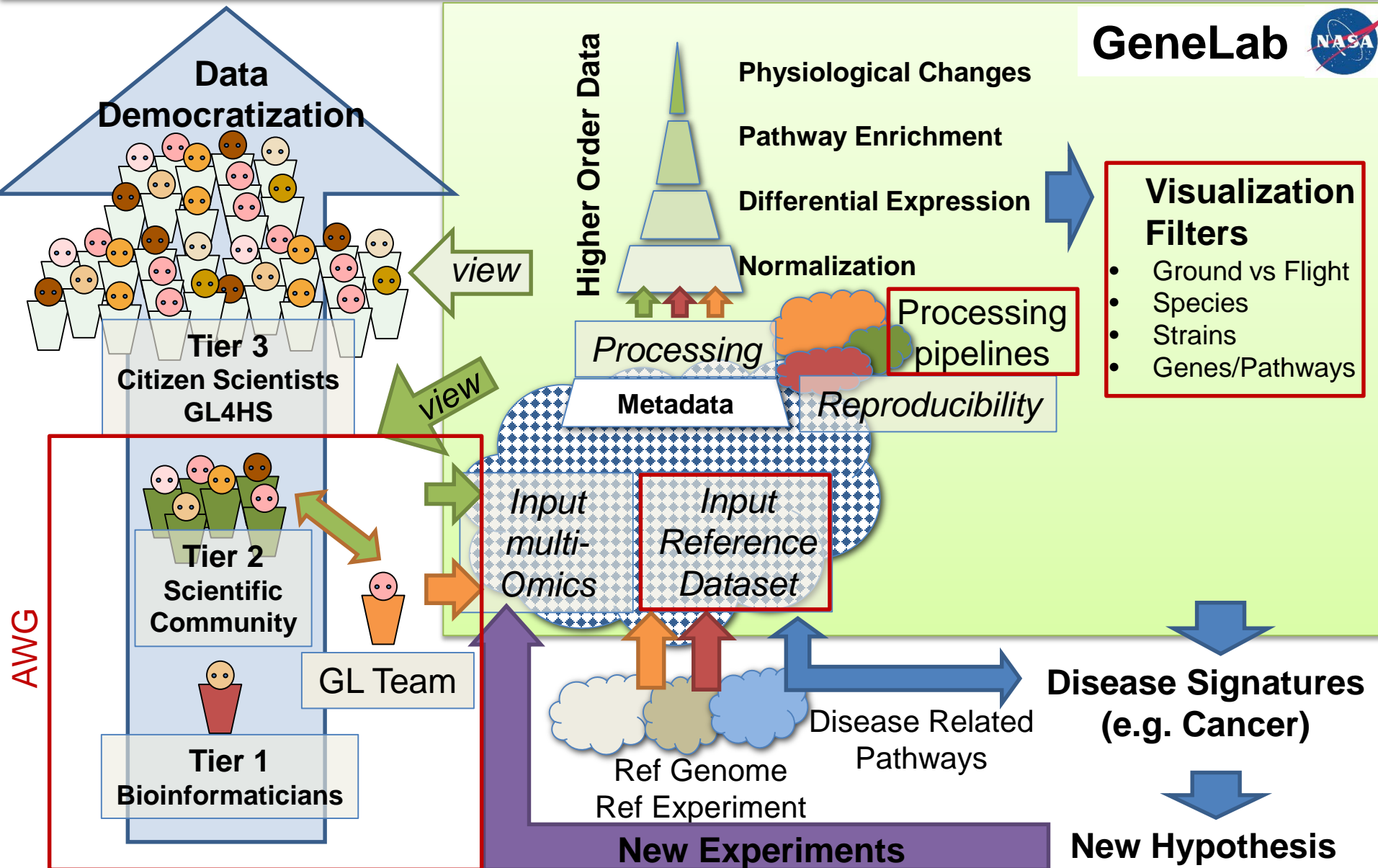


NASA astronaut Barry "Butch" Wilmore setting up the Rodent Research-1 hardware in the Microgravity Science Glovebox aboard the International Space Station.

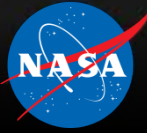
# Three-tier Client Strategy to Democratize Data



GeneLab 



# Engaging the Scientific Community



GeneLab **Analysis Working Groups (AWG)** will be tasked with analyzing all data across the GLDS with relevance to a specific domain to generate higher-order data.

## Goals:

1. Peer-reviewed publications describing AWG's comprehensive analysis.
2. Consensus data analysis pipelines relevant to AWG domains to be used on the GLDS will help domains harmonize their analyses.
  - a) Summer interns will process all data based on AWG recommendation
  - b) Processed "higher-order" data relevant to domains will be posted on the GLDS.
  - c) Strategies needed to link metadata to processed data will be put in place for the visualization portal deployment
3. Feedback for the GLDS to be used for improving its utility; test driving passed along to scientific community via the AWG
  - a) Access to galaxy toolshed and Jupyterlab GenePattern notebook within GeneLab provided with CPU and RAM AWS resources
  - b) Integration of GenomeSpace workspace with processing tools
  - c) GLDS 2.0 search query needs to be improved – What should we do different?

## AWGs emphasis:

1. Animal Group
  - a) Mammals
  - b) Non-mammals
2. Plants
3. Microbes
4. Multi-omics/Systems Biology

# GLDS Phase 2 (Release 2.0) Google-like Search, Federated Search



## Data federation/integration with heterogeneous bioinformatics external databases (GEO, PRIDE, MG-RAST)

Home Repository Data Data Mining Tools Submit Data Help Workspa

Search results for: **mouse myostatin** using filter(s):

Sort by Relevance 25

**Myostatin inactivation effects on myogenesis in vitro and in vivo**  
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE28986

Key words: dystrophin, mdx mouse, Duchenne, fibrosis, dystrophy ABSTRACT Strin (MDSC) into myogenic, as opposed to lipofibrogenic, lineages is a promising therapeutic counteracting myostatin, a negative regulator of muscle mass and a pro-lipofibrotic fibrogenic capacity of MDSC from wild...

Organism: *Mus musculus* Accession: GSE28986 PI/Contact: Robert Gelfand Re

**The transcriptomic signature of myostatin inhibitory influence on the differentia**  
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE59674

GDF8 (myostatin) is a unique cytokine strongly affecting the skeletal muscle phenoty molecular mechanism of myostatin influence on the differentiation of mouse C2C12 m technique. Treatment with exogenous GDF8 strongly affected the growth and develo proliferation and differentiatio...

Organism: *Mus musculus* Accession: GSE59674 PI/Contact: Zofia Wick Relea

**Development of gene expression signature for defining the cell potency of mu**  
**genotypes**  
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE39765

In order to determine the cell potency, by identification of genes responsible for plur isolated from five week old male wild type(WT), C57B6J and another hypertrophied microarray analysis and compared this gene expression to that of a standard mouse and Mstn null mice using an esta...

Organism: *Mus musculus* Accession: GSE39765 PI/Contact: Bipasha Bose Rele

**Rodent Research-3-CASIS: Mouse liver transcriptomic, proteomic and epigen**  
https://genelab-data.nrc.nasa.gov/genelab/accession/GLDS-137

The Rodent Research-3 (RR-3) mission was designed to study the effectiveness of occurs during spaceflight. Myostatin is a protein secreted by myoblasts that inhibits block myostatin cause increases in muscle mass. The RR-3 experiment was sponso Advancement of Science in Space and ass...

Organism: *Mus musculus* Factor: Microarray Treatment Assay Type: transcription profiling p... Accession: GLDS-137

### Federated Search

## Search Filters for GeneLab

Home Repository Data Data Mining Tools Submit Data Help Workspace

Search:

All  GeneLab  NIH GEO  EBI PRIDE  ANL MG-RAST

**Search Filters (GeneLab Only)**

Project Type	Factors	Organisms	Assay Type
<input checked="" type="checkbox"/> Ground	<input checked="" type="checkbox"/> Age	<input checked="" type="checkbox"/> <i>Mus musculus</i>	<input type="checkbox"/> deletion pool profiling
<input type="checkbox"/> Spaceflight	<input type="checkbox"/> Anatomical Stru	<input type="checkbox"/> <i>Mycobacterium ma</i>	<input type="checkbox"/> DNA methylation profiling
<input type="checkbox"/> AND (organism =	<input type="checkbox"/> Antibiotic conce	<input type="checkbox"/> <i>Oryzias latipes</i>	<input type="checkbox"/> environmental gene survey
Sort by Relevance	<input type="checkbox"/> Atmospheric Pre	<input type="checkbox"/> <i>Pantoea conspicua</i>	<input type="checkbox"/> genome sequencing
	<input type="checkbox"/> Bed Rest	<input type="checkbox"/> <i>Pseudomonas aeru</i>	<input type="checkbox"/> metabolite profiling
	<input type="checkbox"/> Bleomycin Treat	<input type="checkbox"/> <i>Rattus norvegicus</i>	<input type="checkbox"/> protein expression profiling
<b>Age and Space Irra</b> https://genelab-app-1-st	<input checked="" type="checkbox"/> cage	<input type="checkbox"/> <i>Rhodospirillum rubr</i>	<input type="checkbox"/> RNA methylation profiling
Age play	<input type="checkbox"/> CANONT:Part	<input type="checkbox"/> <i>Saccharomyces ce</i>	<input type="checkbox"/> transcription profiling
Epidem	<input type="checkbox"/> cell culture	<input type="checkbox"/> <i>Staphylococcus</i>	
accumu	<input type="checkbox"/> clinical treatment	<input type="checkbox"/> <i>Staphylococcus aureus</i>	
decreas			

Factor Name = Age' OR 'Study Factor Name = cage')  
Total Search Results Found: **3**

1

**carcinogenesis Risk**  
modeling the carcinogenesis process or estimating cancer risks. nce increases with age. This effect is commonly attributed to a lifetime g middle-age the incidence begins to decelerate and for many tumor sites it actually ption profiling Accession: GLDS-88 PI/Contact: Christine Afshin Edward L...

# GLDS Phase 2 (Release 2.0) Customized NASA Collaborative Workspace



## User Account Mgmt., Access Controls (e.g., Private, Shared, Public Folders)

The image displays three overlapping screenshots of the GeneLab website. The top-left screenshot shows a search results page for 'Dissecting Low Atmospheric Pressure Stress: Transcriptome Responses to the Components of Hypobaria in Arabidopsis [Experiment 2]'. The top-right screenshot shows the login page with fields for 'USERNAME:' and 'PASSWORD:', and buttons for 'Sign In' and 'Cancel'. The bottom screenshot shows a file browser interface for the 'genelab-data' folder, listing files from 'GLDS-1' to 'GLDS-113'.

**Search Results Page:**

Page 1 of 6 (Total Studies: 133) Next >  
Studies Per Page: 25

Organisms	Factors	Assay Types	Release Date	Description
Arabidopsis thaliana	Atmospheric Pressure	Transcription profiling	11-May-2017	Controlled hypobaric research facilities provide an environment that is never encountered in terrestrial ecology, yet the apparent components of hypobaric are stresses typical of terrestrial ecosystems. It...
Mus musculus	Microgravity	Transcription profiling	23-May-2017	Microgravity as well as chronic muscle disuse are two causes of low back pain originated at least in part from peroneal muscle denervation. All present no study investigated the complexity of

**Login Page:**

NASA GeneLab-GenomeSpace OpenID Login

USERNAME:   
PASSWORD:

Register new NASA GeneLab user  
Forgot your password?

Open Science for Exploration

This is a US Government system and is for authorized users only. By accessing this system you are consenting to complete monitoring with no expectation of privacy. Unauthorized access or use may subject you to disciplinary action and criminal prosecution. Unauthorized use of the computer accounts and computer resources to which I am granted access is a violation of Federal law, constitutes theft, and is punishable by law. I understand that I am the only individual to access these accounts and will not knowingly permit access by others without written approval. I understand that my misuse of assigned accounts and my accessing others' accounts without authorization is not allowed. I understand that this/these system(s) and resources are subject to monitoring and recording and I will have no expectation of

**File Browser:**

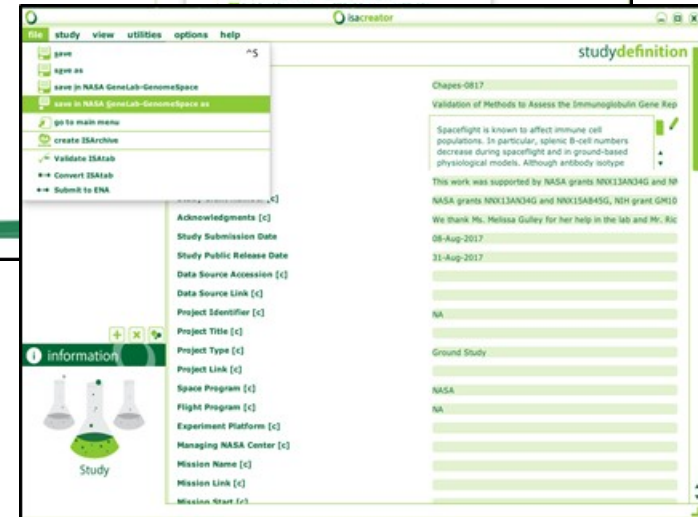
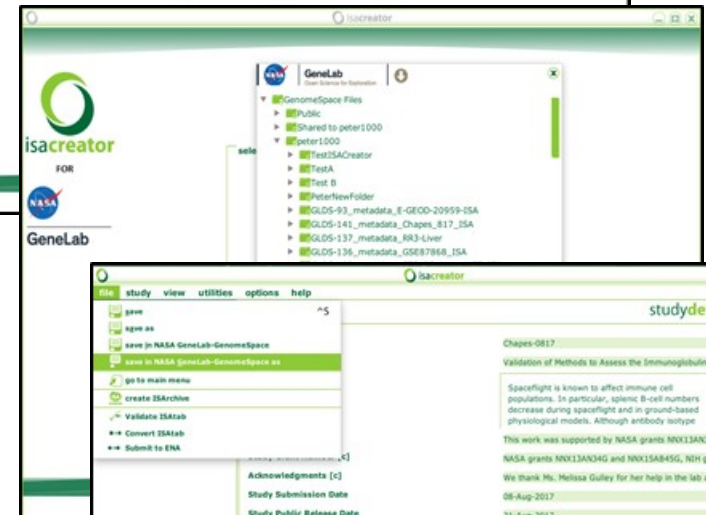
Up to: Home > Public > genelab > genelab-data

Filename	Tags	Owner	Size	Last Modified
GLDS-1		genelab		
GLDS-10		genelab		
GLDS-100		genelab		
GLDS-101		genelab		
GLDS-102		genelab		
GLDS-103		genelab		
GLDS-104		genelab		
GLDS-105		genelab		
GLDS-106		genelab		
GLDS-107		genelab		
GLDS-108		genelab		
GLDS-109		genelab		
GLDS-11		genelab		
GLDS-110		genelab		
GLDS-111		genelab		
GLDS-112		genelab		
GLDS-113		genelab		

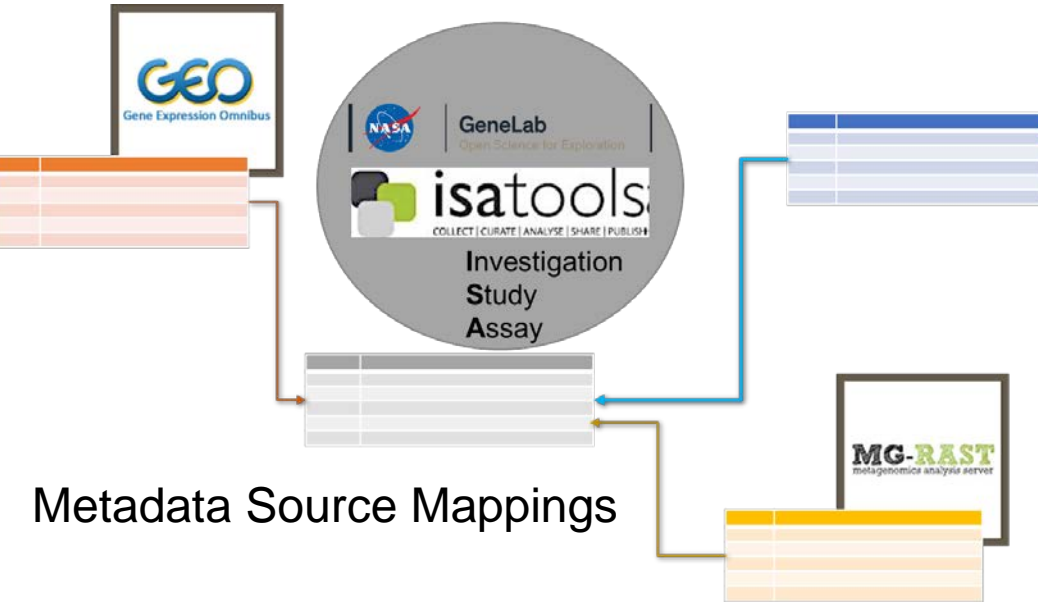
# GLDS Phase 2 (Release 2.0) Metadata Curation via ISACreator Tool



## GeneLab-GenomeSpace Integration with ISACreator for Streamlining Data Processing Operations

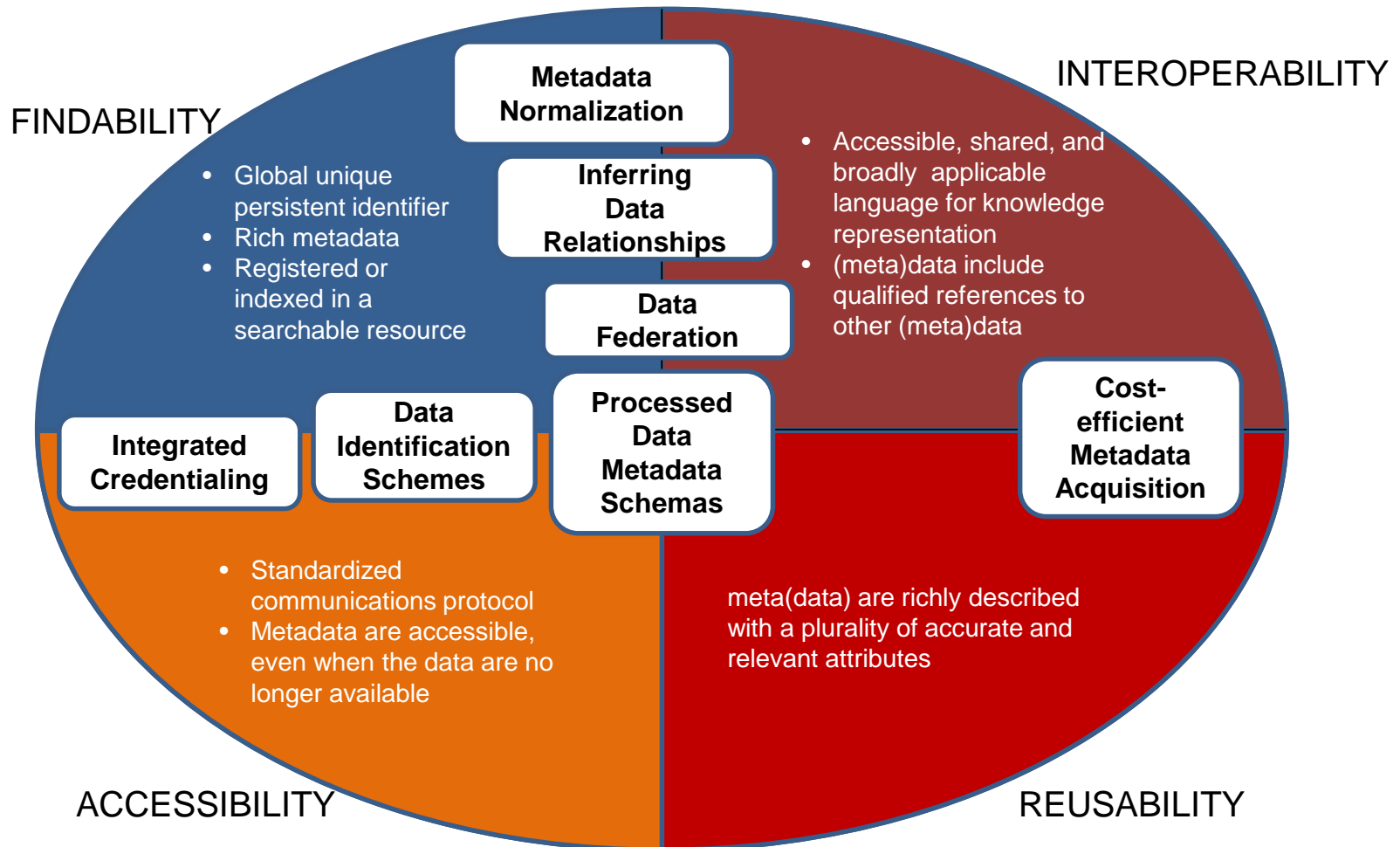


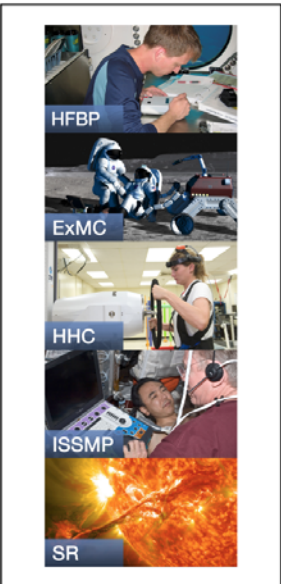
### Metadata Source Mappings



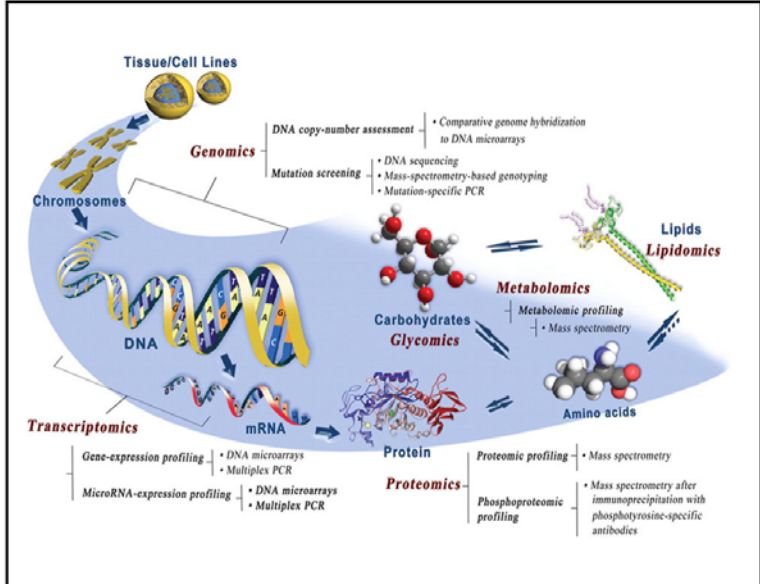


# GeneLab has adopted the FAIR principle





# OMICS



# GENE LAB

**DATA REPOSITORY**

**ANALYSIS TOOLS**

**COLLABORATIVE WORKSPACE**

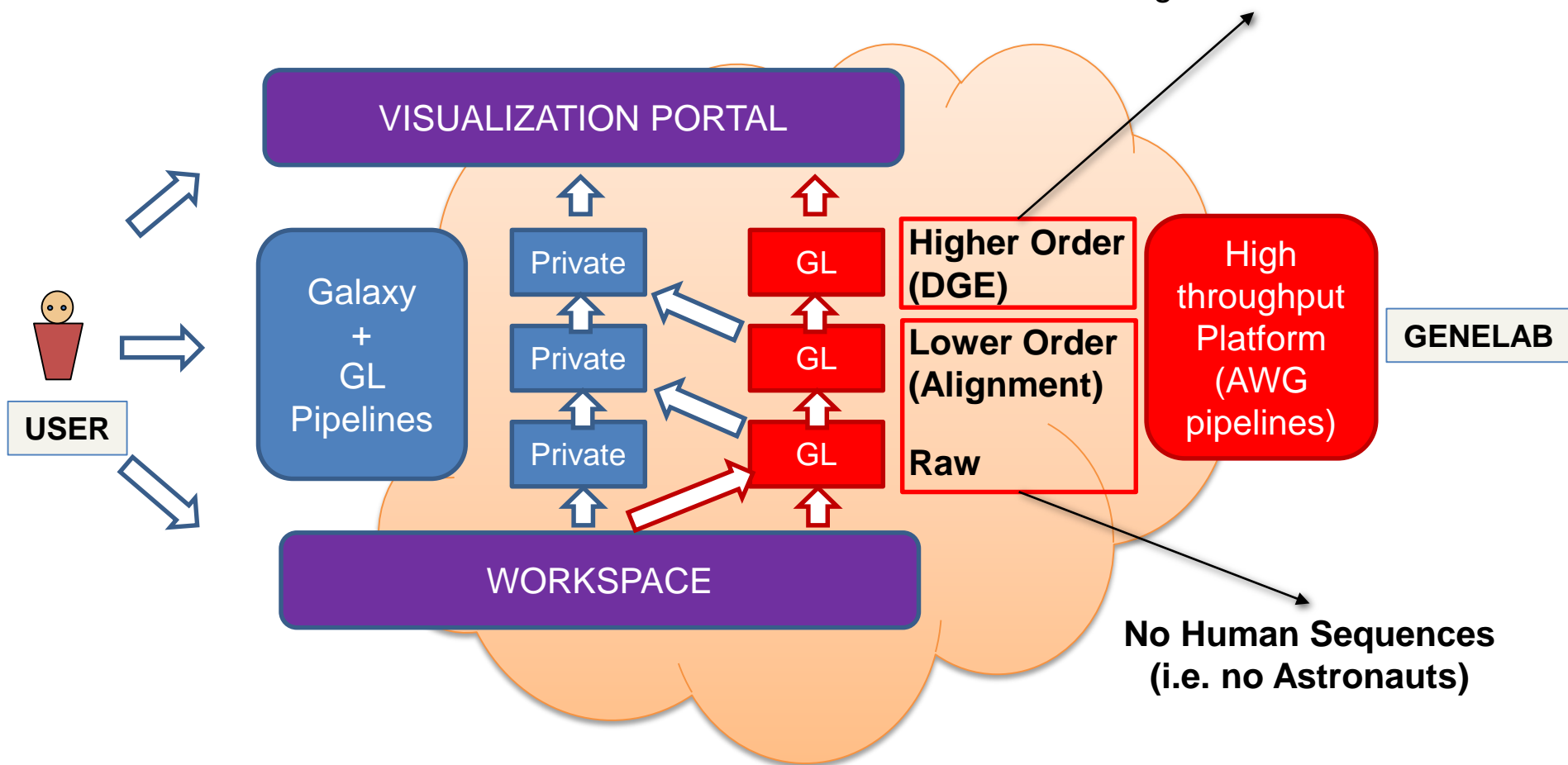
**FEDERATED DATABASE**

The GeneLab database infrastructure provides a platform for storage, retrieval and analysis of omics datasets – with the ultimately goal to support the missions of HRP

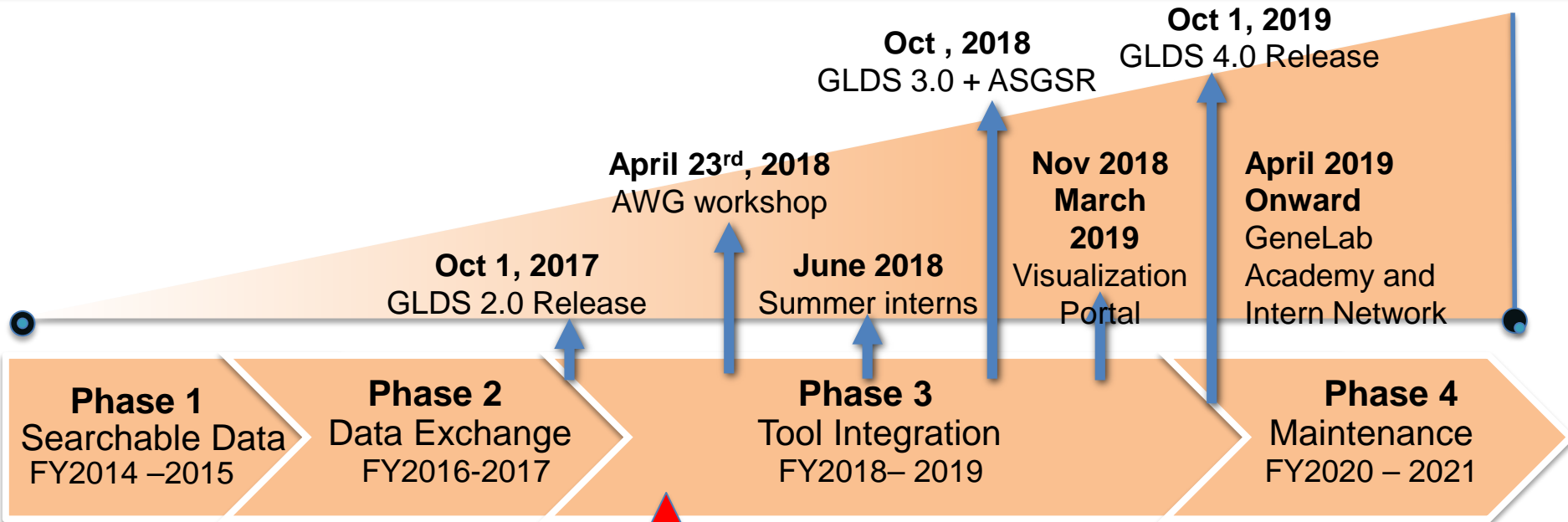
# GLDS 4.0



**Astronaut Data should be possible for Higher Order Data**  
Providing minimum metadata



# Phased Implementation



## Data System

- ✓ Public Website
- ✓ Searchable Data Repository
- ✓ Top Level Requirements
- ✓ New Data and Legacy Data

## Data System

- ✓ Link to Public Databases via Data Federation
- ✓ Integrated Search (e.g., data mashup)

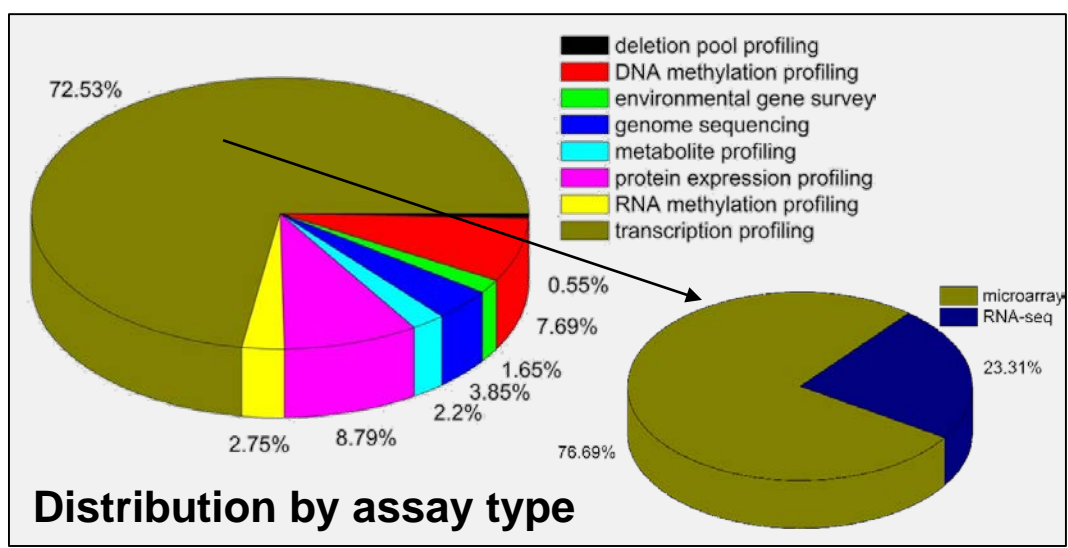
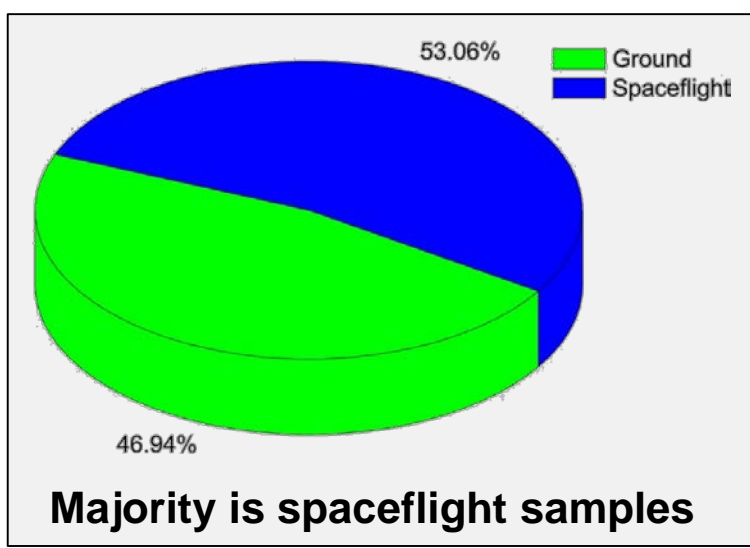
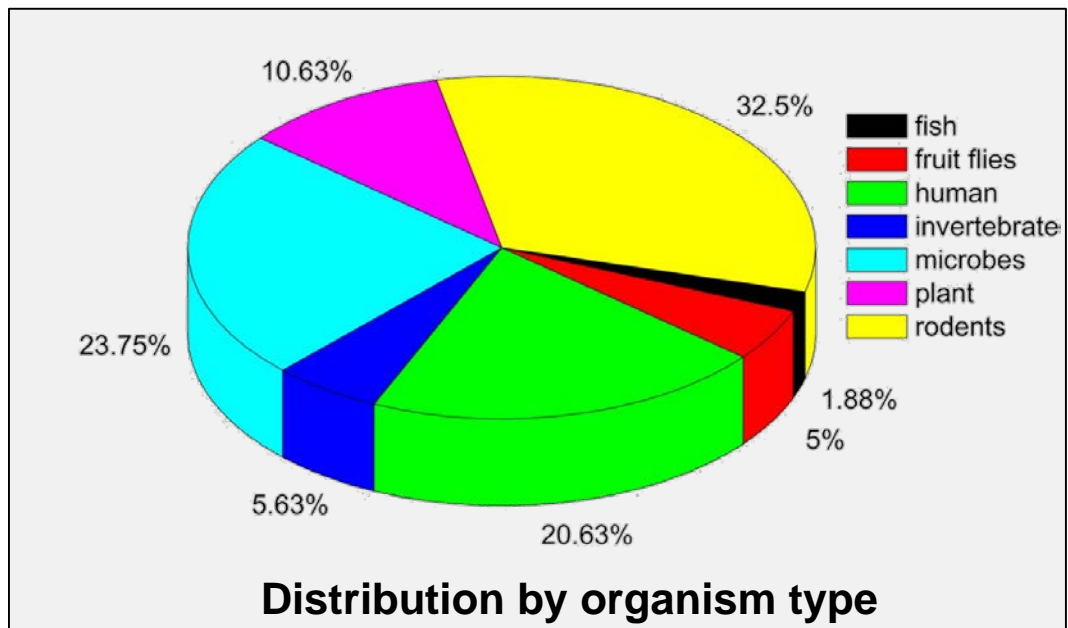
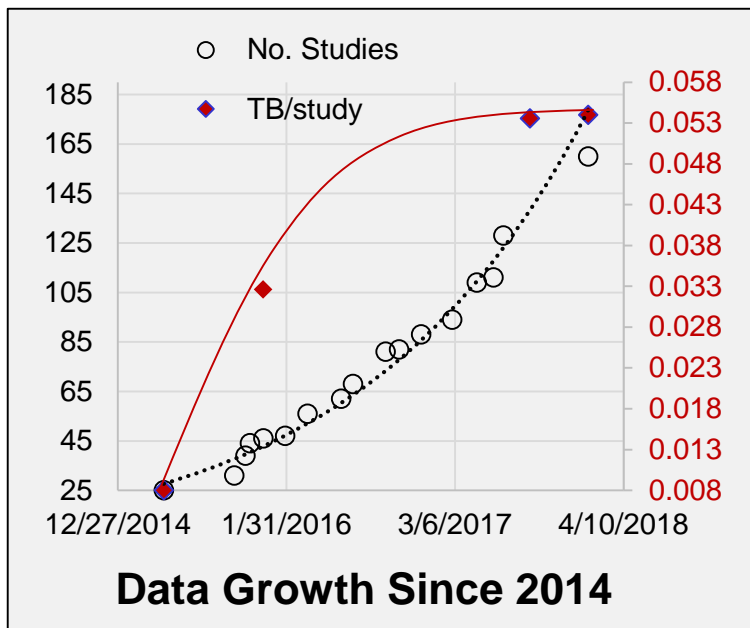
## Data System

- Integrated Platform across model organisms
- Build Community via AWG
- Provide access to biocomputational tools for omics analysis
- Provide collaboration framework and tools

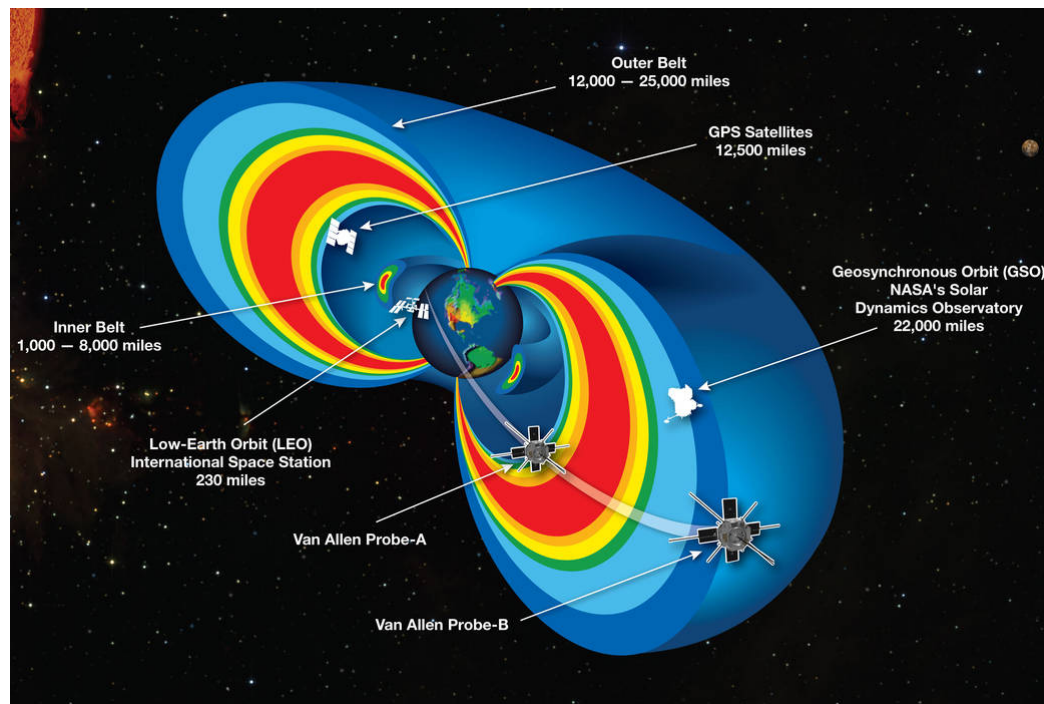
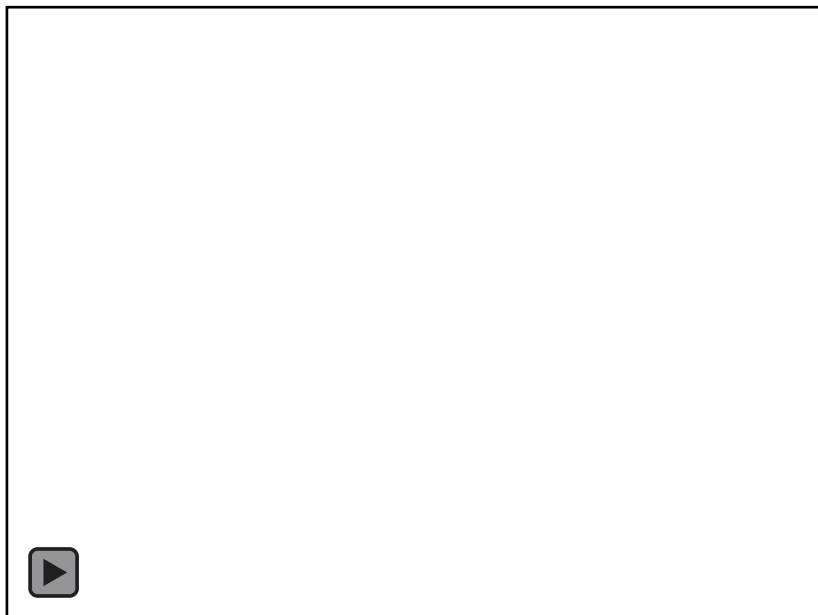
## Open Source Maintenance

- User community becomes primary provider of new tools/knowledge
- Maintain integrity of data, and data system

# GeneLab Database: 154 data sets



# Earth's magnetic field protects us from cosmic radiation

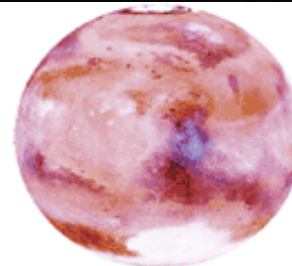


	MILLIREM:
CHEST X-RAY	8 to 50
AVG. YEARLY RADON DOSE	200
U.S. AVG. YEARLY DOSE	350
PET SCAN	1,000
1 YEAR IN KERALA, INDIA	1,300
U.S. NUCLEAR WORKER LIMIT PER YEAR	5,000
APOLLO 14 (9 DAYS)	1,140
SHUTTLE 41-C (18 DAYS)	5,600
SKYLAB 4 (84 DAYS)	17,800
<b>MARS MISSION TOTAL</b>	<b>130,000</b>

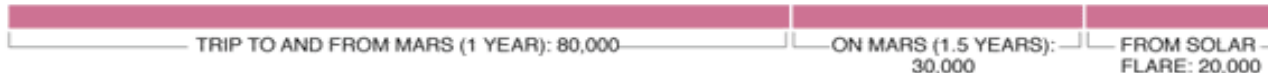
## 2½ Years, 2,600 X-Rays

Americans on average absorb the radiation equivalent of at least 7 chest X-rays each year.

Space missions, outside of Earth's protective atmosphere and magnetic field, expose astronauts to many times more.

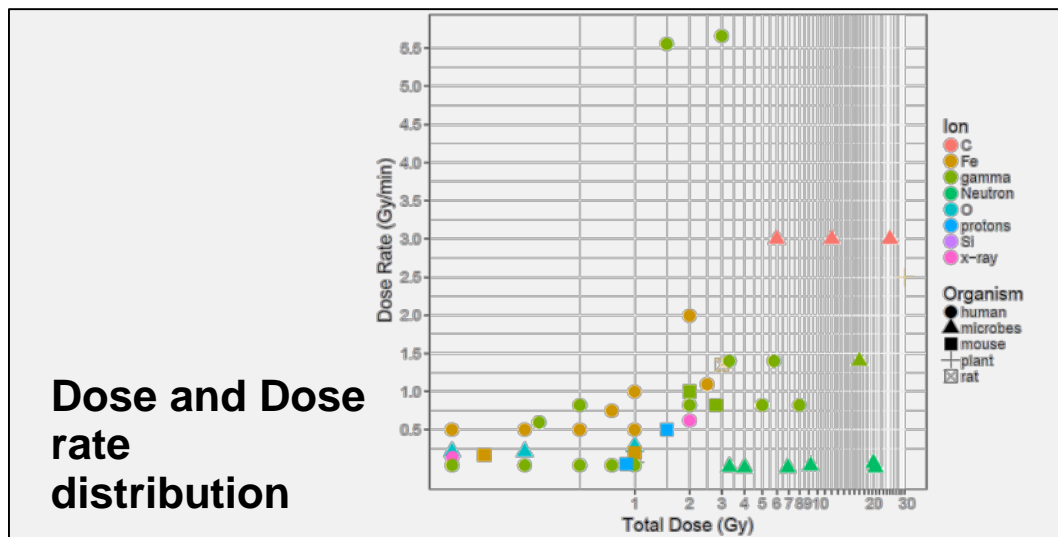
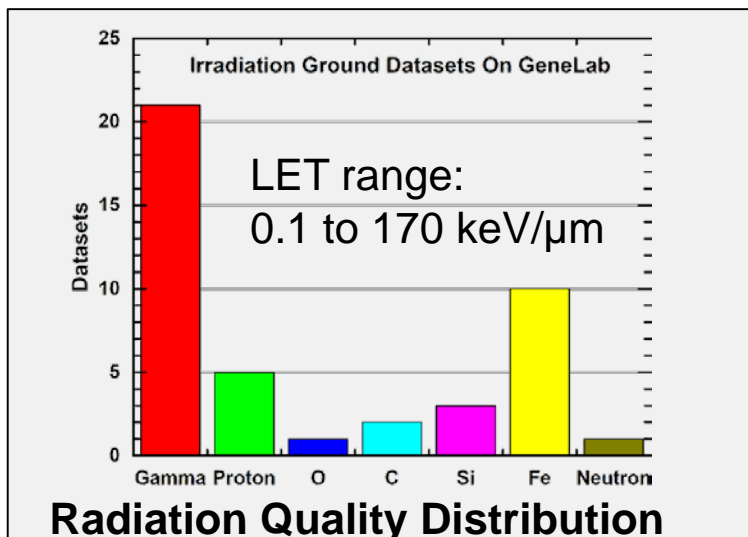
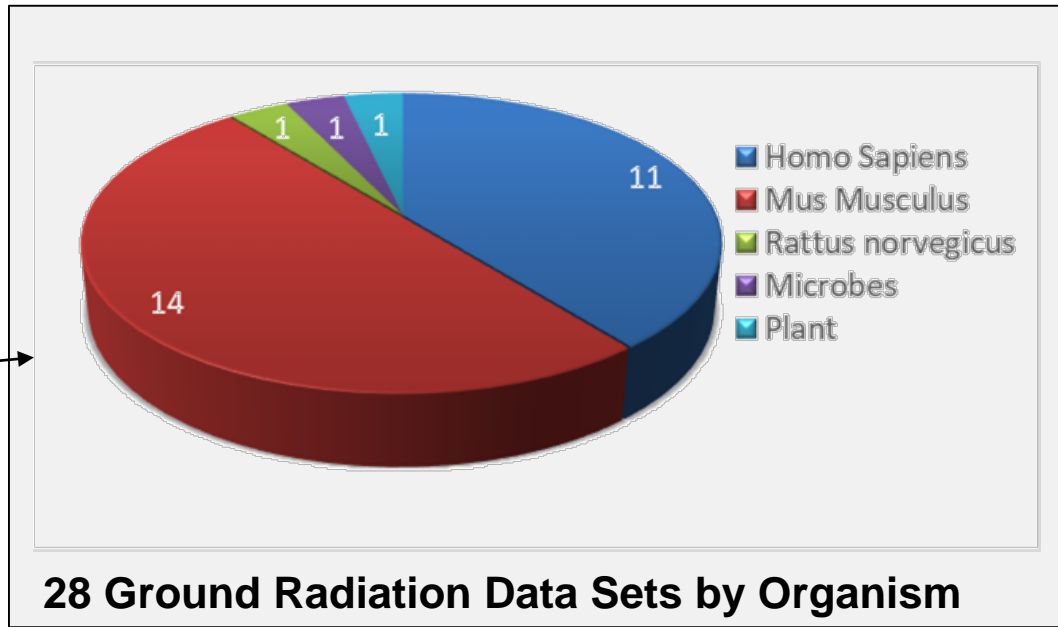
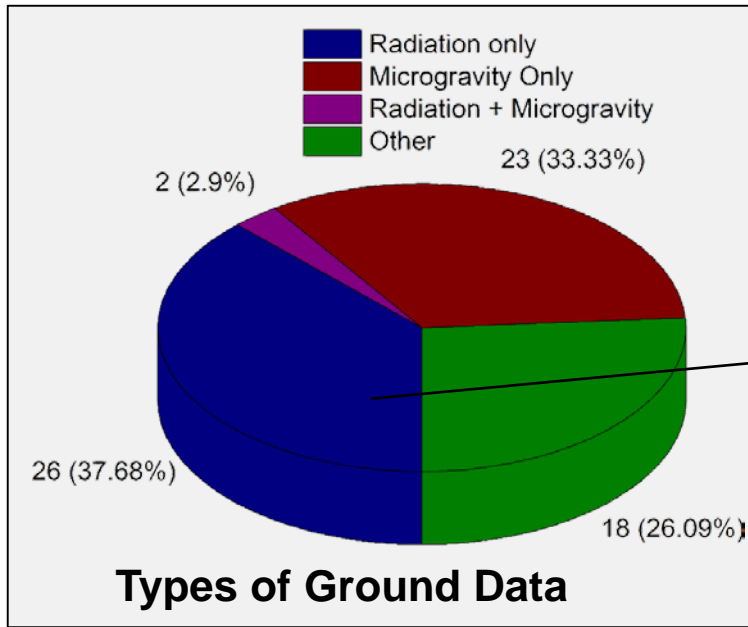


NASA

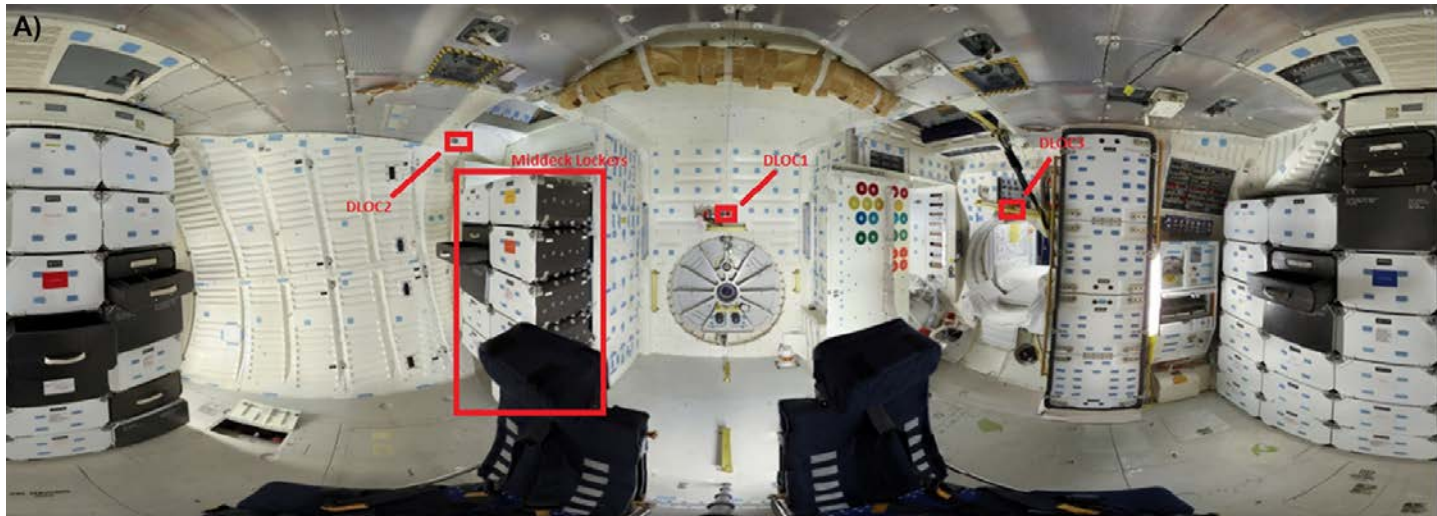


Source: Brookhaven National Laboratory, U.S. Department of Energy

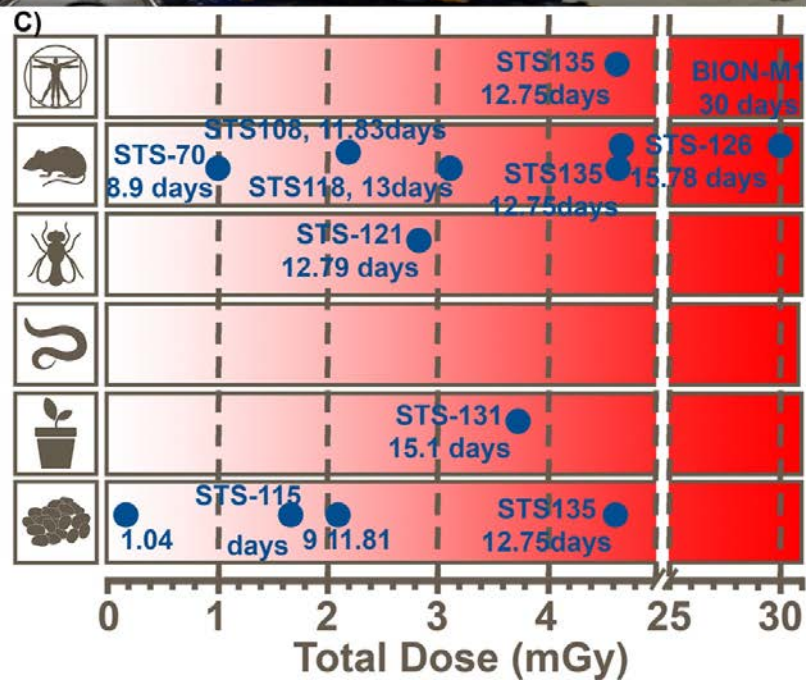
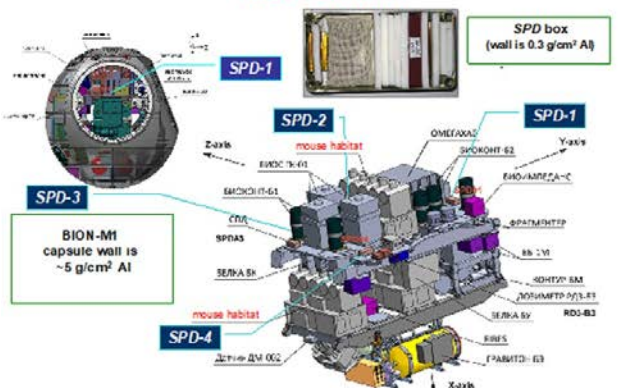
# 69 Ground Data Sets



# STS Samples: Radiation Dosimetry



B) Locations of Radiation Detectors and Animal Holders inside BION-M1





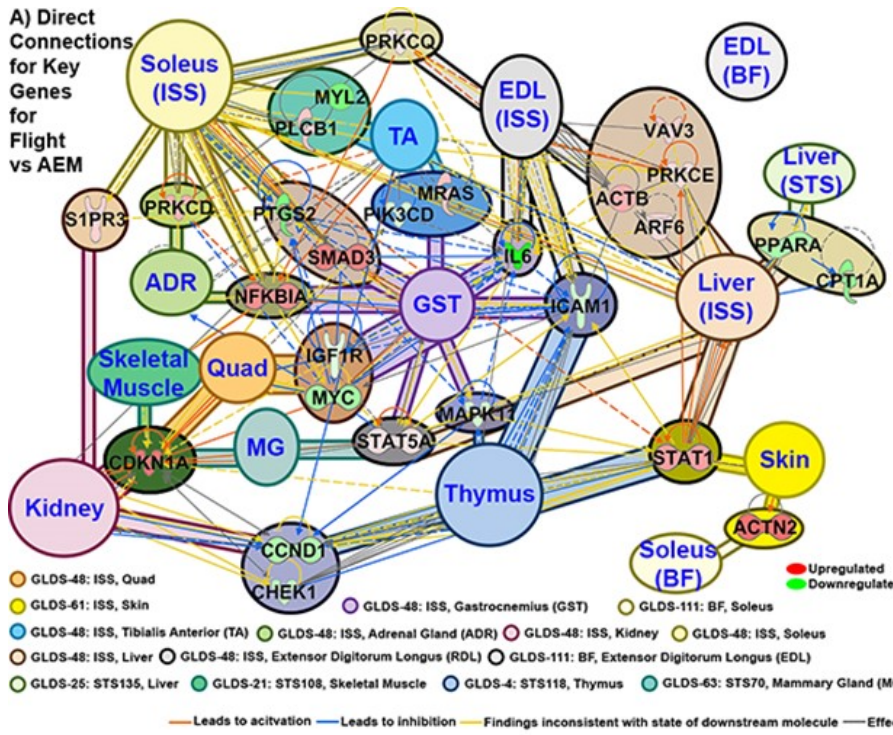


# Building a database to support studies on human health and countermeasures

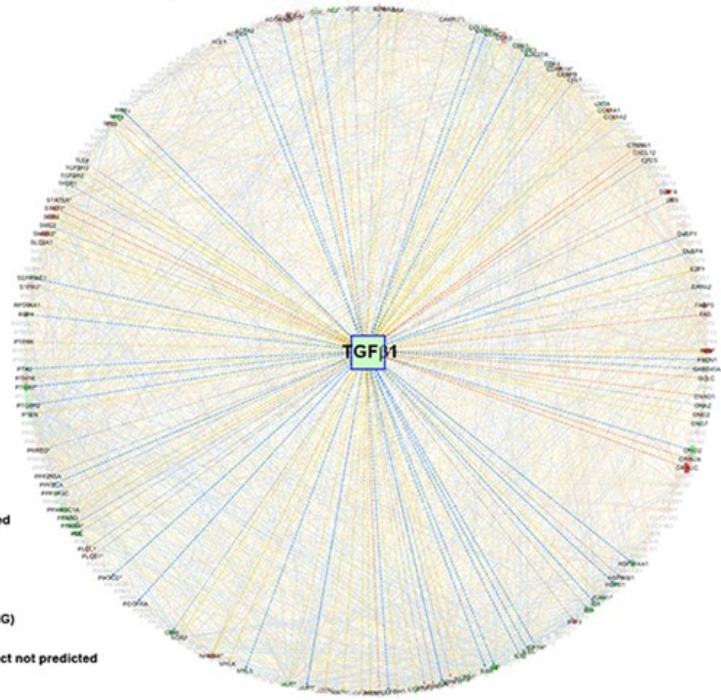
## Future analysis capabilities

### 1. Cohort comparison

- Display the expression of a gene query or its frequency of differential regulation based on sex, species, tissue, or age
  - Example: From a systems biology analysis, TGFβ1 was found to be a master regulator impacting spaceflight



B) Connections Between all Key Genes for all Datasets (Flight vs AEM): Radial Plot with the most Connected Gene in the Middle



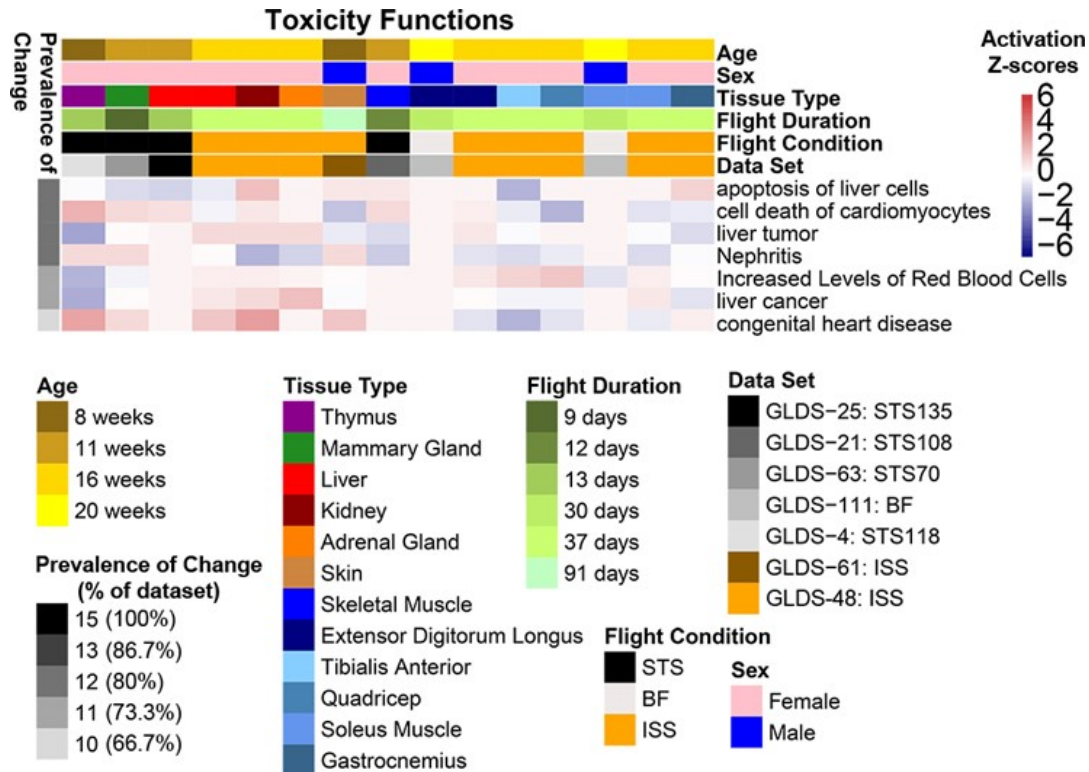


# Building a database to support studies on human health and countermeasures

## Future analysis capabilities

### 2. Relevance to human disease

- Display the expression of a query gene or its frequency of differential regulation in disease types
  - Example: Using the GeneLab data we are able to make predictions on impact on health and risk of diseases due to space flight



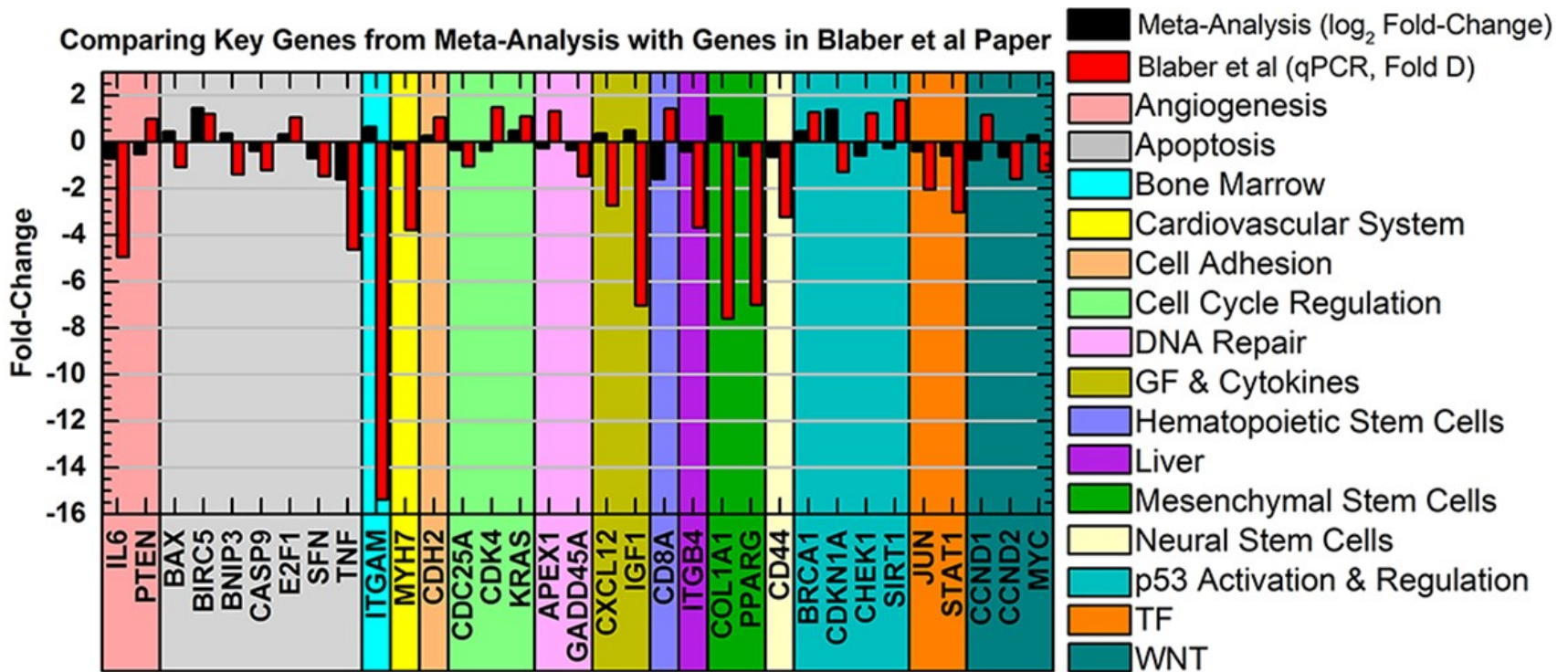
# Building a database to support studies on human health and countermeasures



## Future analysis capabilities

### 3. Tissue expression

- Display the expression of a query gene based on cell or tissue type
  - Example: Can make direct comparisons from of key genes to data from the literature.



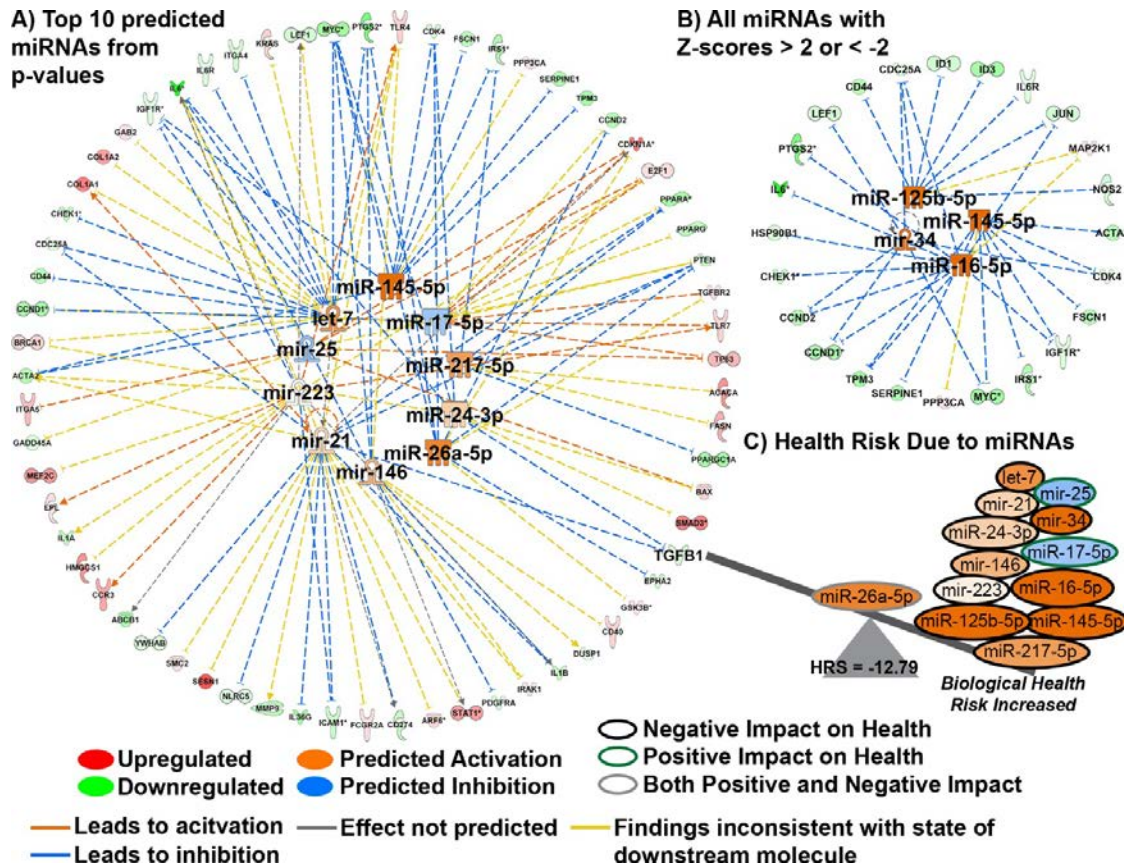


# Building a database to support studies on human health and countermeasures

## Future analysis capabilities

### 4. Countermeasure identification

- Display countermeasures reported to impact expression of a gene query
  - Example: Hypothesis generated from GeneLab datasets that miRNAs can be used as countermeasure against spaceflight health risks.





# Current studies

**Sylvain Costes, Ph.D.**  
**Afshin Beheshti, Ph.D.**



# The Data Reproducibility Challenge



- Space omics datasets are sparse
  - Need to reduce level of noise
  - Need a method for assay bias identification and correction
- Started a collaboration with NIST (National Institute of Standards and Technology)
  - Implement methods to make the best use of precious flight samples
  - NIST showed high level of variation for RNAseq between 12 different core processing centers in the US



**NIST's collaborators**  
Dr. Munro and Dr. Salit

The image shows a horizontal banner. On the left is the Nature Communications logo, which consists of a stylized wave graphic in red and yellow above the text "nature COMMUNICATIONS". On the right, the text "NIST's collaborators" is in bold, with "Dr. Munro and Dr. Salit" below it.

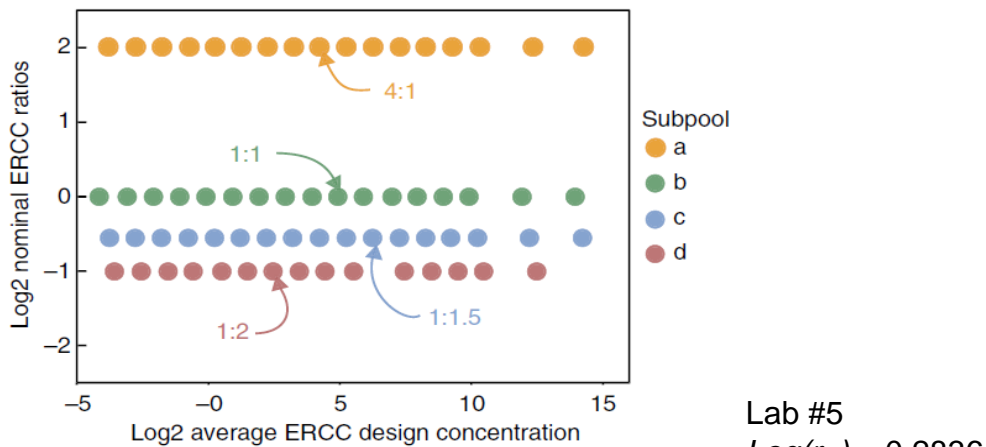
## ARTICLE

Received 11 Aug 2014 | Accepted 1 Sep 2014 | Published 25 Sep 2014

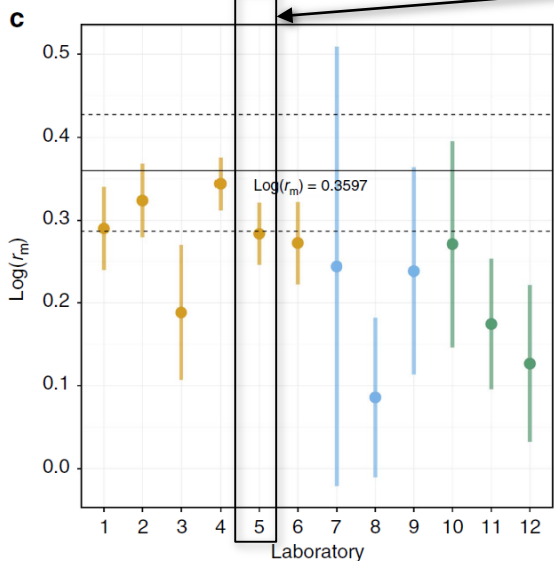
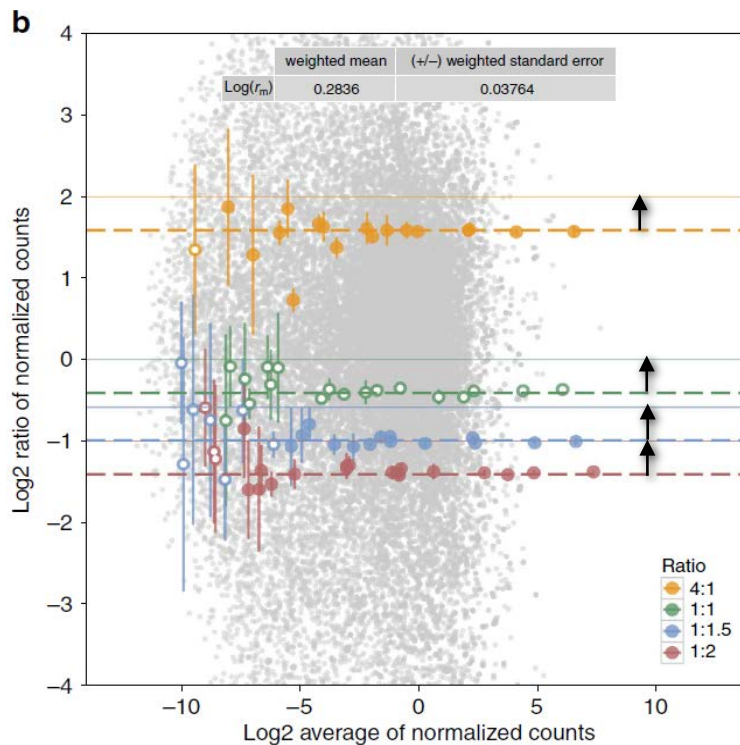
DOI: 10.1038/ncomms6125

Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures

# #1 Risk: Data Reproducibility



Lab #5  
 $\text{Log}(r_m) = 0.2836$

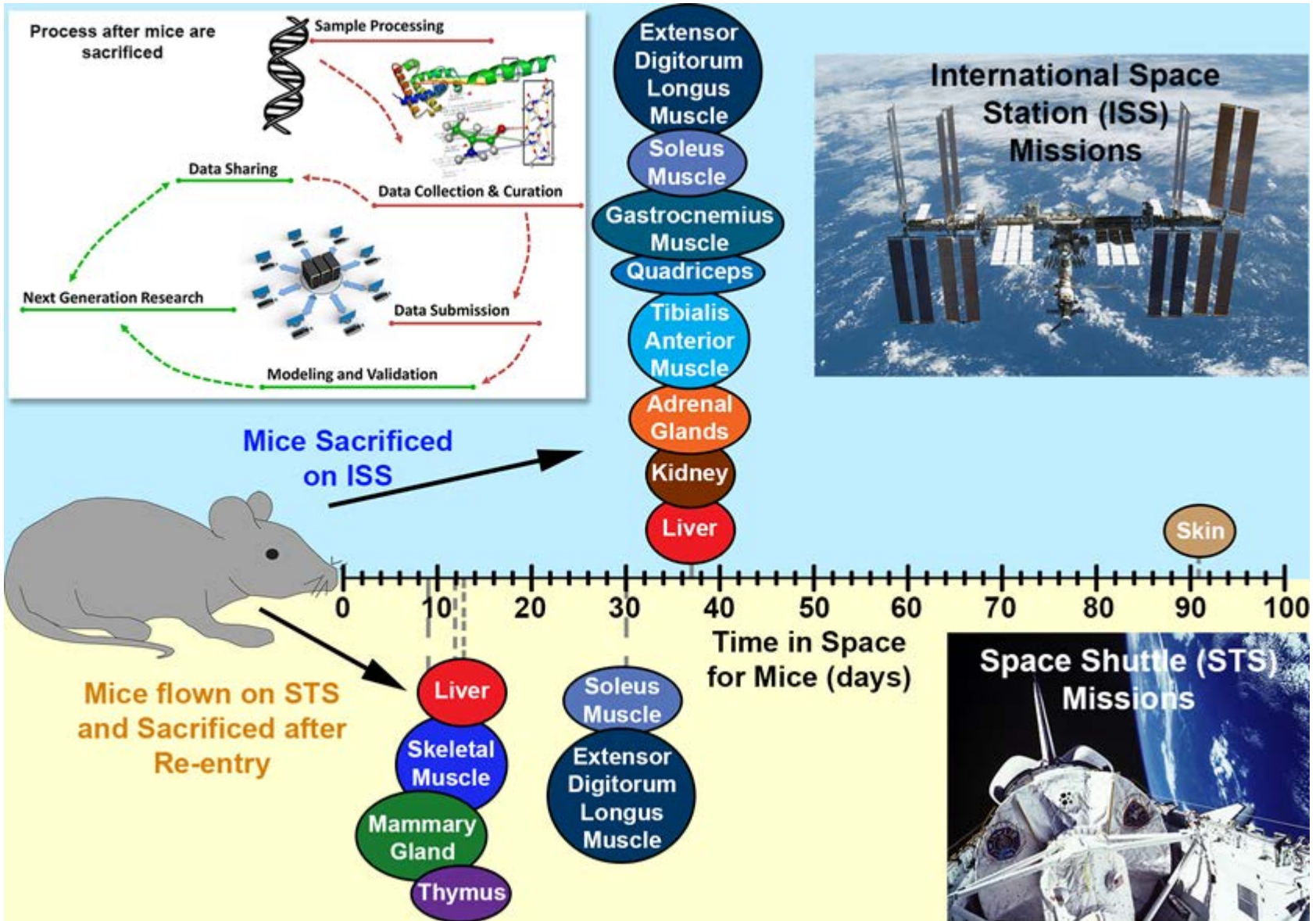


$r_m$  = Weighted mean estimates of mRNA fraction differences for the sample set with error bars representing weighted standard errors

$$R_S = r_m \left( \frac{E_1}{E_2} \right)_S$$

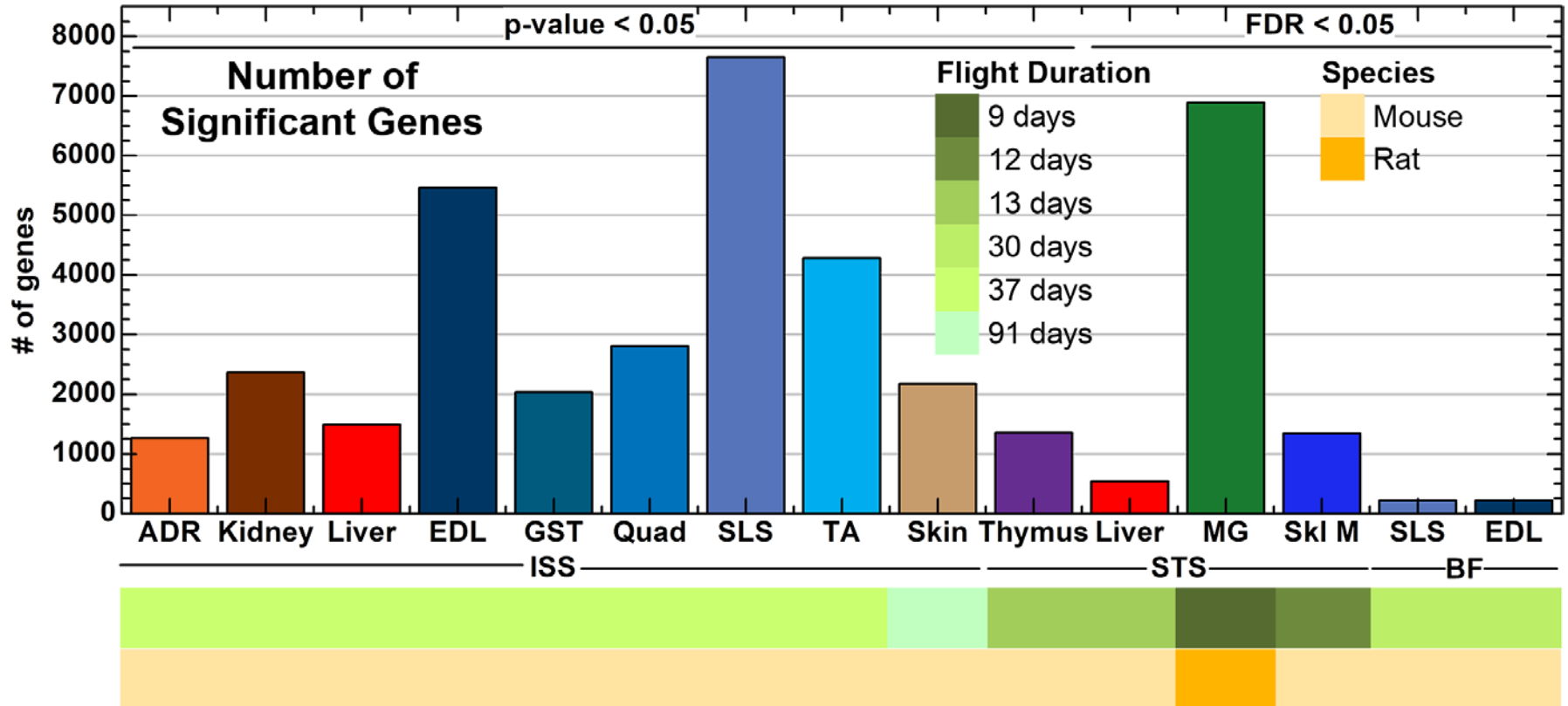
$$\text{Log}(R_S) = \text{Log}(r_m) + \text{Log}(E_1) - \text{Log}(E_2)$$

# General Overview of GeneLab Mice Data

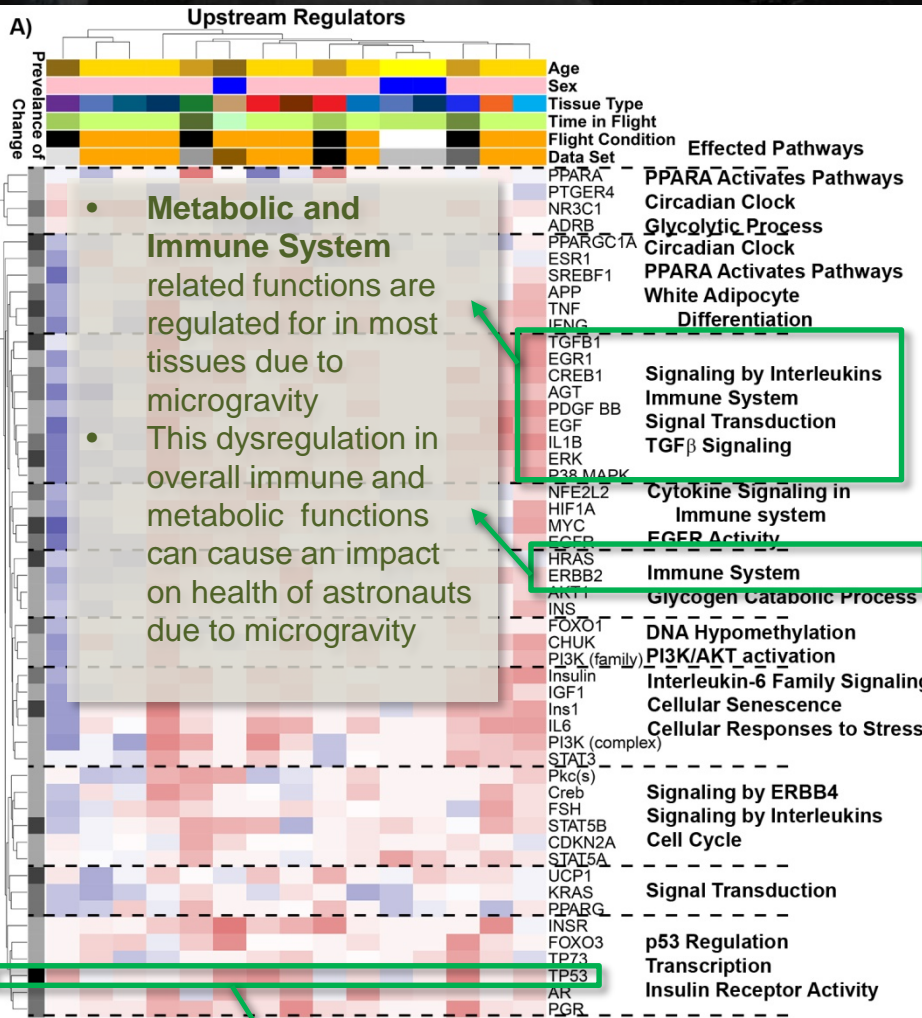




# Number of Significant Genes from Multiple Datasets



# Predicted Master Regulators



Metabolic and Immune System related functions are regulated for in most tissues due to microgravity

This dysregulation in overall immune and metabolic functions can cause an impact on health of astronauts due to microgravity

Signaling by Interleukins  
Immune System  
Signal Transduction  
TGF $\beta$  Signaling

Immune System  
Glycogen Catabolic Process

TP53

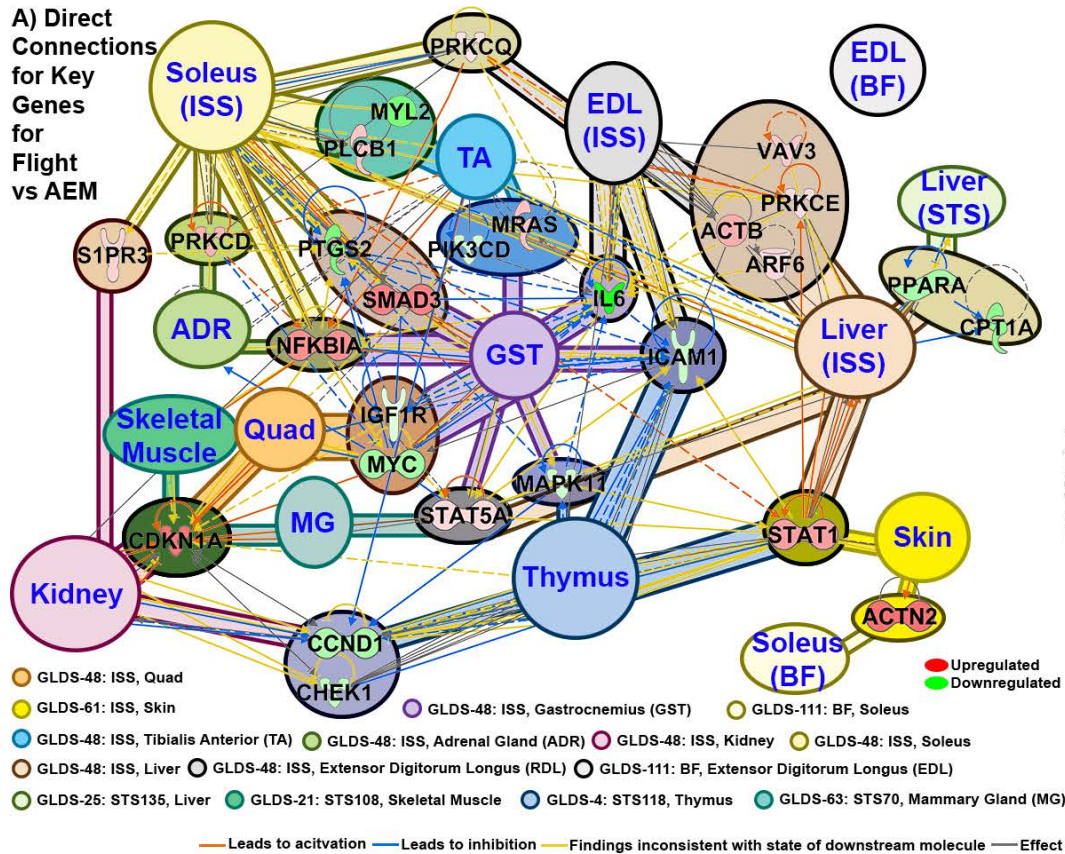


- p53 common in all tissue and conditions when comparing tissue from mice Flight vs Controls.
- p53 known to be involved in: tumor suppressor, conserving stability by preventing genome mutation, DNA repair, cell cycle, apoptosis

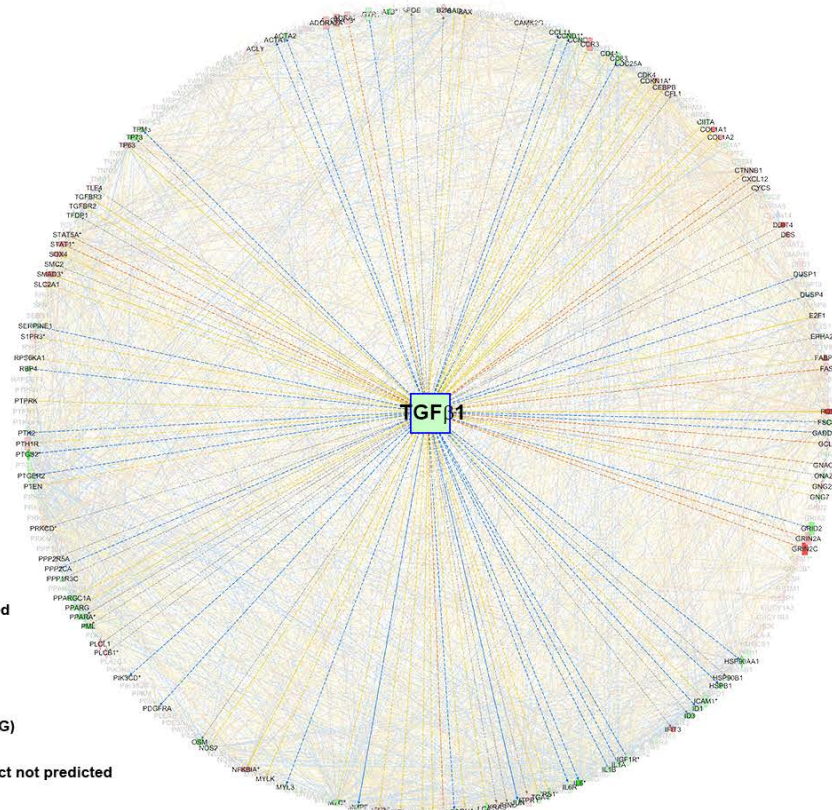
# Key Genes and the Connections: Flight vs Ground (AEM – Rodent Habitat)



A) Direct Connections for Key Genes for Flight vs AEM



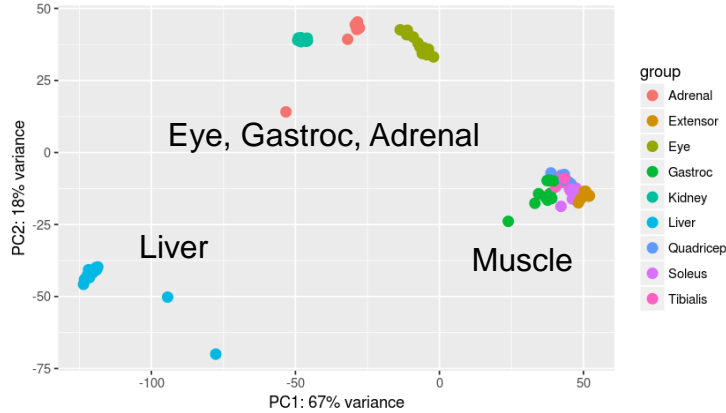
B) Connections Between all Key Genes for all Datasets (Flight vs AEM): Radial Plot with the most Connected Gene in the Middle



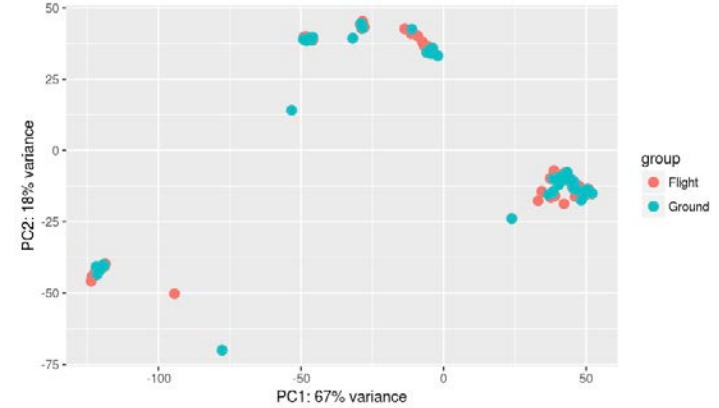
# Mission-specific analysis: RR-1 Transcriptomics



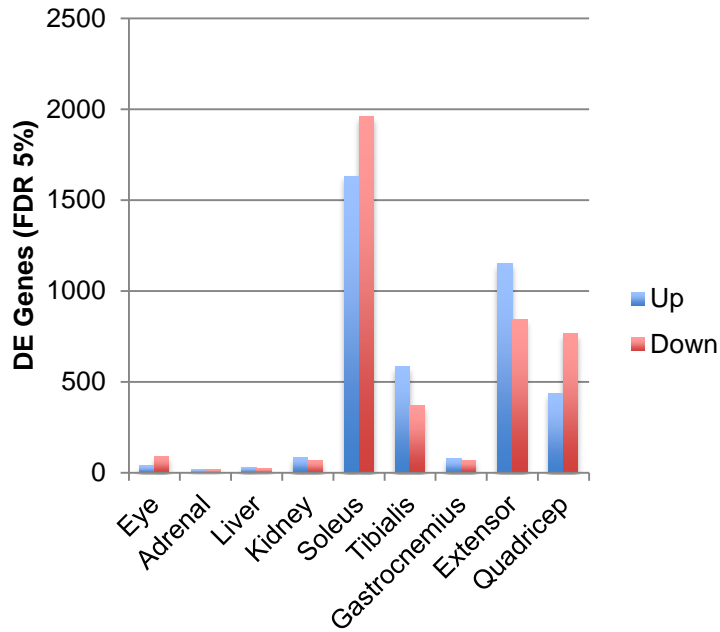
## Samples cluster by tissue type



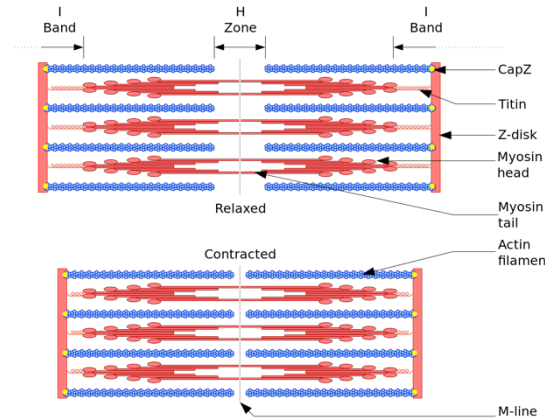
## Samples do not cluster by flight/ground



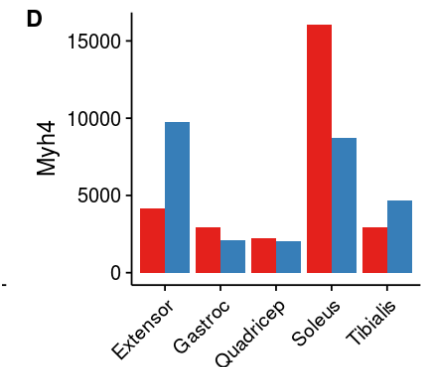
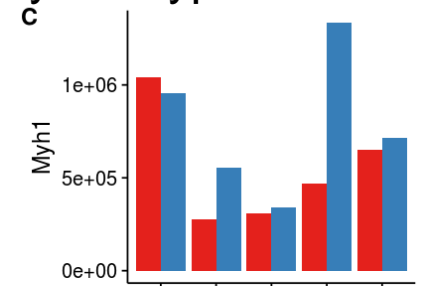
## Many changes in muscles



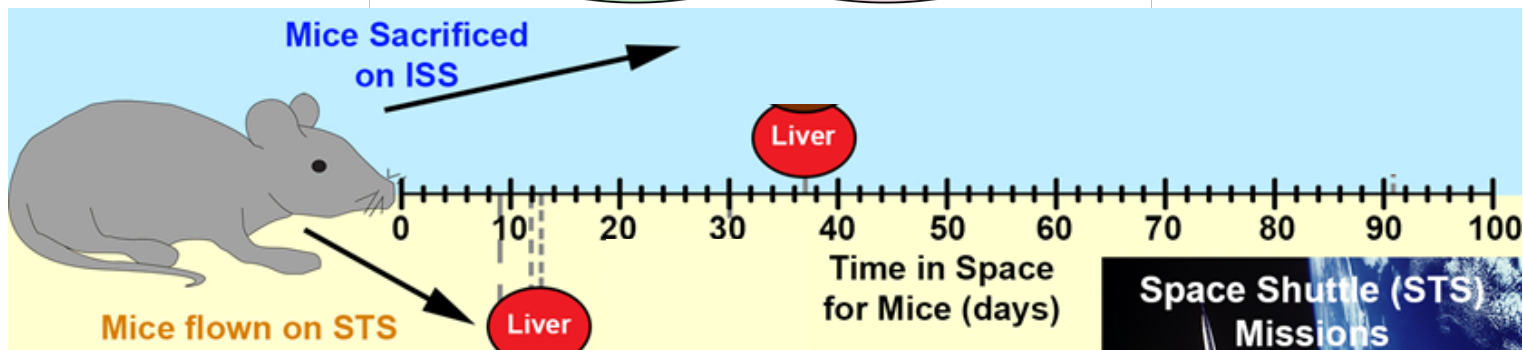
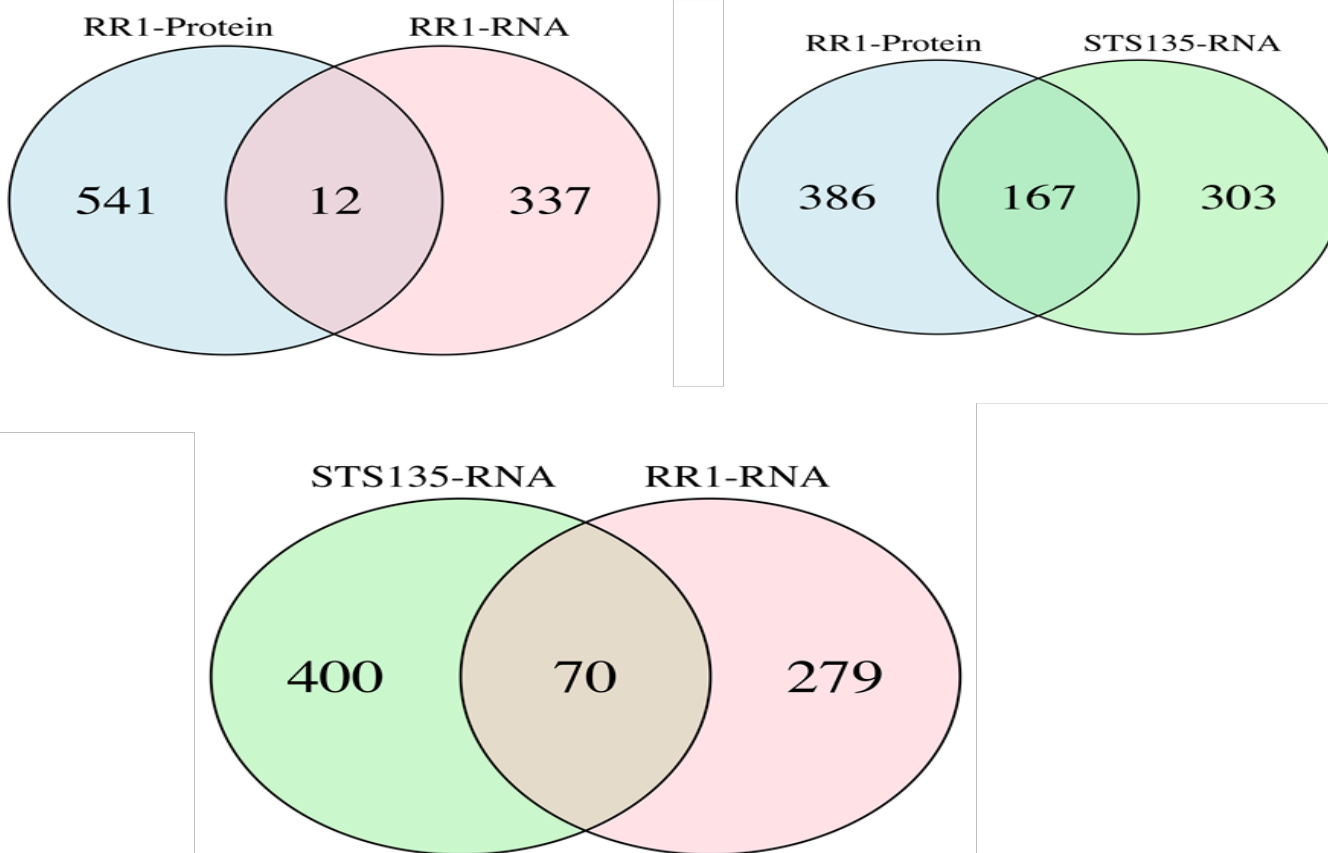
## Changes to muscle myosin types



## Muscle structure



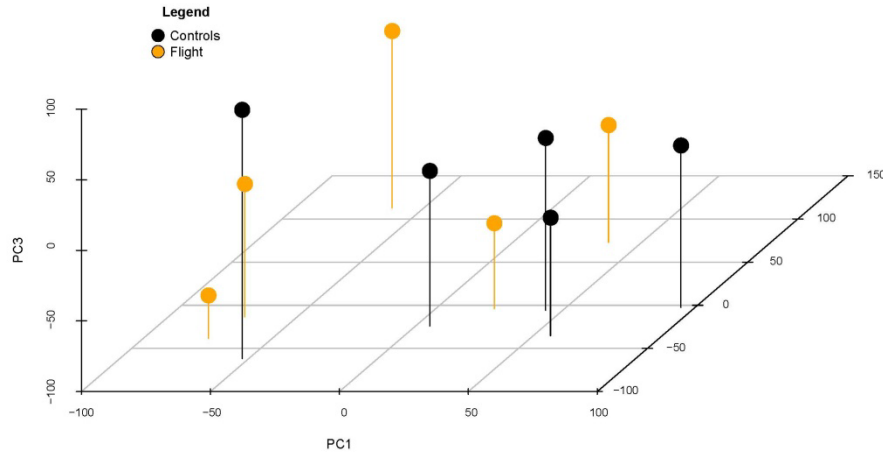
# Impact of Microgravity on Liver Tissue: STS135 & RR1 Intersect Venn Diagram Analysis



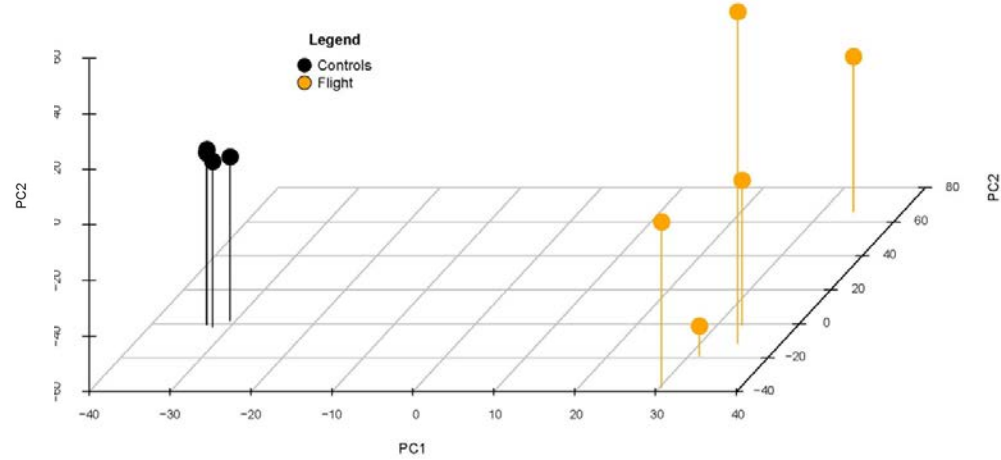
# Impact of Microgravity on Liver Tissue: STS135 & RR1 Principle Component Analysis



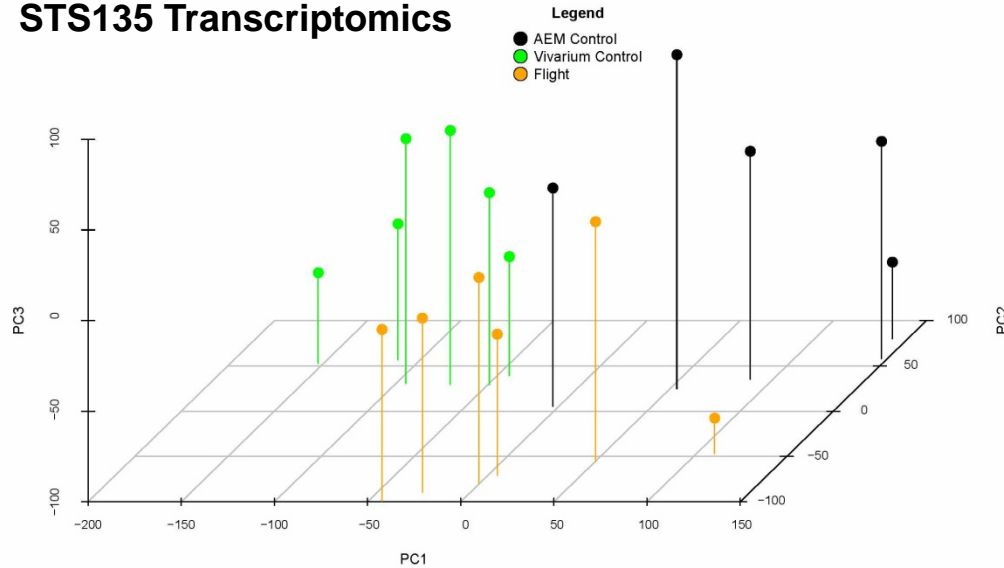
## RR1 Transcriptomics



## RR1 Proteomics



## STS135 Transcriptomics

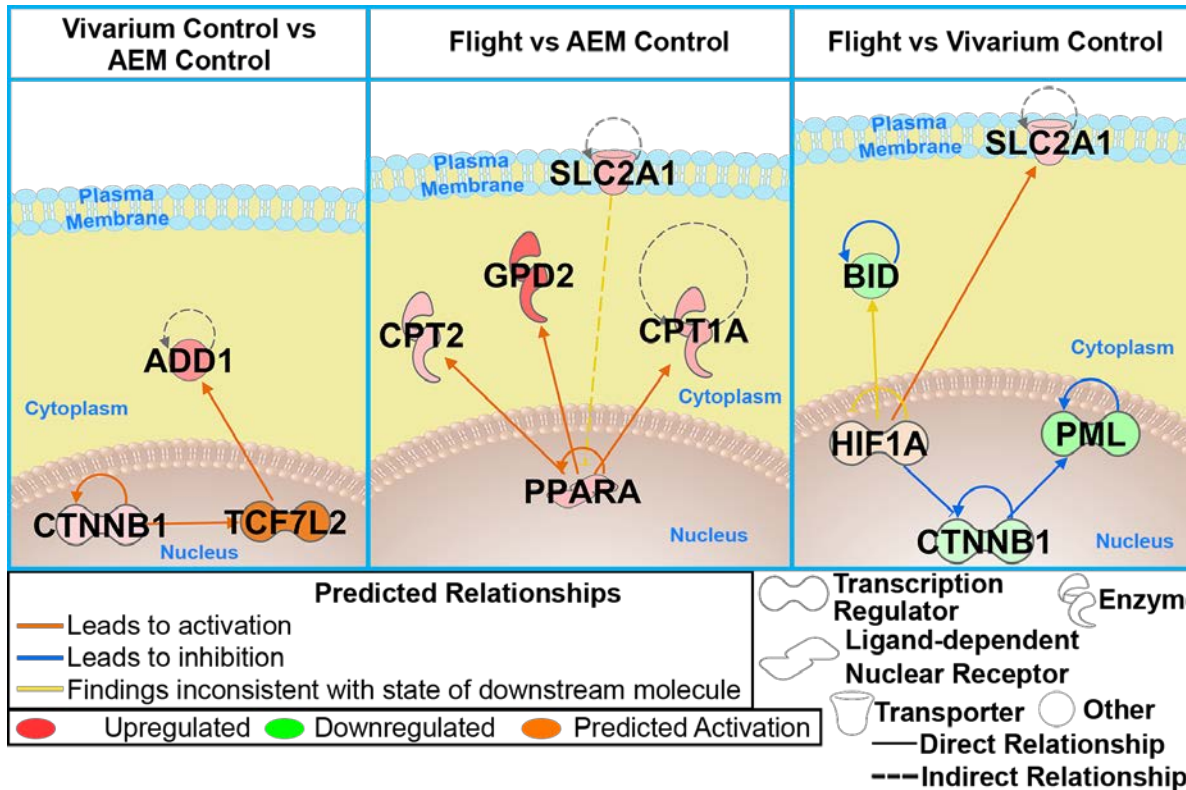


# RR1 & STS135 Mice Liver KEGG Enrichment Pathways

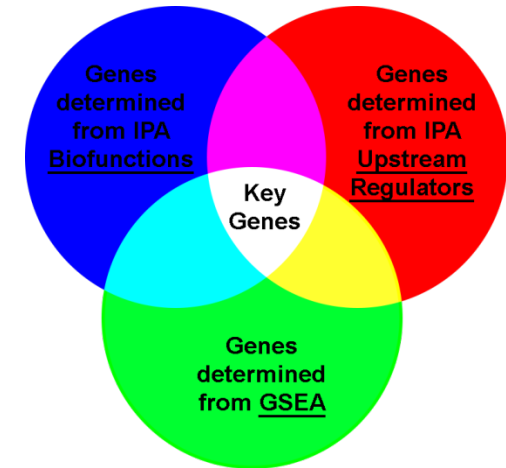


Pathway	STS-135 RNA	RR1 Protein	RR1 RNA
<b>mmu01100:Metabolic pathways</b>	****	****	****
<b>mmu01200:Carbon metabolism</b>	****	****	**
<b>mmu01130:Biosynthesis of antibiotics</b>	****	****	**
<b>mmu01212:Fatty acid metabolism</b>	****	****	**
<b>mmu00640:Propanoate metabolism</b>	****	****	*
<b>mmu00062:Fatty acid elongation</b>	***	*	*
<b>mmu00620:Pyruvate metabolism</b>	**	*	*
<b>mmu00380:Tryptophan metabolism</b>	**	***	**
<b>mmu00520:Amino sugar and nucleotide sugar metabolism</b>	*	*	*
<b>mmu00190:Oxidative phosphorylation</b>	****	**	*
<b>mmu00280:Valine, leucine and isoleucine degradation</b>	****	****	NS
<b>mmu04146:Peroxisome</b>	****	**	NS
<b>mmu04141:Protein processing in endoplasmic reticulum</b>	****	*	NS
<b>mmu00020:Citrate cycle (TCA cycle)</b>	****	****	NS
<b>mmu03013:RNA transport</b>	****	**	NS
<b>mmu03010:Ribosome</b>	****	****	NS
<b>mmu00071:Fatty acid degradation</b>	****	****	NS
<b>mmu00650:Butanoate metabolism</b>	****	****	NS
<b>mmu01210:2-Oxocarboxylic acid metabolism</b>	***	***	NS
<b>mmu00630:Glyoxylate and dicarboxylate metabolism</b>	***	****	NS
<b>mmu01230:Biosynthesis of amino acids</b>	**	***	NS
<b>mmu00970:Aminoacyl-tRNA biosynthesis</b>	**	**	NS
<b>mmu05010:Alzheimer's disease</b>	**	**	NS
<b>mmu00310:Lysine degradation</b>	**	**	NS
<b>mmu05012:Parkinson's disease</b>	**	**	NS
<b>mmu03050:Proteasome</b>	**	**	NS
<b>mmu00410:beta-Alanine metabolism</b>	**	**	NS
<b>mmu00920:Sulfur metabolism</b>	**	**	NS
<b>mmu00270:Cysteine and methionine metabolism</b>	**	*	NS
<b>mmu00010:Glycolysis / Gluconeogenesis</b>	**	*	NS
<b>mmu05016:Huntington's disease</b>	*	**	NS
<b>mmu00072:Synthesis and degradation of ketone bodies</b>	*	**	NS
<b>mmu00250:Alanine, aspartate and glutamate metabolism</b>	*	**	NS
<b>mmu00860:Porphyrin and chlorophyll metabolism</b>	*	*	NS
<b>mmu04932:Non-alcoholic fatty liver disease (NAFLD)</b>	*	*	NS
<b>mmu01040:Biosynthesis of unsaturated fatty acids</b>	**	NS	*
<b>mmu04922:Glucagon signaling pathway</b>	**	NS	*
<b>mmu00061:Fatty acid biosynthesis</b>	**	NS	*
<b>mmu04710:Circadian rhythm</b>	*	NS	*

# Key Genes Affected by Microgravity in Liver – Astronauts may develop NASH disease



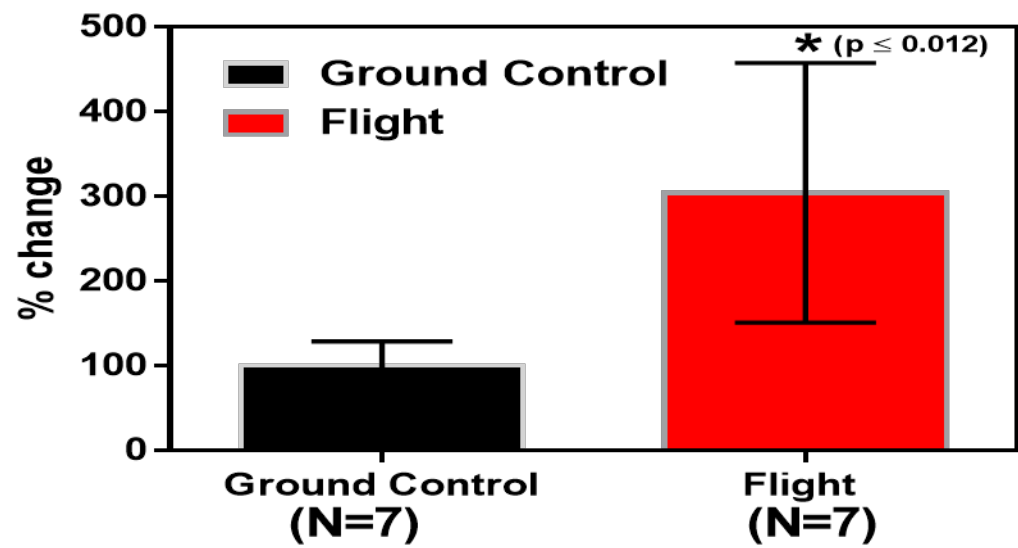
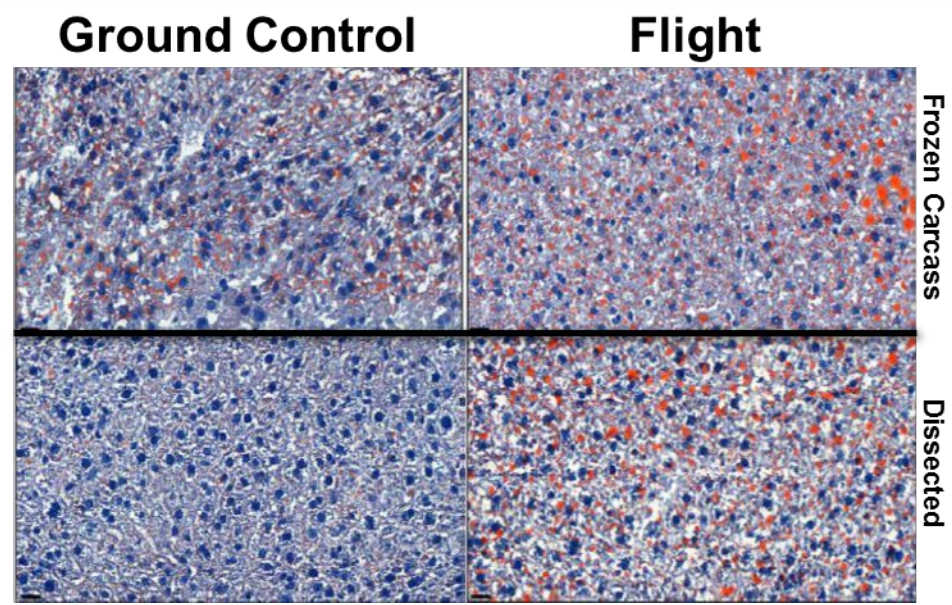
Key genes determined by the following:



- Common theme shows **PPARA** being putative key regulator in the liver
- Disruption of PPARA pathways is typically a precursor to liver disease
- Leads to hypothesis generation of possible mechanism occurring in the liver that is impacted by space radiation and microgravity.



# Histopathology Confirms Liver Disease



# Confounding Factor 1: Cage Effects

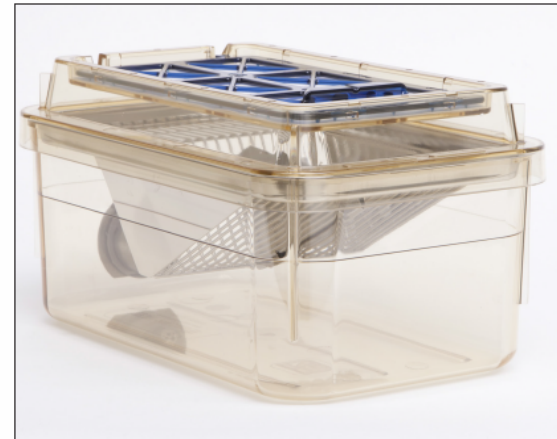
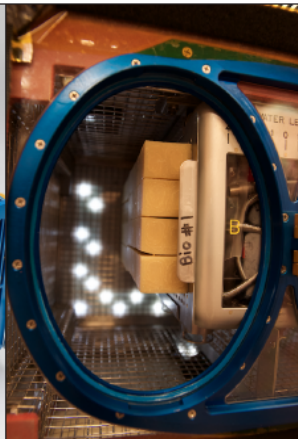


Vivarium vs Rodent Habitat control (AEM) across 5 different rat/mice studies, (no flight samples – CO2 level matches flight info)

## Cage Types

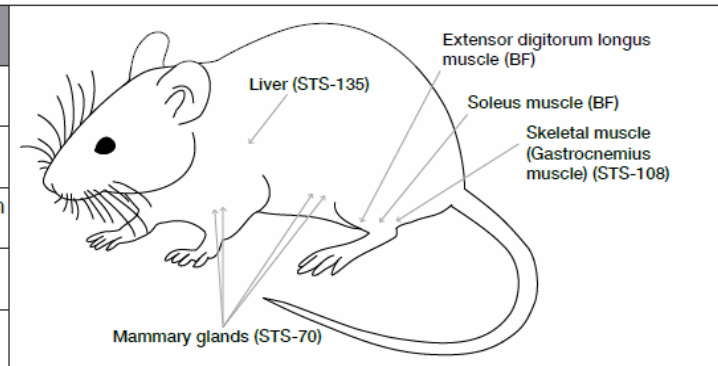


Animal Enclosure Module (AEM)



Sample vivarium cage

GeneLab study	Mission	Species	CO <sub>2</sub> (ppm)	Tissue type
GLDS-21	STS-108	mouse	~3000	skeletal muscle (gastrocnemius)
GLDS-111	BF	mouse	~600	soleus muscle
GLDS-111	BF	mouse	~600	extensor digitorum longus muscle
GLDS-25	STS-135	mouse	~3000	liver
GLDS-63	STS-70	rat	~3000 (est.)	mammary gland



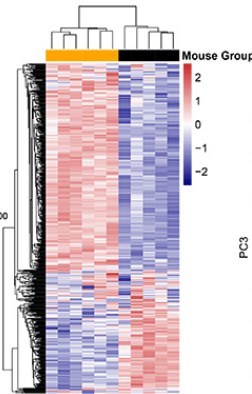
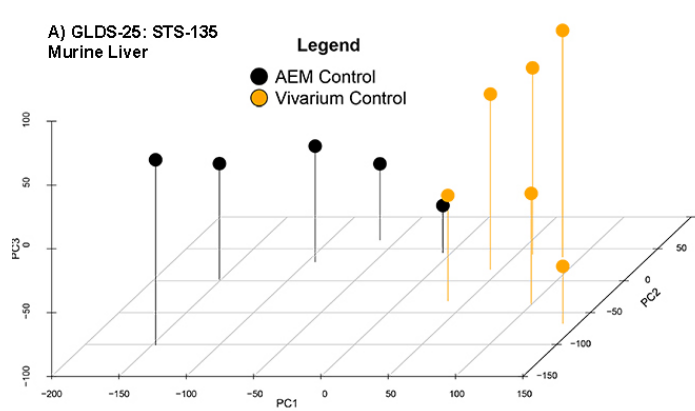
# PCA Plots Suggest Strong Cage Effect



3000 ppm

A) GLDS-25: STS-135  
Murine Liver

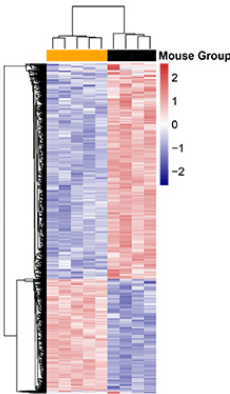
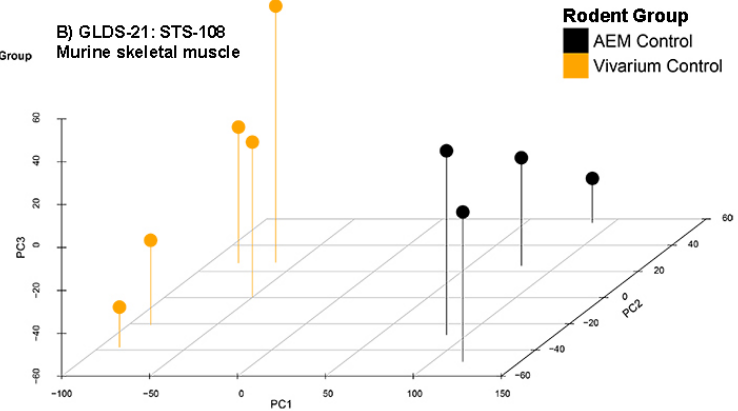
**Legend**  
 ● AEM Control  
 ● Vivarium Control



3000 ppm

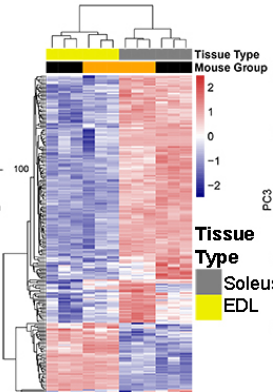
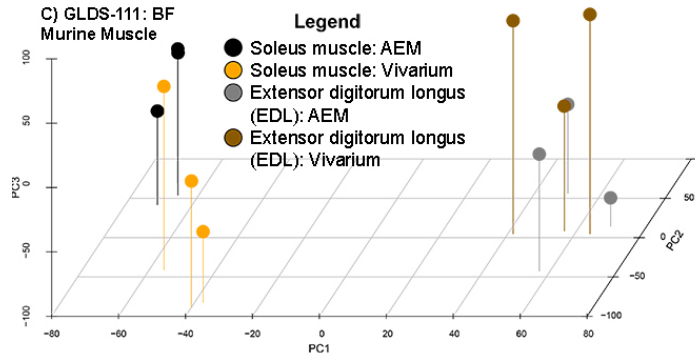
B) GLDS-21: STS-108  
Murine skeletal muscle

**Rodent Group**  
 ● AEM Control  
 ● Vivarium Control



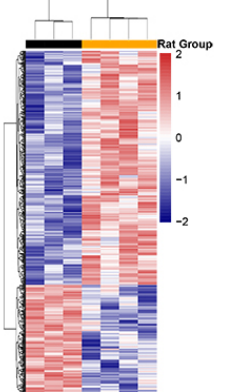
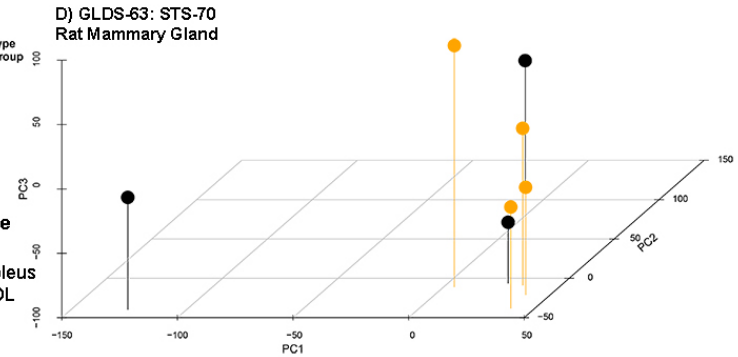
C) GLDS-111: BF  
Murine Muscle

**Legend**  
 ● Soleus muscle: AEM  
 ● Soleus muscle: Vivarium  
 ● Extensor digitorum longus (EDL): AEM  
 ● Extensor digitorum longus (EDL): Vivarium



600 ppm

D) GLDS-63: STS-70  
Rat Mammary Gland



3000 ppm

# Differential Gene Expression: Cage or CO2 Effect?



A) Venn Diagram of all significant genes

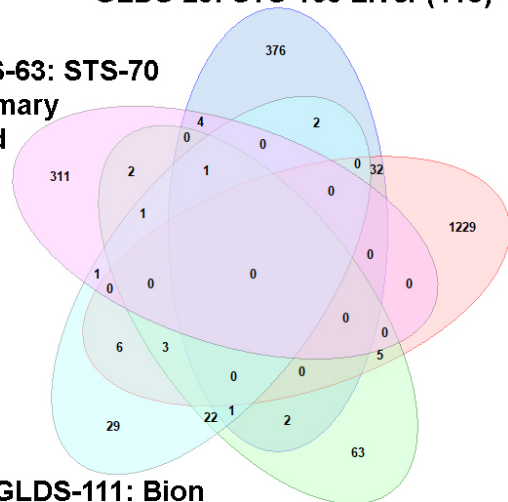
GLDS-25: STS-135 Liver (418)

GLDS-63: STS-70  
Mammary  
Gland  
(348)

GLDS-21: STS-108  
Skeletal Muscle  
(1303)

GLDS-111: Bion  
Extensor Digitorum  
Longus (66)

GLDS-111: Bion  
Soleus Muscle  
(100)



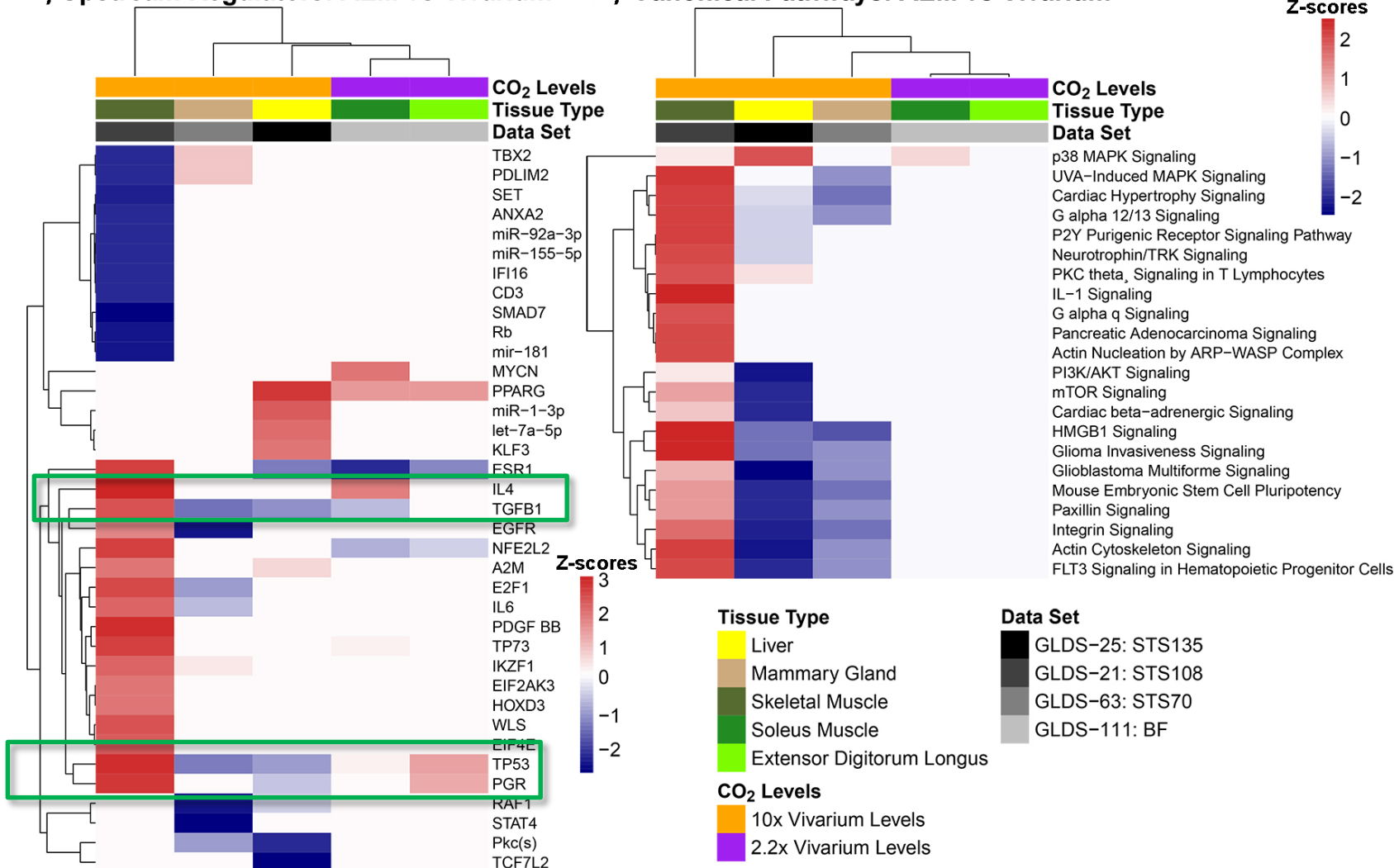
An increase in aldosterone is associated with metabolic syndrome, which is characterized by chronic inflammation; aldosterone secretion can be triggered by hypoxia.

# Upstream regulators and canonical pathways show response is tissue specific and highest for high CO<sub>2</sub>



A) Upstream Regulators: AEM vs Vivarium

B) Canonical Pathways: AEM vs Vivarium

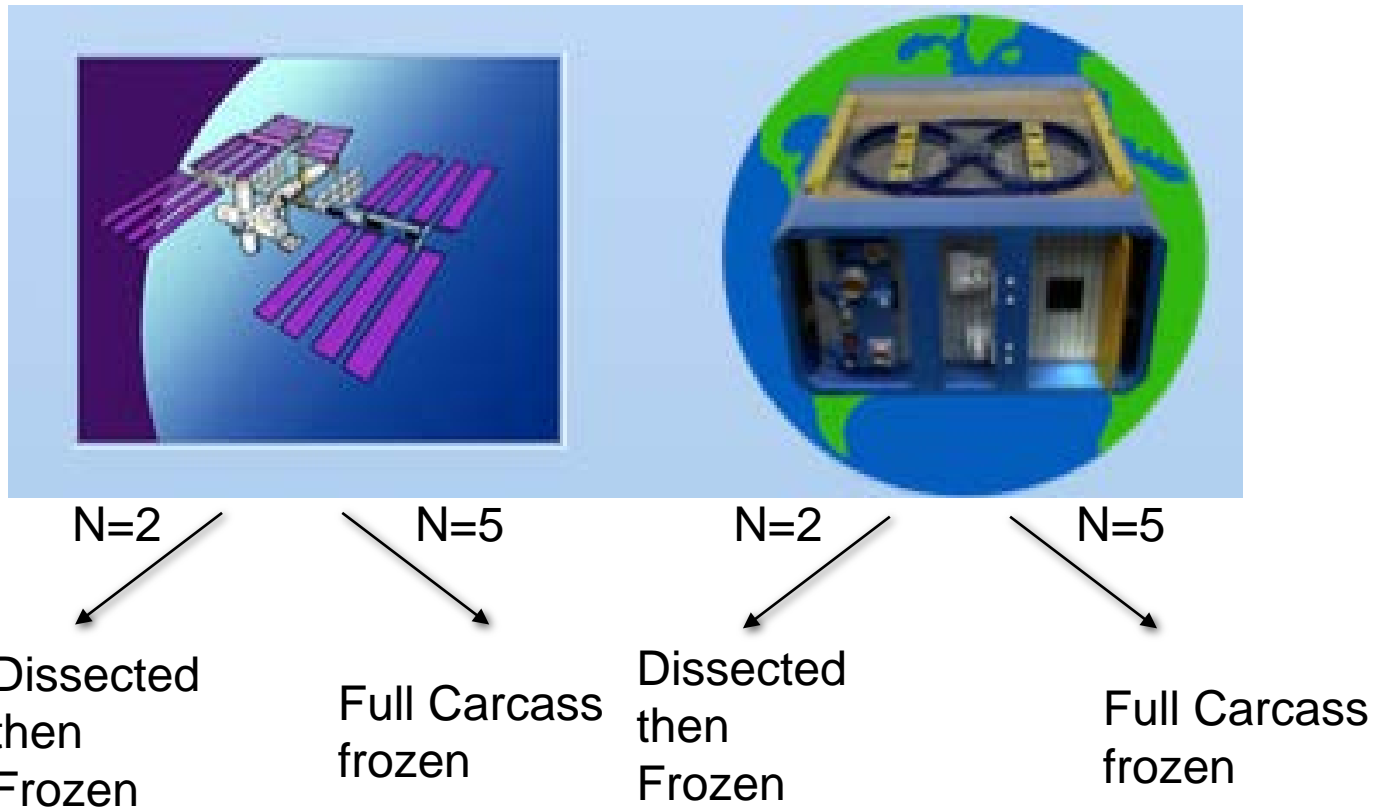


Mild chronic hypoxia due to increased CO<sub>2</sub> levels could explain both the increase in immune responses and a reduction in metabolism – **Need to confirm with AEM experiments at ambient CO<sub>2</sub> levels.**

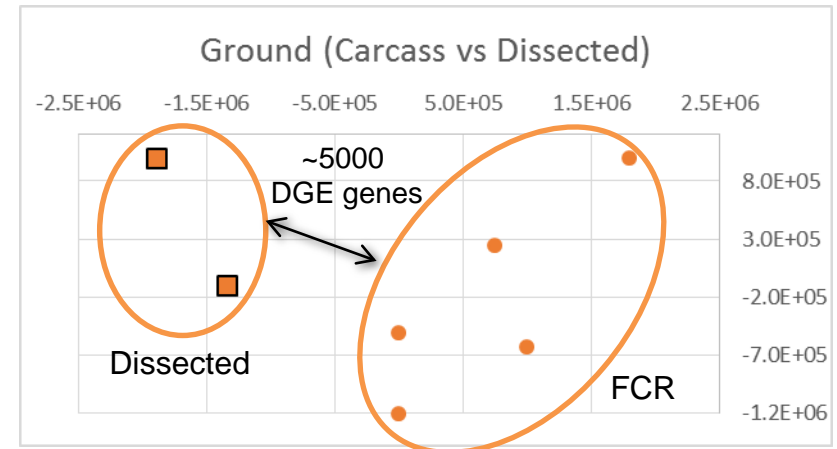
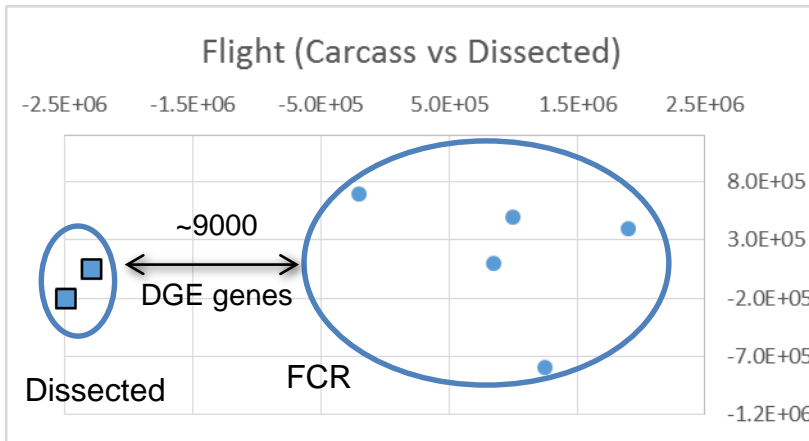
# Confounding Factor 2: Preservation Methods in Space



## Liver collection for RR1




# Principal Component Analysis of On-Orbit Dissected vs Frozen Carcass Livers

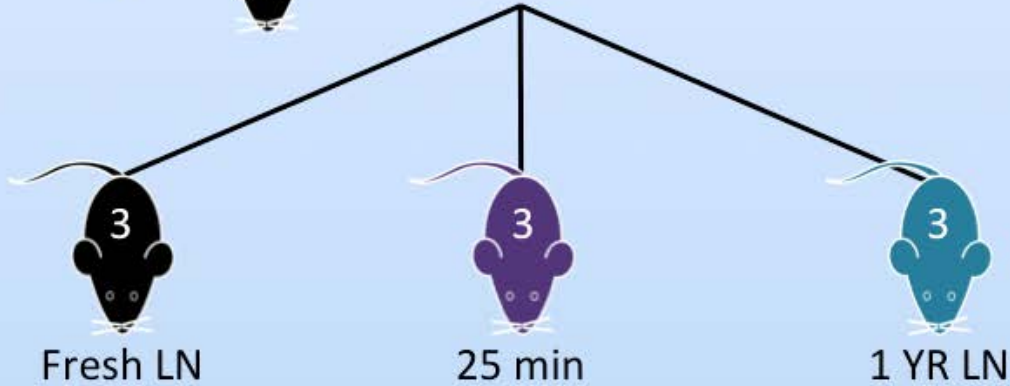


➔ Strong separation of differentially expressed genes between FCR and frozen tissue, either in space or on the ground (worst in space) – 4000 genes in common, principally linked to catabolic pathways (i.e. tissue degradation).

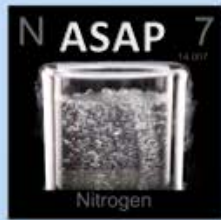
# Transcriptomics Data: Pre-validation Experiment



N =  9 C57BL/6J female mice, 12 weeks



Dissection

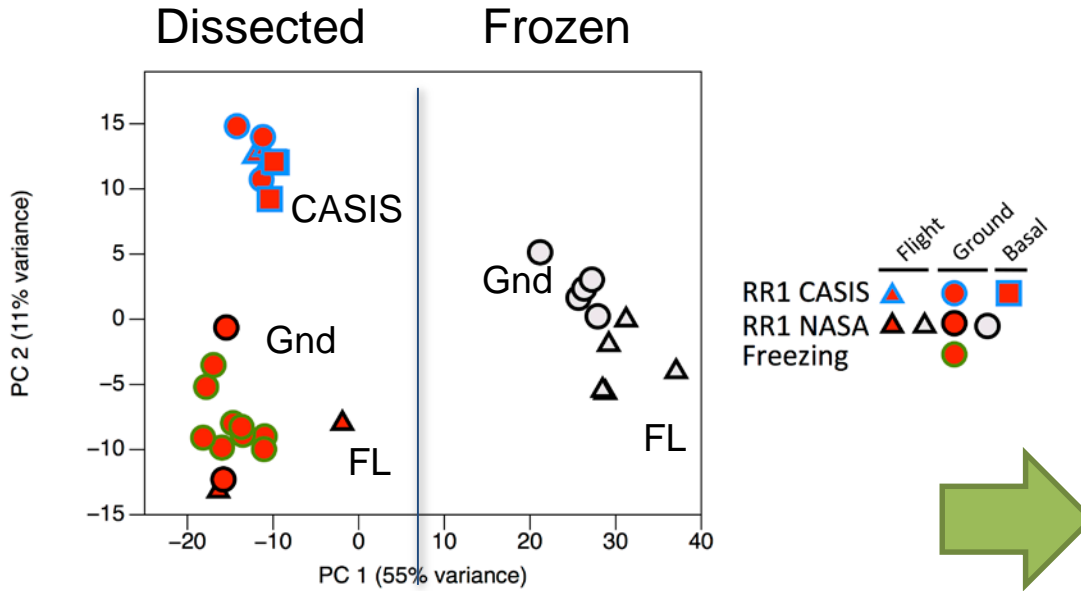


Storage Time





# Freezing Before Dissection Changes RNA



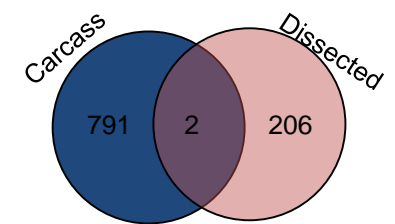
## New experimental design to understand:

1. Is this effect specific to liver?
2. Are drugs used for euthanasia creating a system effect?
3. Can conclusions be reached by having proper controls?

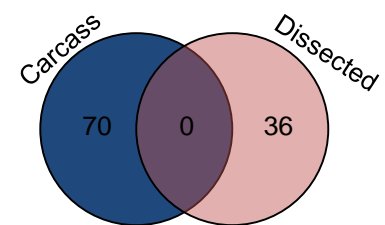
## Principal component analysis of liver samples:

- Triangles - flight samples
- Circles - ground samples
- Squares - basal controls
- Red fill - dissected
- Gray fill - frozen carcass
- Blue outline: RR1 CASIS
- Black outline: RR1 NASA,
- Green outline: Freezing study

DGE



GSEA



# Science Communications



The screenshot shows the GeneLab website interface. At the top, there's a header with the NASA logo and 'GeneLab' text. Below the header, there's a navigation menu with links like 'Home', 'About', 'Latest Data Releases', 'GeneLab Data System', 'Analysis Working Groups', 'Upcoming Events', 'Newsletters', 'FAQ', and 'Contact Us'. The main content area is divided into several sections: 'LATEST NEWS' featuring a 'GeneLab Analysis Working Group' announcement with a 'SIGN UP NOW!' button and a photo of Sylvain Costes; 'DATA REPOSITORY' with a search bar and a table of data releases; 'ANALYSIS WORKING GROUPS' with a 'Join the GeneLab Analysis Working Groups' link; 'SOCIAL MEDIA' with links to ResearchGate, Facebook, and Twitter; and 'LATEST DATA RELEASES' with a link to 'Gene expression data from 4T1 irradiated tumors treated with TGFbeta blockade'. A large 'OMICS' graphic is also visible on the right side of the screenshot.

Engage broadest community of researchers, industry, and citizen scientists to advance innovations

<https://genelab.nasa.gov>

- Weekly social media posts:
  - @NASA Ames **Facebook**
  - **Twitter** #GeneLab
  - **ResearchGate**: <https://www.researchgate.net/project/Omics-for-Space-Biology-The-GeneLab-project>
- GeneLab database listed in science journals:
  - *Scientific Data*, Oxford e-Research
- GeneLab issues Digital Object Identifiers (DOI) via DataCite
- Customer Support: Respond and resolve all inquiries from science community, academia, public

# GeneLab Acknowledgements



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Egle Cekanaviciute  
John Costa  
**Sylvain Costes (PM)**  
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Qiang Li  
Shu-Chun Lin  
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Andrew Williamson

