



GeneLab: “Omics” Data Systems for Spaceflight and Simulated Spaceflight Environment

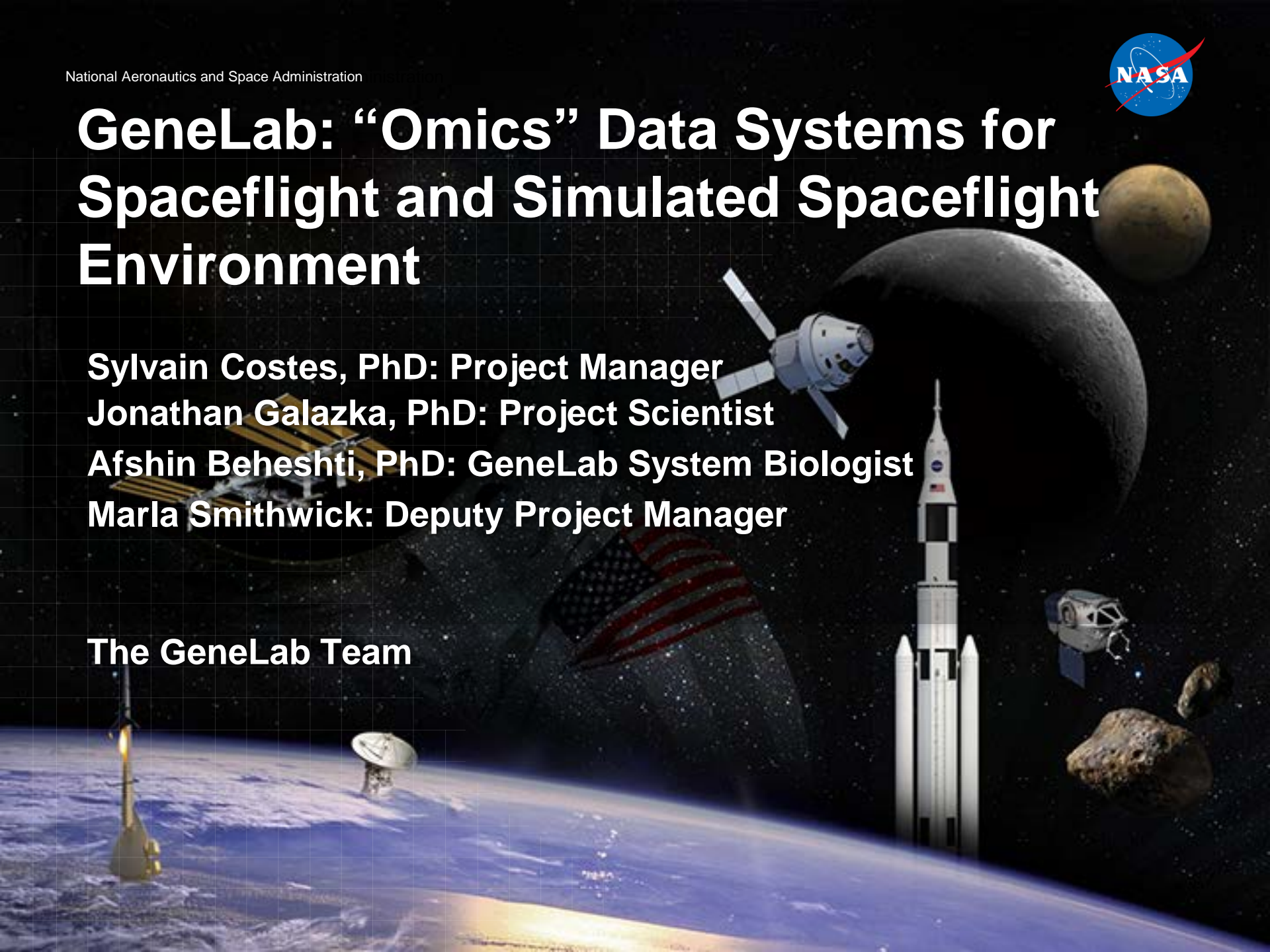
Sylvain Costes, PhD: Project Manager

Jonathan Galazka, PhD: Project Scientist

Afshin Beheshti, PhD: GeneLab System Biologist

Marla Smithwick: Deputy Project Manager

The GeneLab Team



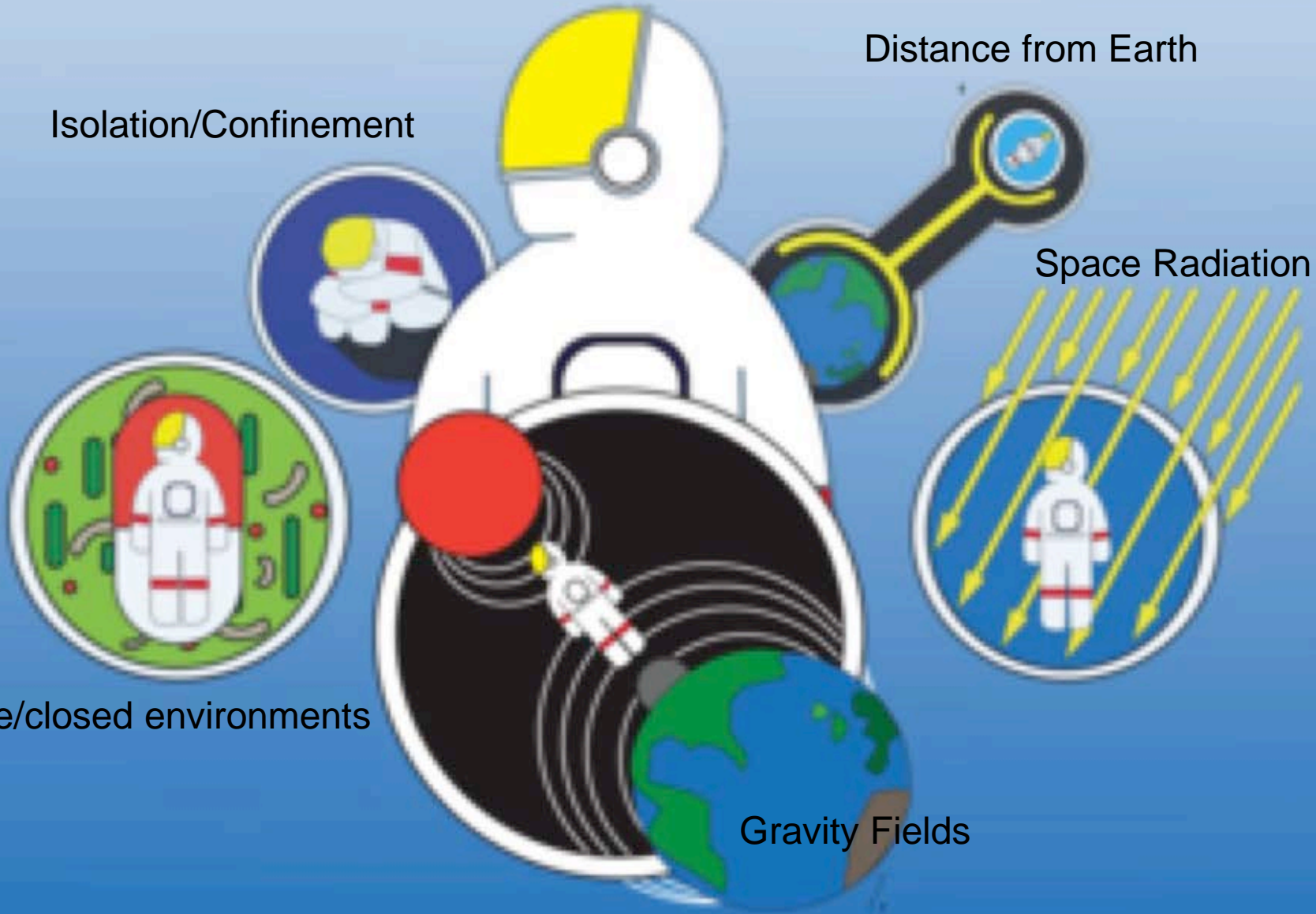
Isolation/Confinement

Distance from Earth

Space Radiation

Hostile/closed environments

Gravity Fields

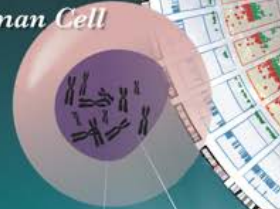




OMICS

A Circular Genome Visualization

Human Cell



Telomere

Chromosome

Chromatin

Methyl Groups

DNA

Telomere

Metabolites

Proteins

RNA

Telomere

A Journey to See More Than Ever Before





**Recapturing a Future
for Space Exploration**

Life and Physical Sciences Research for a New Era

NATIONAL RESEARCH COUNCIL
OF THE NATIONAL ACADEMIES

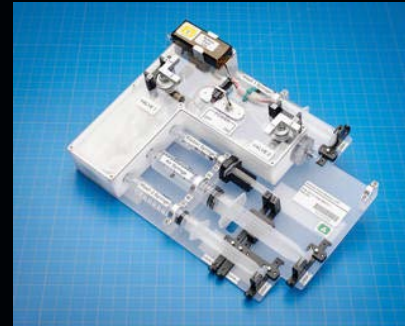
*“...**genomics, transcriptomics, proteomics, and metabolomics** offer an immense opportunity to understand the effects of spaceflight on biological systems...”*

*“...Such techniques generate considerable amounts of **data that can be mined and analyzed** for information by multiple researchers...”*

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



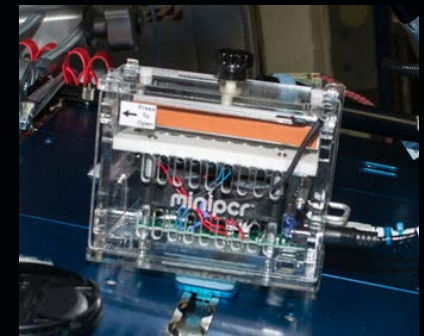
Oxford Nanopore MinION Gene Sequencer



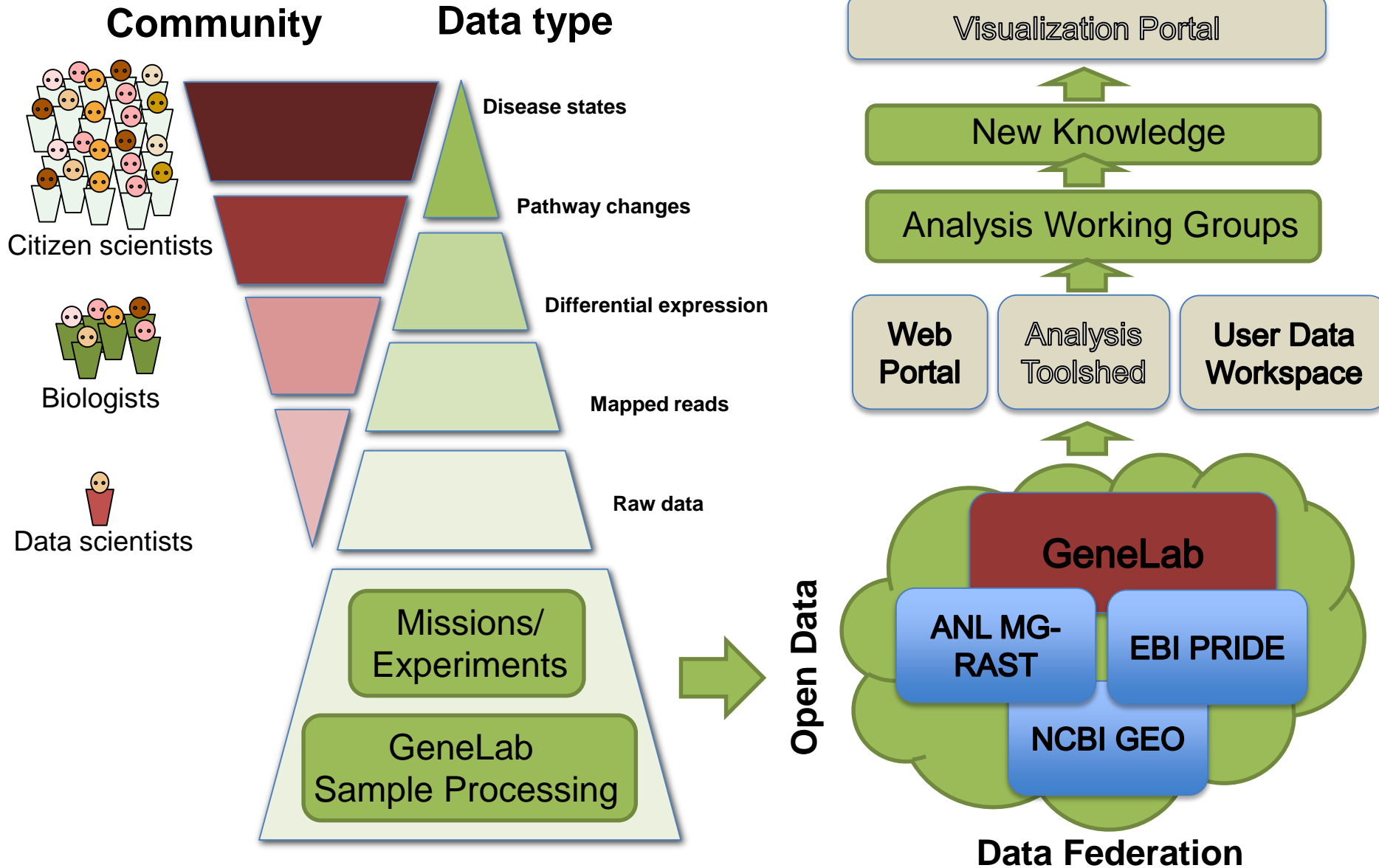
Cepheid Smart Cycler qRT-PCR



Reaction tube containing lyophilized chemical assay bead (proprietary)



Mini-PCR



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 Stim (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 differenti
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 devel proliferation and differentiatio...

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

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.nci.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: Microarxiv Treatment Assay Type: transcription profilin 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"/> Spaceflight	<input type="checkbox"/> Antibiotic conce	<input type="checkbox"/> <i>Oryzias latipes</i>	<input type="checkbox"/> environmental gene survey
<input type="checkbox"/> Spaceflight	<input type="checkbox"/> Atmospheric Pre	<input type="checkbox"/> <i>Pantoea conspicua</i>	<input type="checkbox"/> genome sequencing
<input type="checkbox"/> Spaceflight	<input type="checkbox"/> Bed Rest	<input type="checkbox"/> <i>Pseudomonas aeru</i>	<input type="checkbox"/> metabolite profiling
<input type="checkbox"/> Spaceflight	<input type="checkbox"/> Bleomycin Treat	<input type="checkbox"/> <i>Rattus norvegicus</i>	<input type="checkbox"/> protein expression profiling
<input type="checkbox"/> Spaceflight	<input checked="" type="checkbox"/> cage	<input type="checkbox"/> <i>Rhodospirillum rubr</i>	<input type="checkbox"/> RNA methylation profiling
<input type="checkbox"/> Spaceflight	<input type="checkbox"/> CANONT:Part	<input type="checkbox"/> <i>Saccharomyces ce</i>	<input type="checkbox"/> transcription profiling
<input type="checkbox"/> Spaceflight	<input type="checkbox"/> cell culture	<input type="checkbox"/> <i>Staphylococcus</i>	
<input type="checkbox"/> Spaceflight	<input type="checkbox"/> clinical treatment	<input type="checkbox"/> <i>Staphylococcus aureus</i>	

Factor Name = Age' OR 'Study Factor Name = cage'

Total Search Results Found: **3**

1

cinogenesis Risk

modeling the carcinogenesis process or estimating cancer risks. ance 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

tion profiling Accession: GLDS-88 PI/Contact: Christine Afshin Edward L...



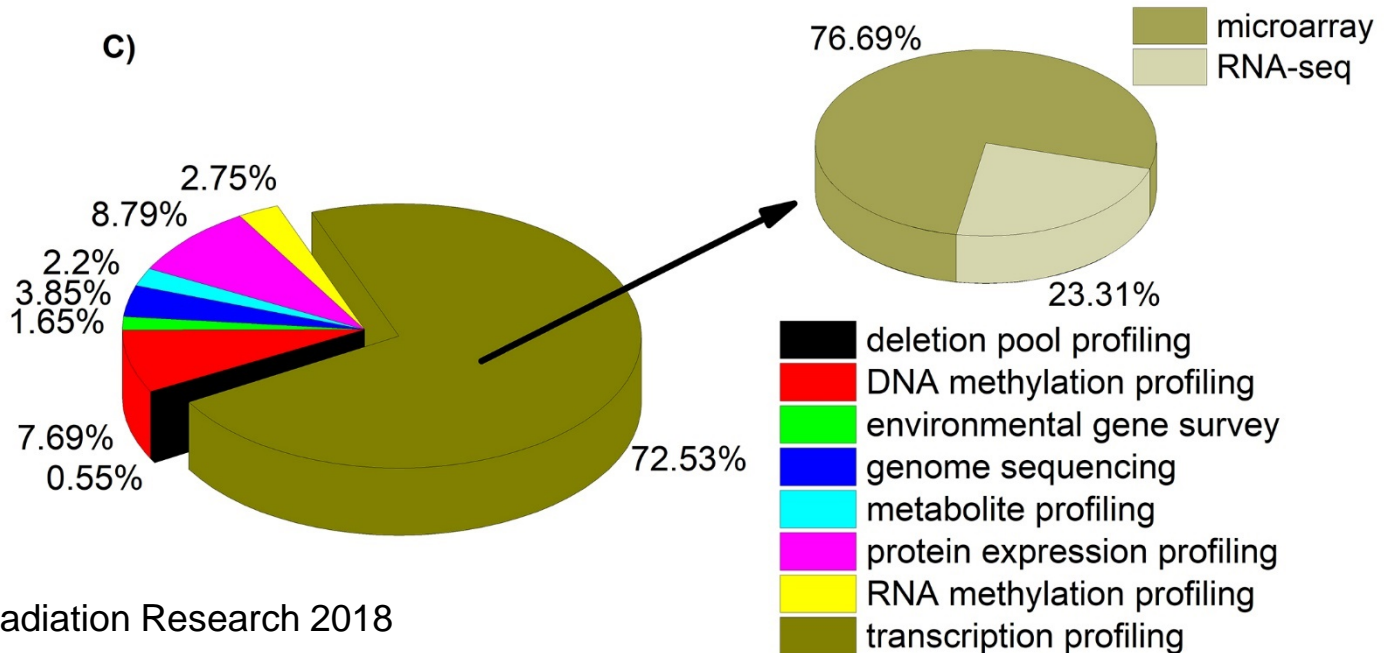
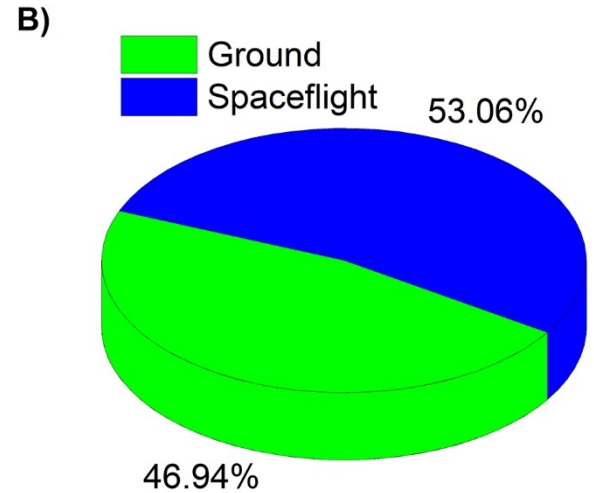
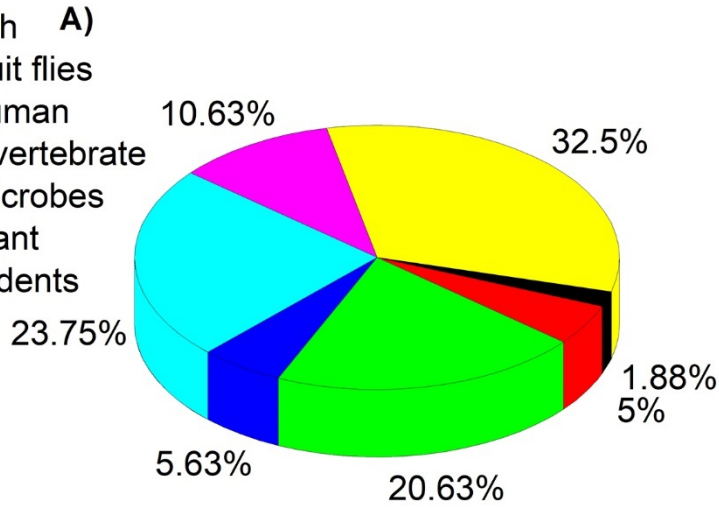
User Account Mgmt., Access Controls (e.g., Private, Shared, Public Folders)

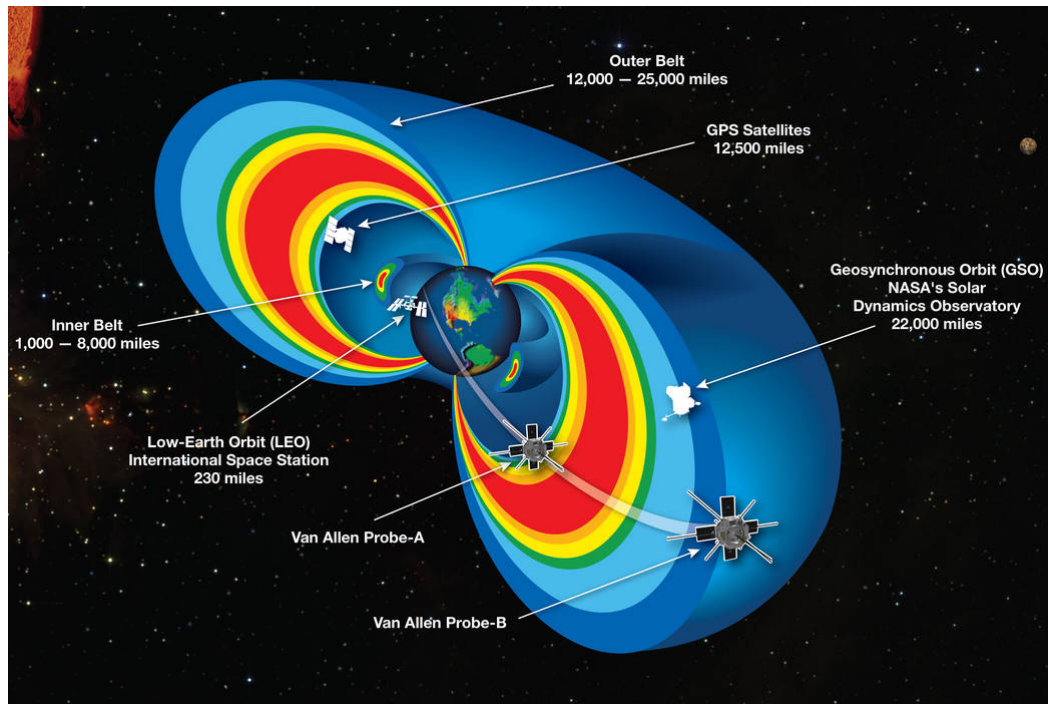
The image displays three overlapping screenshots of the GeneLab web interface:

- Top Left:** The main GeneLab homepage. It features a search bar, navigation tabs (Home, Repository, Data, Data Mining Tools, Submit Data, Contact Us, Workspace), and a list of studies. Two study entries are visible:
 - GLDS-136:** Dissecting Low Atmospheric Pressure Stress: Transcriptome Responses to the Components of Hypobaria in Arabidopsis [Experiment 2]. Organism: Arabidopsis thaliana. Factors: Atmospheric Pressure. Assay Types: Transcription profiling. Release Date: 11-May-2017.
 - GLDS-137:** Global gene expression analysis highlights microgravity sensitive key genes in longissimus dorsi and tongue of 30 days space-flown mice. Organism: Mus musculus. Factors: Microgravity. Assay Types: Transcription profiling. Release Date: 23-May-2017.
- Top Right:** The login page titled "NASA GeneLab-GenomeSpace OpenID Login". It includes fields for USERNAME and PASSWORD, "Sign In" and "Cancel" buttons, and links for "Register new NASA GeneLab user" and "Forgot your password?". A disclaimer box at the bottom states: "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..."
- Bottom:** A file browser view of the "genelab-data" directory. The breadcrumb path is "Home > Public > genelab > genelab-data". The interface shows a sidebar with a folder tree, a main file list, and a toolbar with "FireBrowse" and "GenePattern" options. The file list contains the following entries:

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		

- fish
- fruit flies
- human
- invertebrate
- microbes
- plant
- rodents



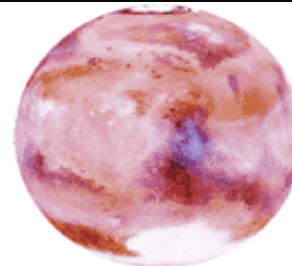


	MILLIREM:
CHEST X-RAY	8 to 50
AVG. YEARLY RADON DOSE	200
U.S. AVG. YEARLY DOSE	350
PET SCAN	1,000
1 YEAR IN KERALA, INDIA	1,300
U.S. NUCLEAR WORKER LIMIT PER YEAR	5,000
APOLLO 14 (9 DAYS)	1,140
SHUTTLE 41-C (18 DAYS)	5,600
SKYLAB 4 (84 DAYS)	17,800
MARS MISSION TOTAL	130,000

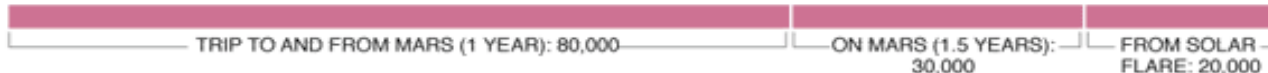
2½ Years, 2,600 X-Rays

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



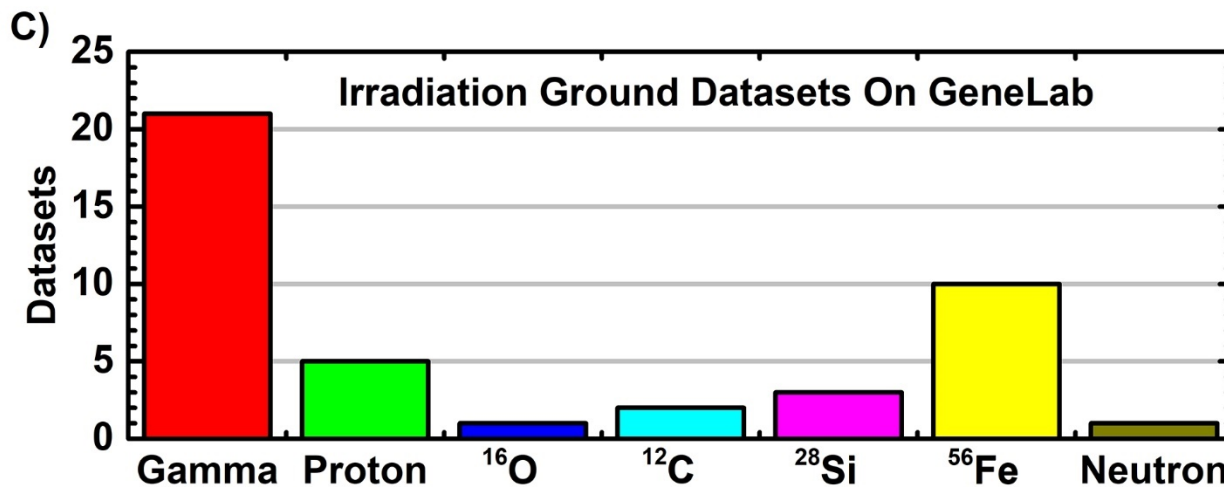
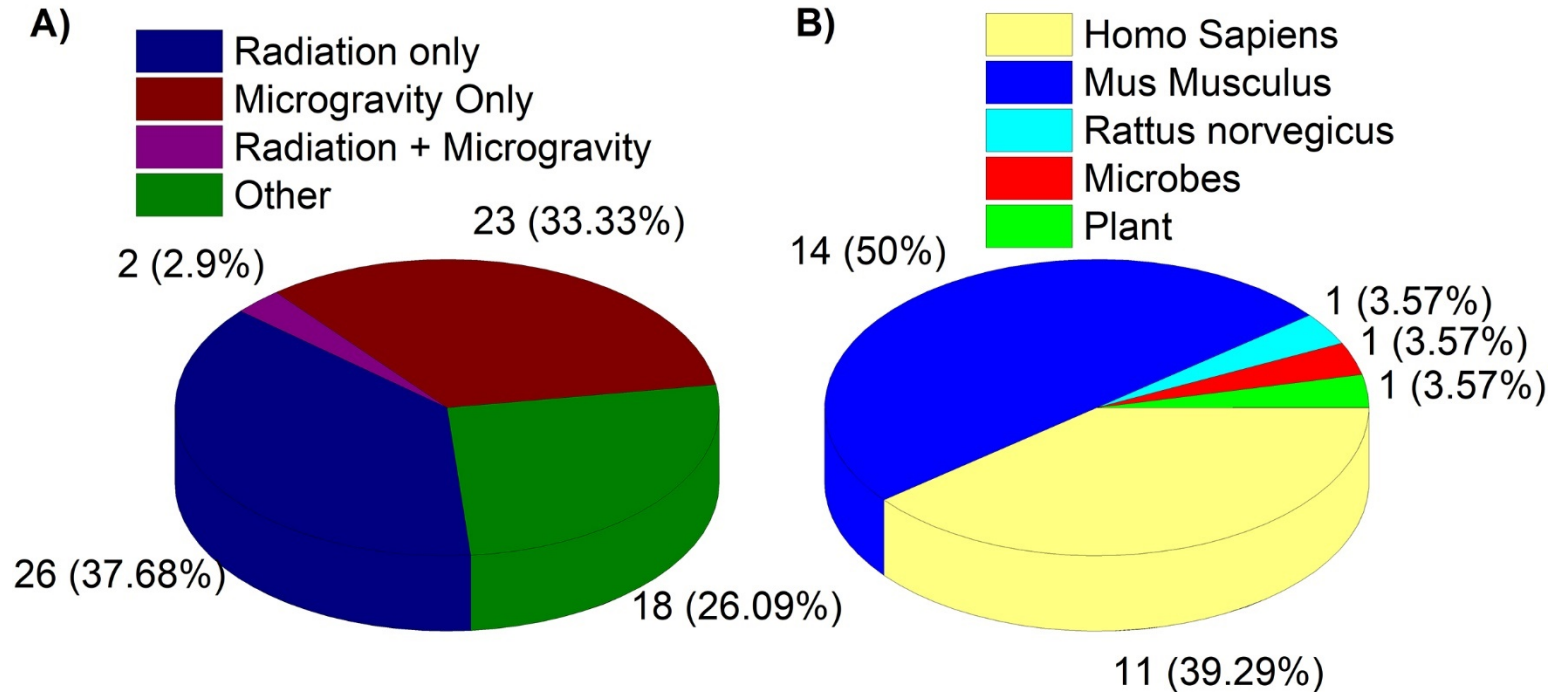
Source: Brookhaven National Laboratory, U.S. Department of Energy



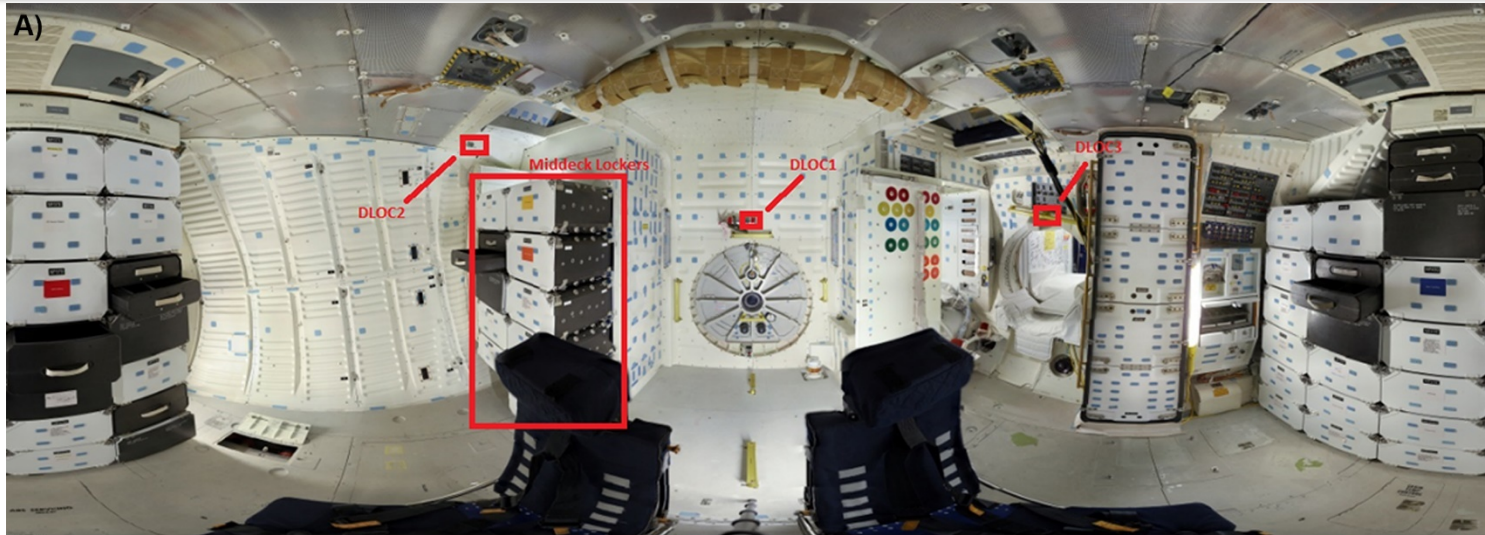
343

CAUTION
LASER RADIATION
DO NOT STARE INTO BEAM
★
CLASS 3 RADIATION
630-690 nm (RED)
- 1 mW CONTINUOUS

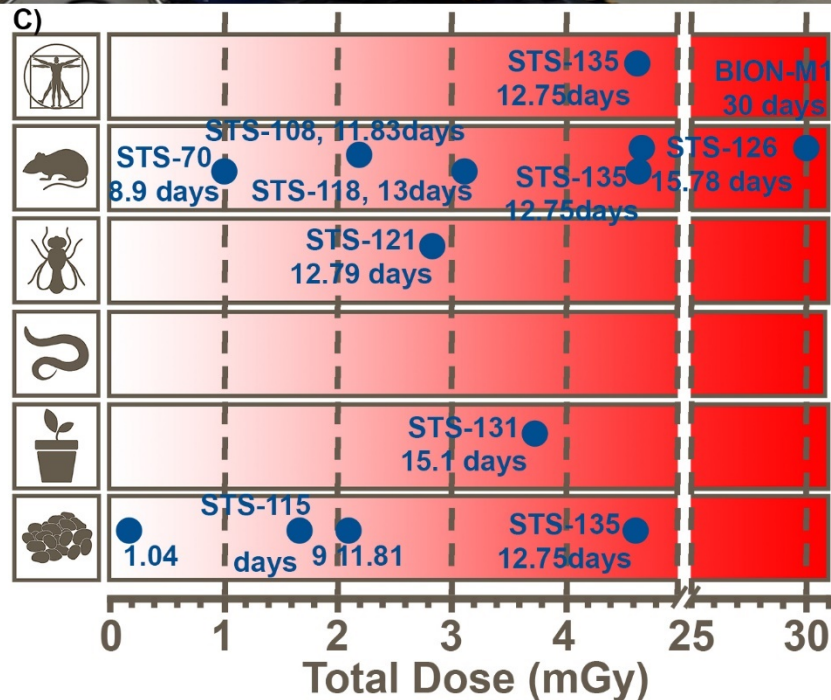
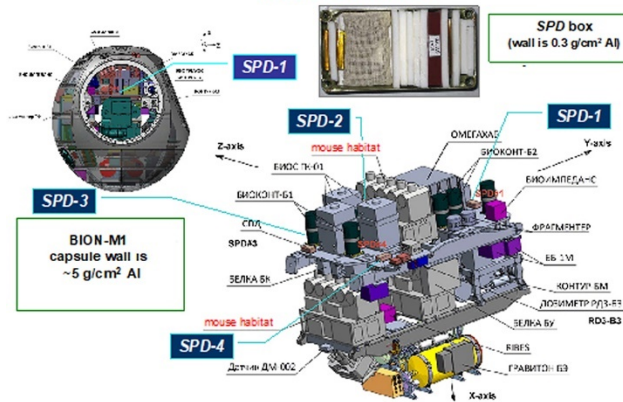
69 Ground Data Sets: Radiation and simulated microgravity



Radiation Dosimetry for STS samples (ISS to follow)



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



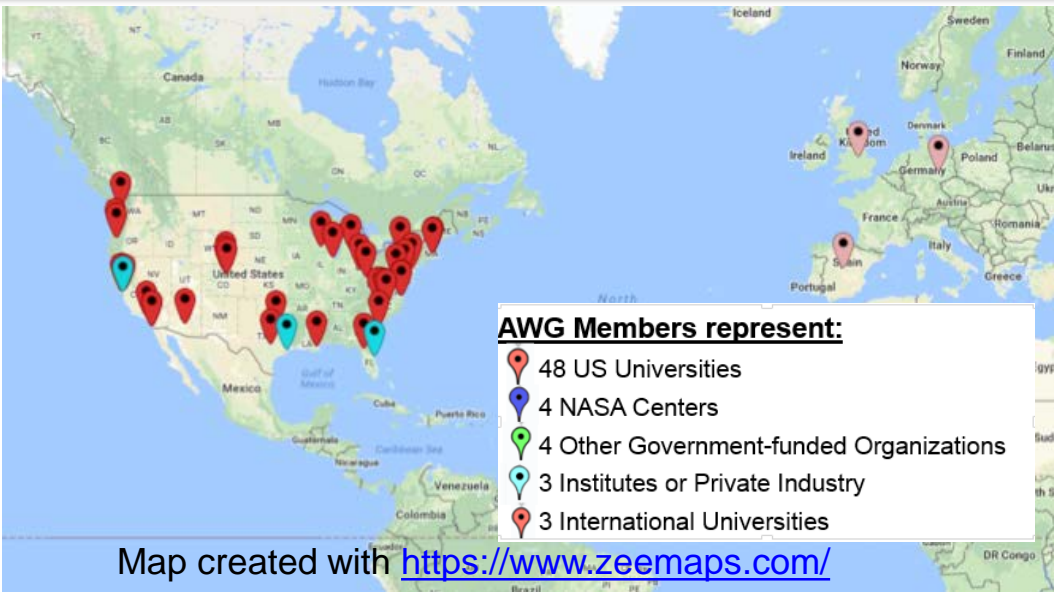
Barriers to reproducible analysis of omics data:

1. Large files are difficult to move around and process
2. Workflows vary from user to user and details are sometimes poorly documented

Galaxy platform:

1. Open source, extensible platform for cloud based analysis of omics data
2. Allows any command line tool or script to be run and chained together into workflows
3. Workflows can published, shared and downloaded



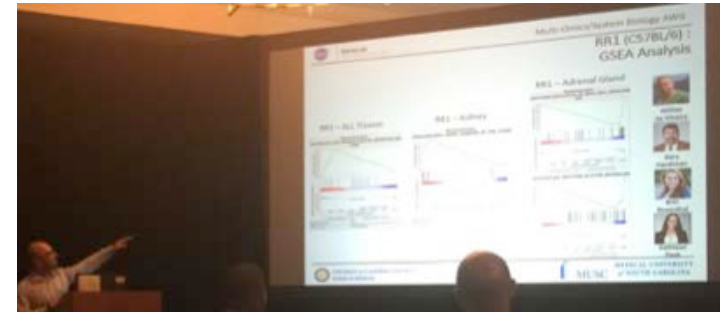


Total AWG Members: 114

AWG Members Per Group:

Animal	47
Multi-Omics/System Biology	33
Plants	24
Microbes	21

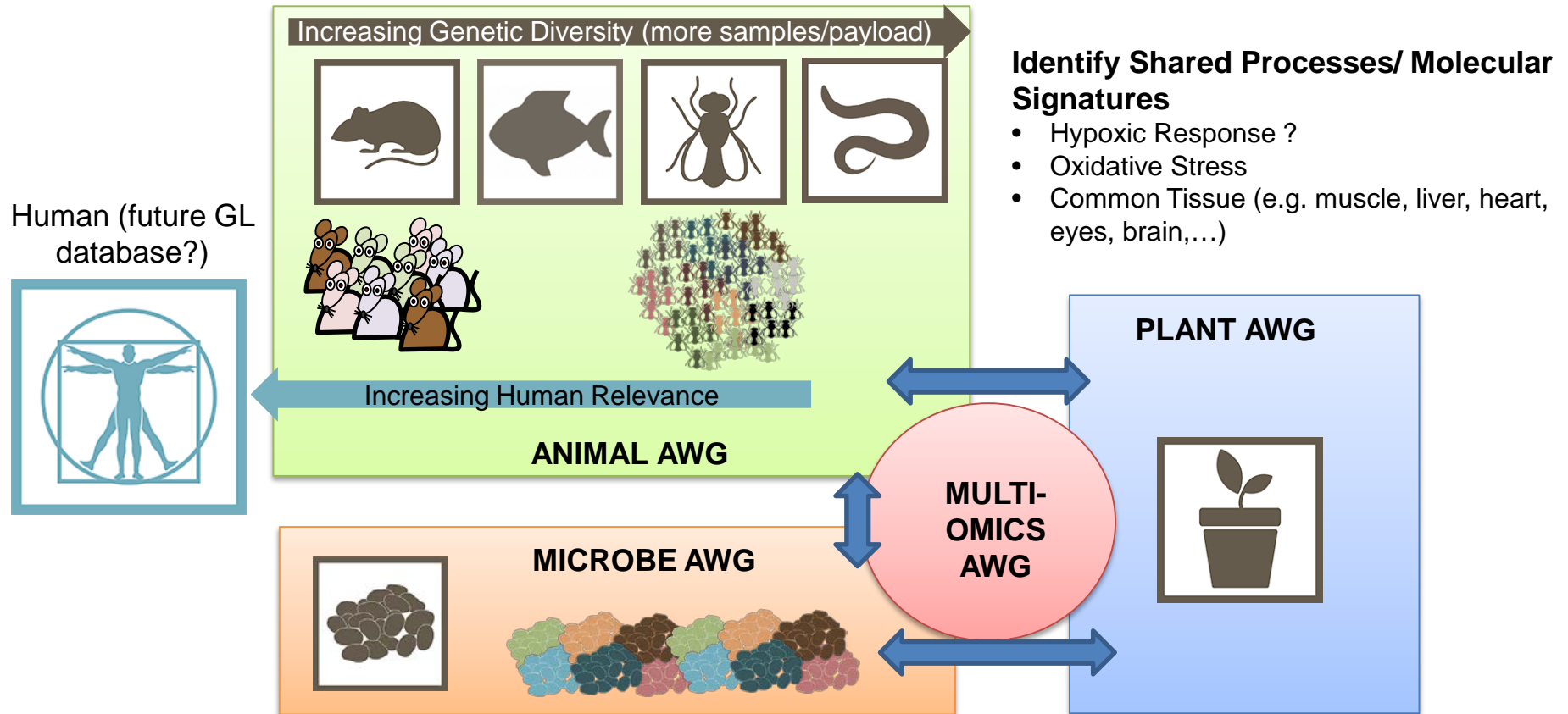
**Some members are in multiple groups*

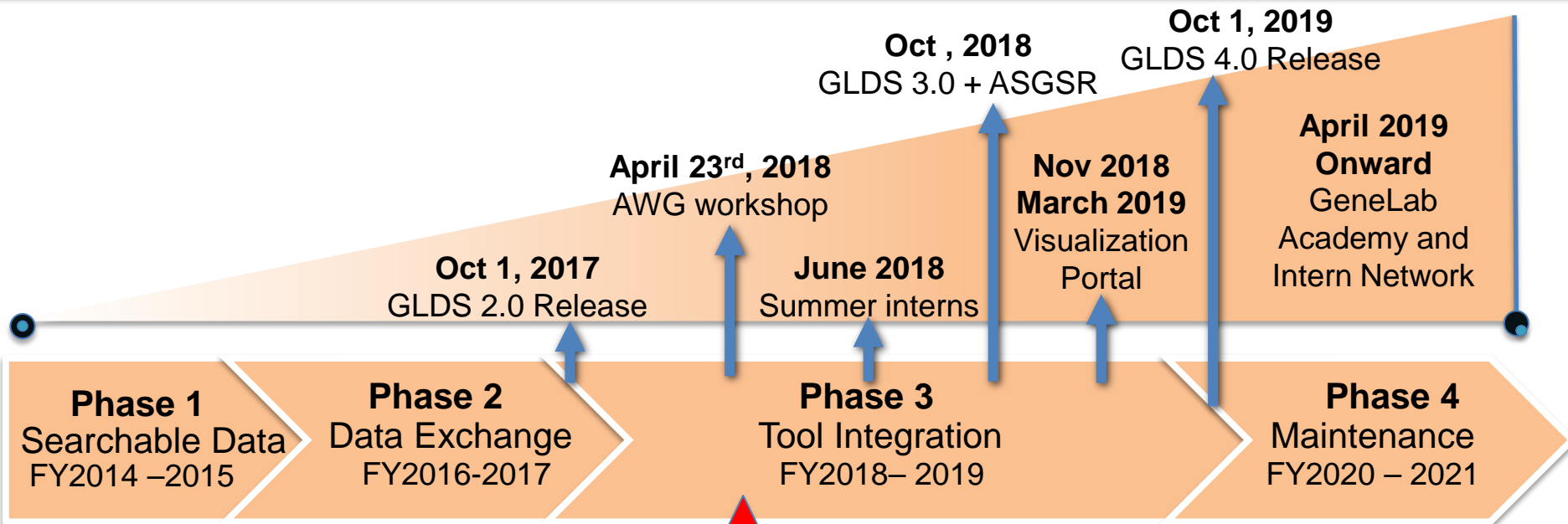


- **Monthly meetings + “Homework”**
- **One Annual Workshop (April)**
- **Summer internship (8 – 10 students for 10 weeks)**
- **Deliverables:**
 - Consensus pipelines for primary analysis of data (Microarray, RNASeq, Bisulfite sequencing, Proteomics, 16S metagenomics, Whole genome metagenomics)
 - Recommendations for visualization of data



Guiding principles to look at GeneLab data



**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)

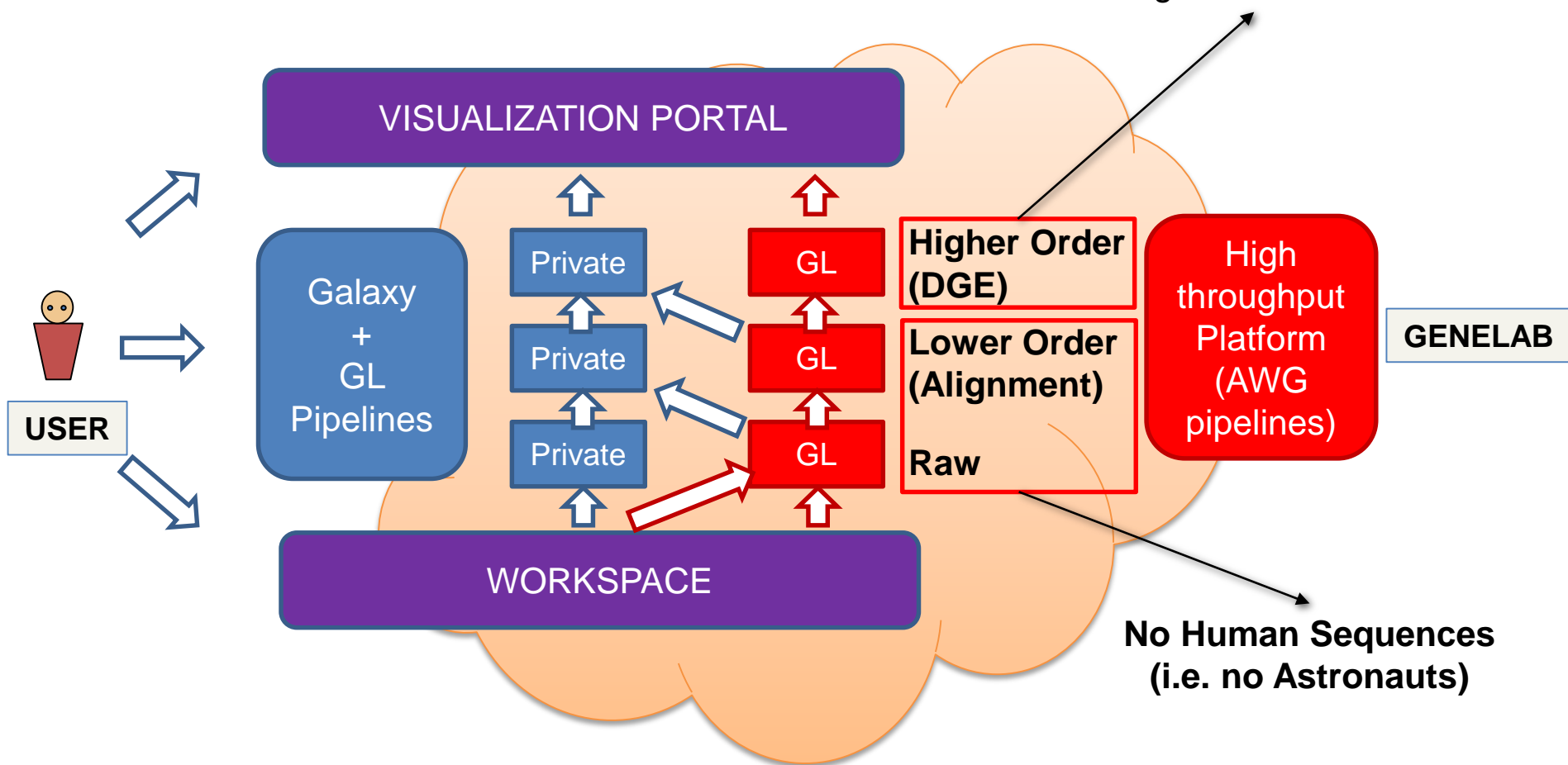
Data System

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

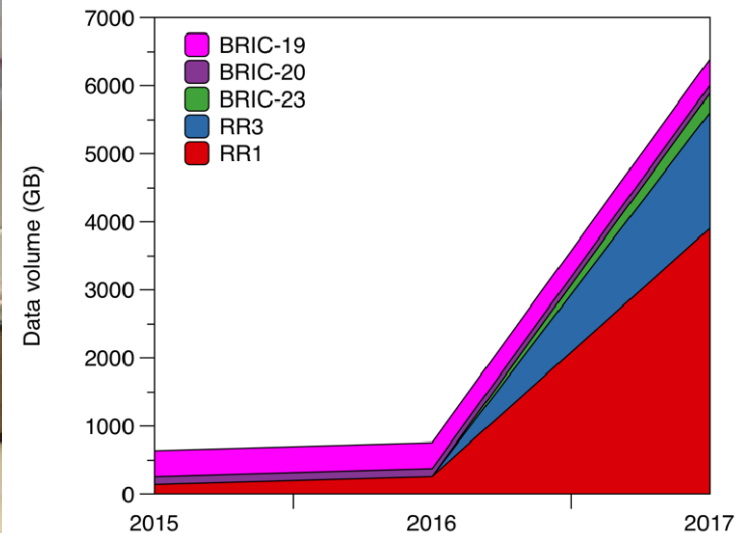
Open Source Maintenance

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

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



- Expertise:
 - DNA/RNA/protein extraction
 - Animal work
 - In-house Sequencing (including Library Prep)
- Develop standards for sample processing (species dependent)
- Responsible for ~50% of GeneLab data by volume – NCI TCGA model: keeping data as consistent as possible.





- Cage Effects with rodent experiments: Carbon Dioxide as an Environmental Stressor in Spaceflight
- Systems Biology analysis reveals biological spaceflight master regulators
- AWG related work determines novel systemic biological factors causing damage due to spaceflight

Cage Effects with rodent experiments: Carbon Dioxide as an Environmental Stressor in Spaceflight

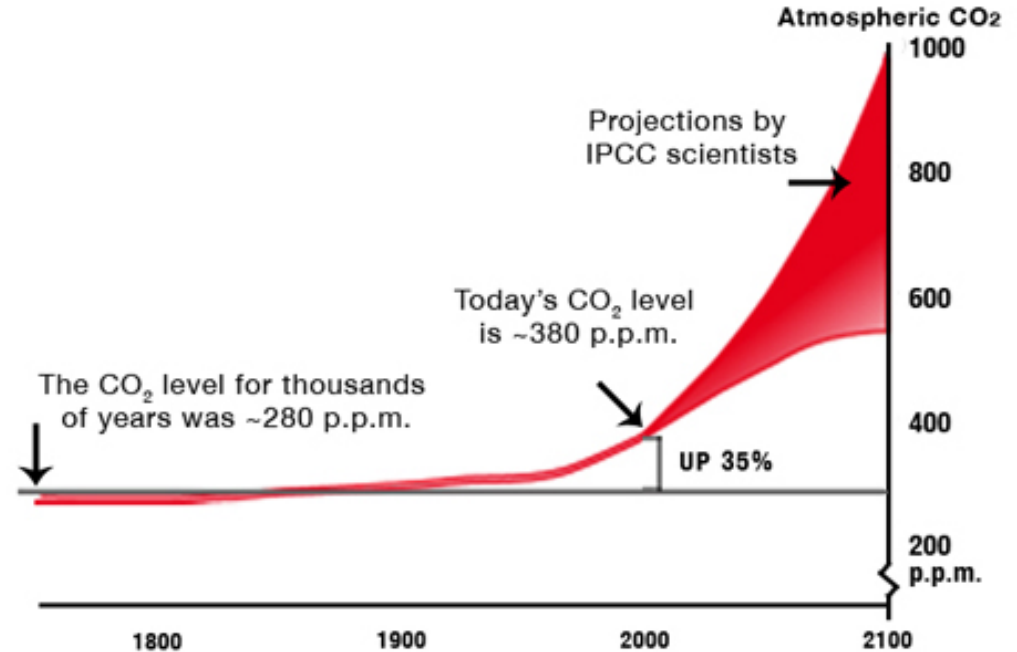
Beheshti A, Cekanaviciute E, Smith DJ, Costes SV. Global transcriptomic analysis suggests carbon dioxide as an environmental stressor in spaceflight: A systems biology GeneLab case study. *Sci Rep.* 2018;8(1):4191. doi: 10.1038/s41598-018-22613-1. PubMed PMID: 29520055; PMCID: PMC5843582.

A) Cage Types



Animal Enclosure Module (AEM)

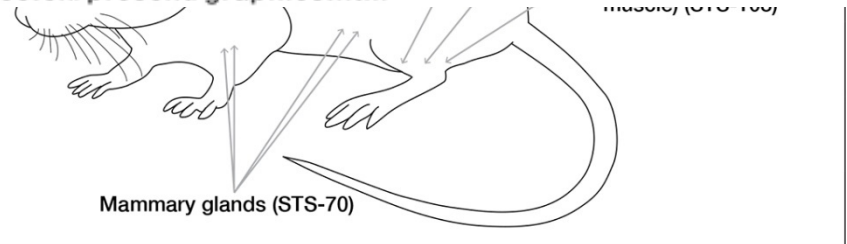
Historic and Projected CO₂ Atmospheric Concentrations



Source: IPCC
<http://www.ipcc.ch/present/graphics.htm>

B)

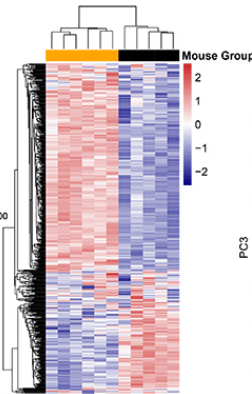
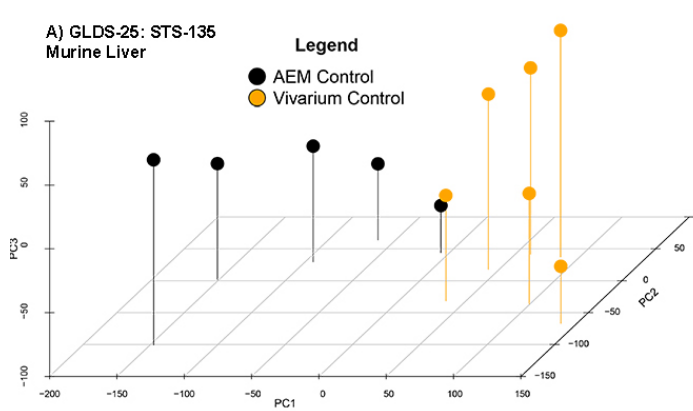
GeneLab Study	Mission	Species	CO ₂ (ppm)	Duration (days)	
GLDS-21	STS-108	mouse	~3000	11.8	
GLDS-111	BF	mouse	~600	30	
GLDS-111	BF	mouse	~600	30	extensor digitorum
GLDS-25	STS-135	mouse	~3000	13	liver
GLDS-63	STS-70	rat	~3000 (est)	9	mammary gland



3000 ppm

A) GLDS-25: STS-135
Murine Liver

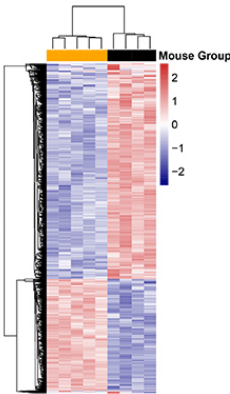
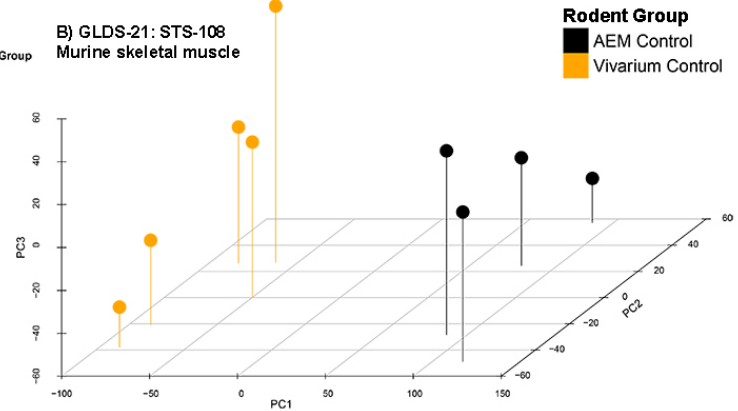
Legend
● AEM Control
● Vivarium Control



3000 ppm

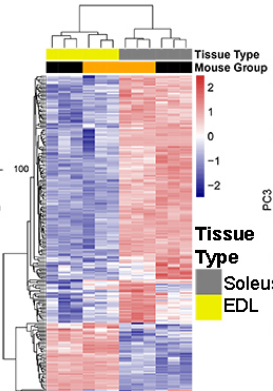
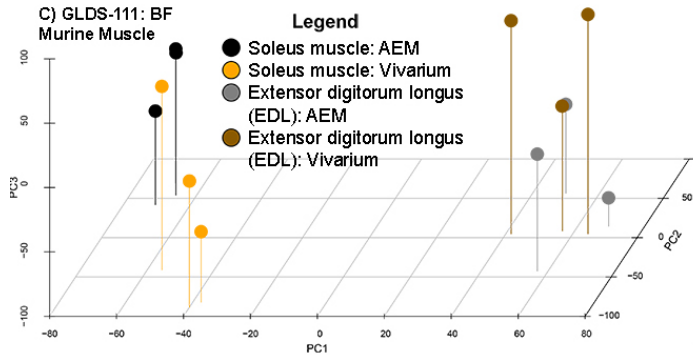
B) GLDS-21: STS-108
Murine skeletal muscle

Rodent Group
● AEM Control
● Vivarium Control



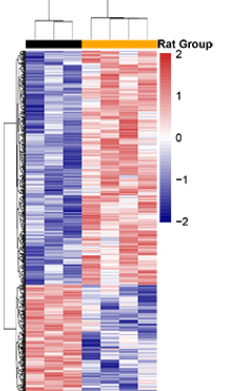
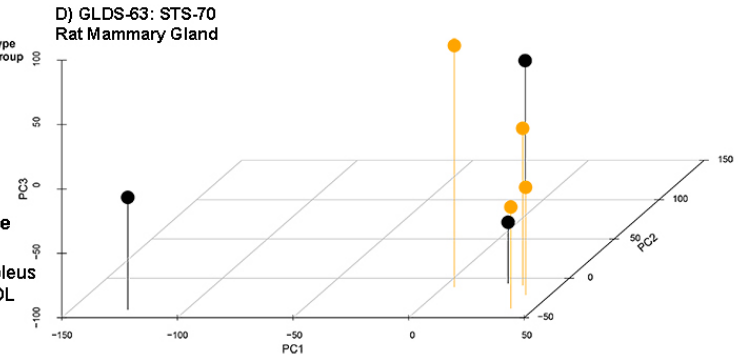
C) GLDS-111: BF
Murine Muscle

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

AEM = Animal Enclosure Modules (now referred to as Rodent Habitats)
Vivarium = normal ground based rodent cages

A) Venn Diagram of all significant genes

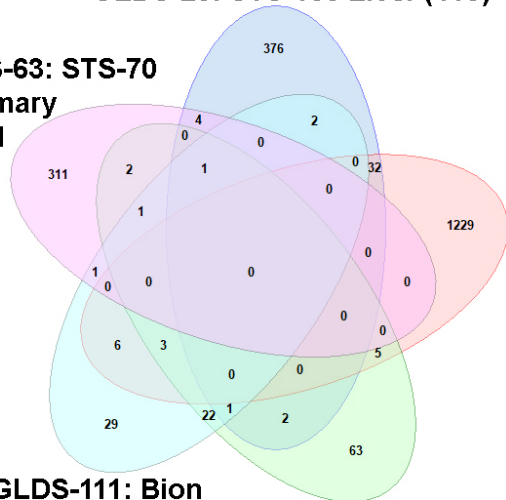
GLDS-25: STS-135 Liver (418)

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)



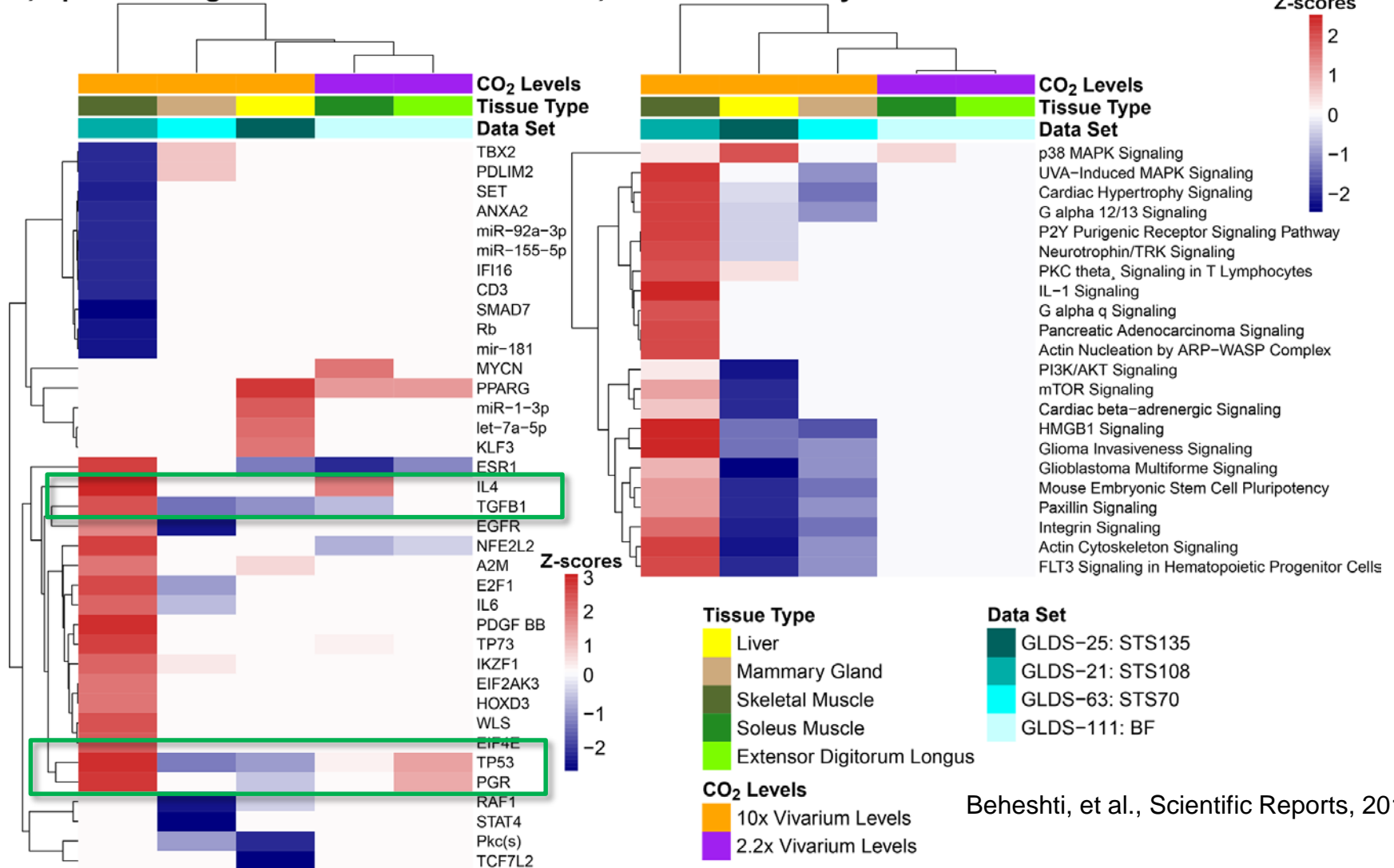
An increase in aldosterone is associated with metabolic syndrome, which is characterized by chronic inflammation; aldosterone secretion can be triggered by hypoxia.

Upstream regulators and canonical pathways show response is tissue specific and highest for high CO₂



A) Upstream Regulators: AEM vs Vivarium

B) Canonical Pathways: AEM vs Vivarium



Mild chronic hypoxia due to increased CO₂ levels could explain both the increase in immune responses and a reduction in metabolism – **Need to confirm with AEM experiments at ambient CO₂ levels.**

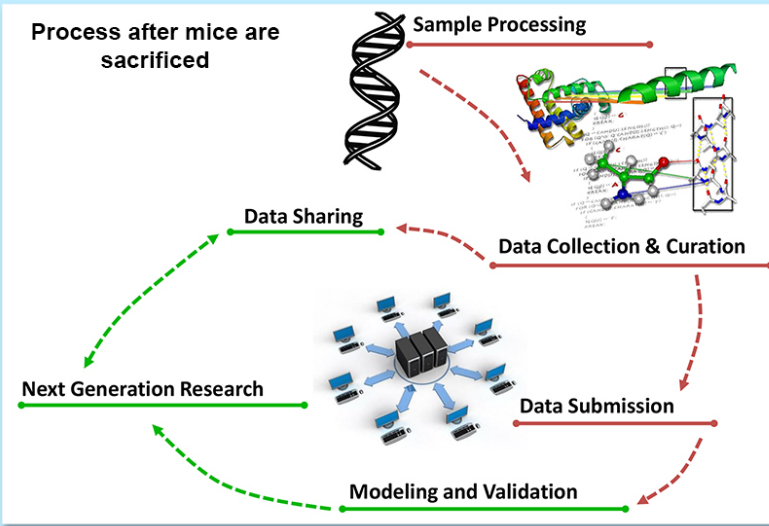


- Through a systems biology approach we observed global transcriptomic changes in rodents induced by spaceflight-matched environment in AEM cages.
- Identify spaceflight CO₂ levels as a potential environmental stressor that merits experimental investigation
- Systematically changing one environmental aspect at a time (gas concentration, radiation, microgravity, etc.) and analyzing and comparing transcriptional responses could be used to create a network that could predict the most relevant causes and countermeasures for spaceflight-associated conditions, as well as confounding factors for spaceflight experiments.

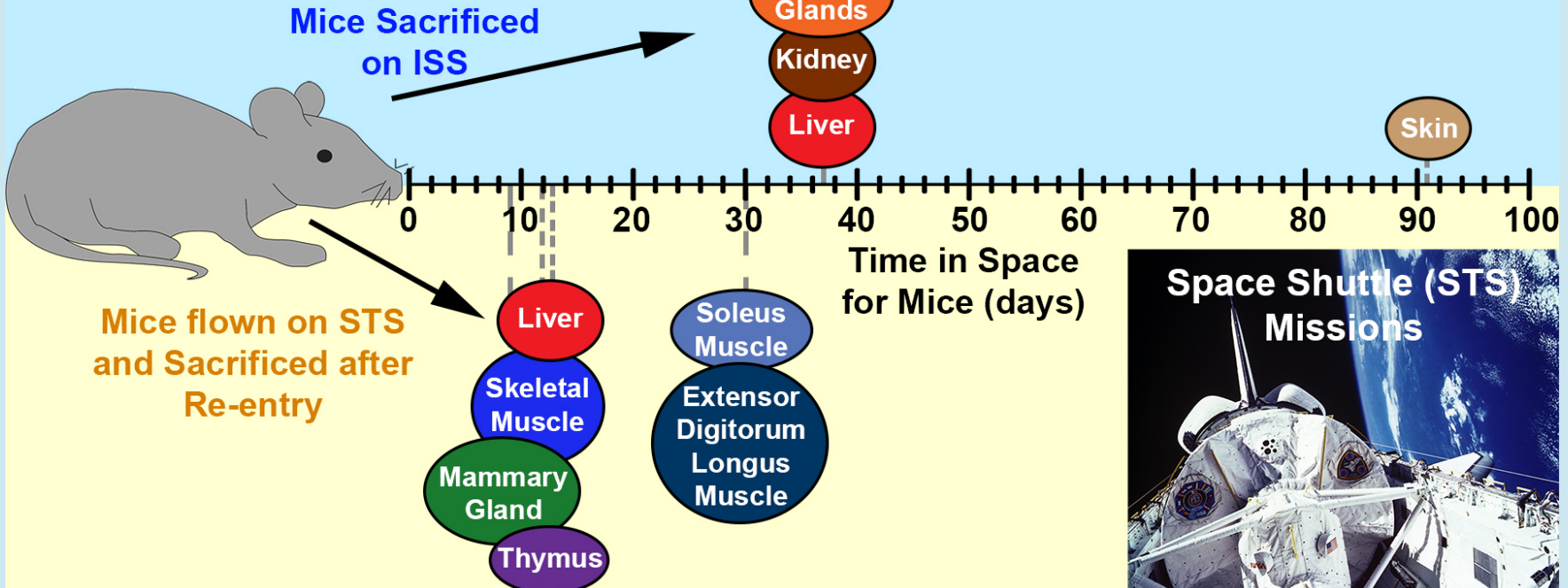
Systems Biology analysis reveals biological spaceflight master regulators

Beheshti, et al., PLOS One, 2018

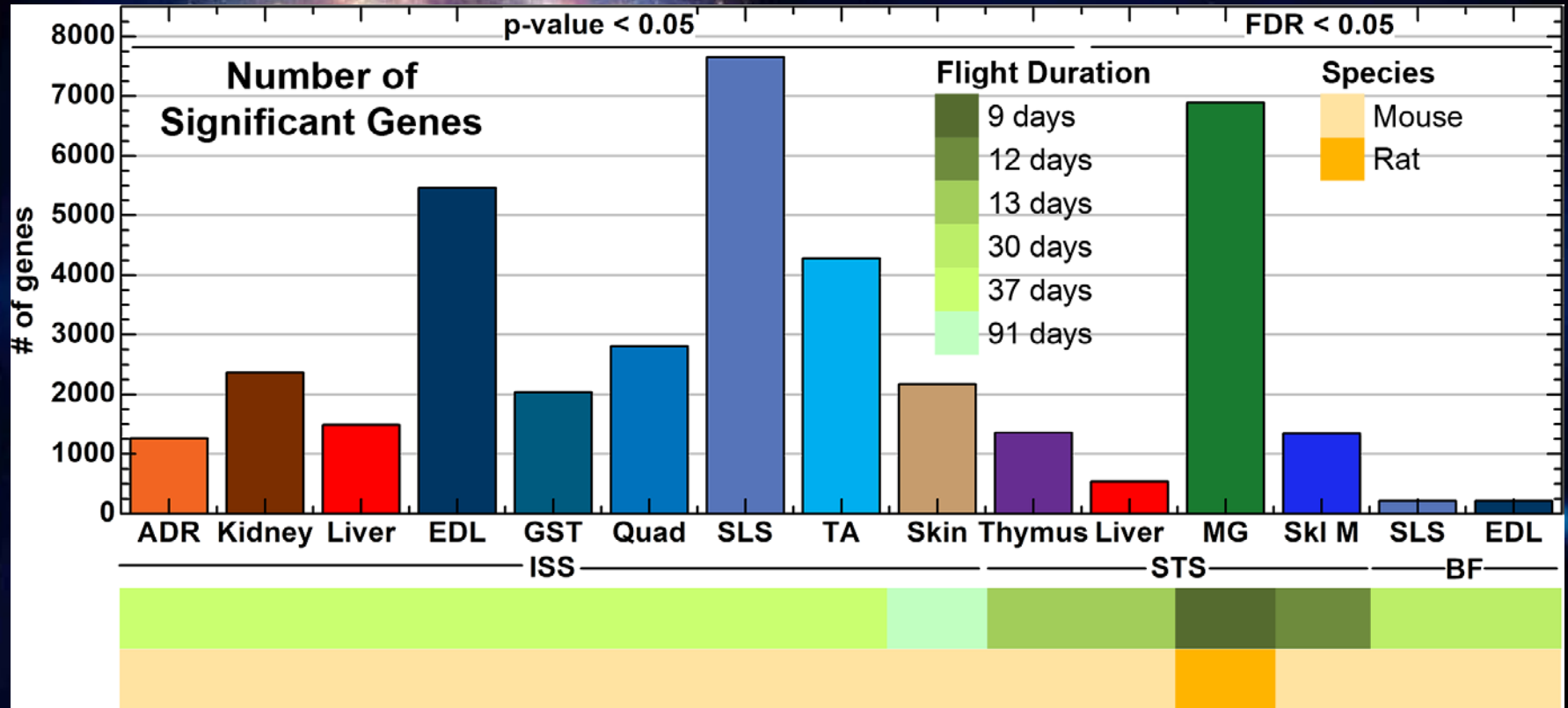
GeneLab Data Used to Generate Results



- Extensor Digitorum Longus Muscle
- Soleus Muscle
- Gastrocnemius Muscle
- Quadriceps
- Tibialis Anterior Muscle
- Adrenal Glands
- Kidney
- Liver

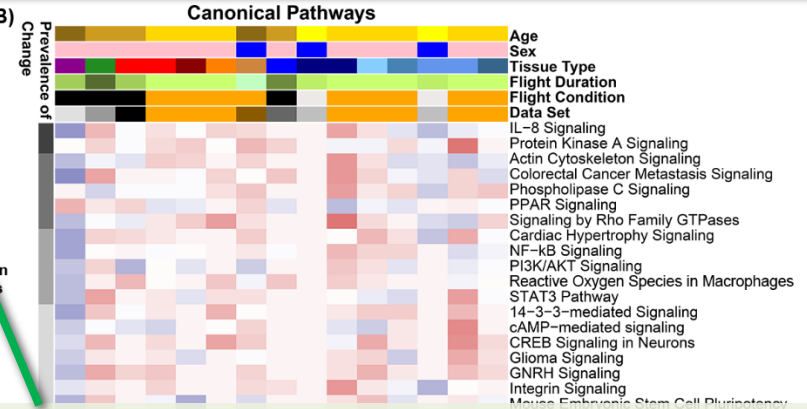
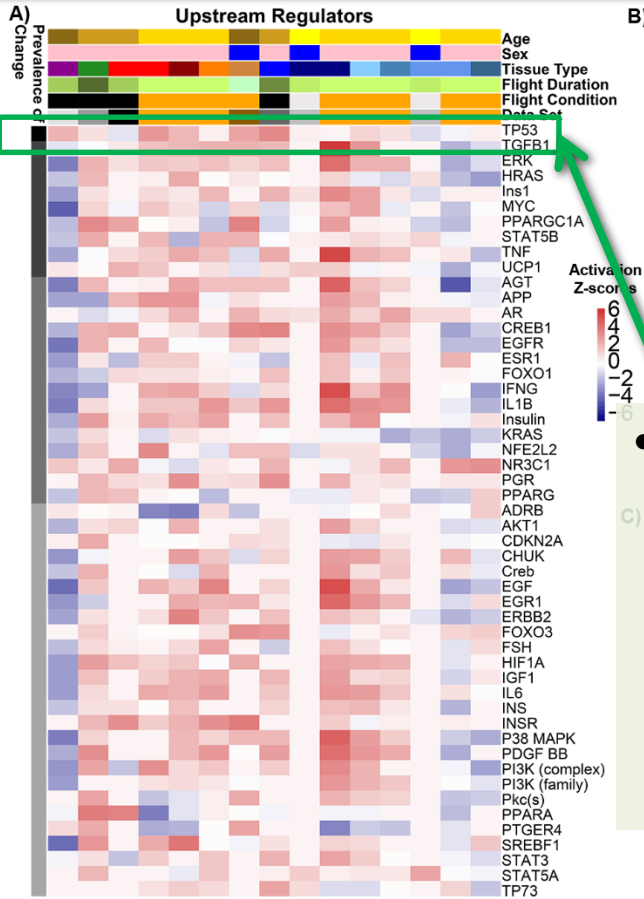


Number of Significant Genes from Each Dataset

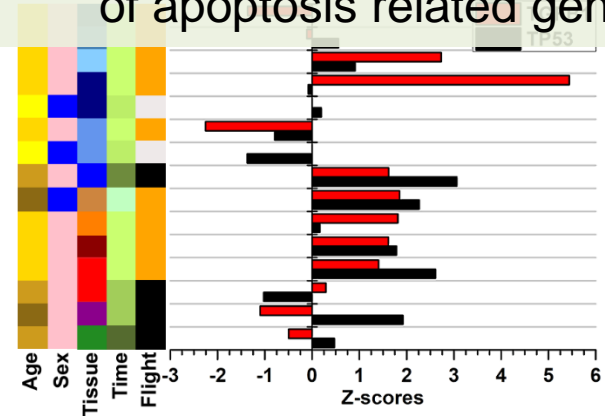
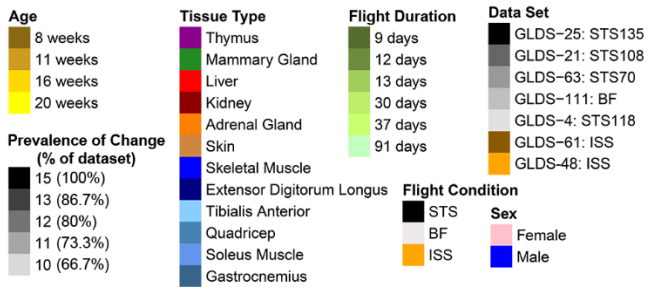


Fold-Change \geq
| 1.2 |

Pathway/Functional Predictions:
Ingenuity Pathway Analysis (IPA)
Gene Set Enrichment Analysis (GSEA)



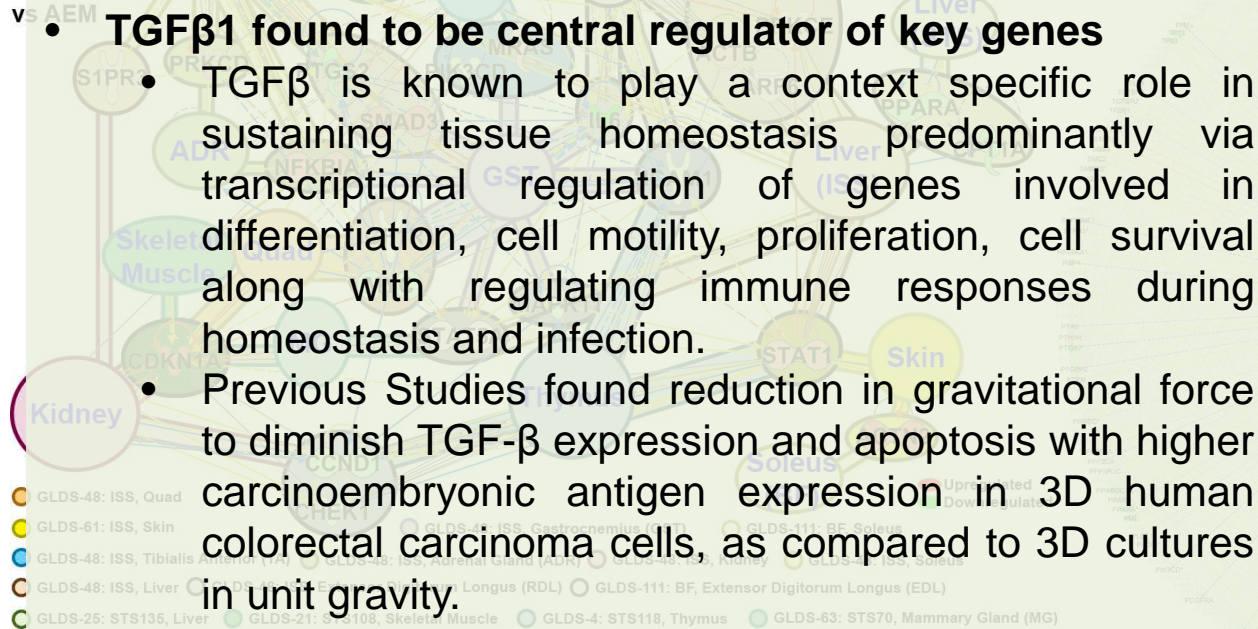
- **p53 found in all tissues**
 - p53 is a transcription factor and in response to genotoxic stress, DNA damage, oncogene activation, and hypoxia, it is recruited to sites in chromatin, thus promoting transcription of apoptosis related genes



A) Direct Connections for Key Genes for Flight vs AEM

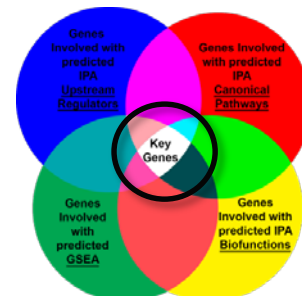
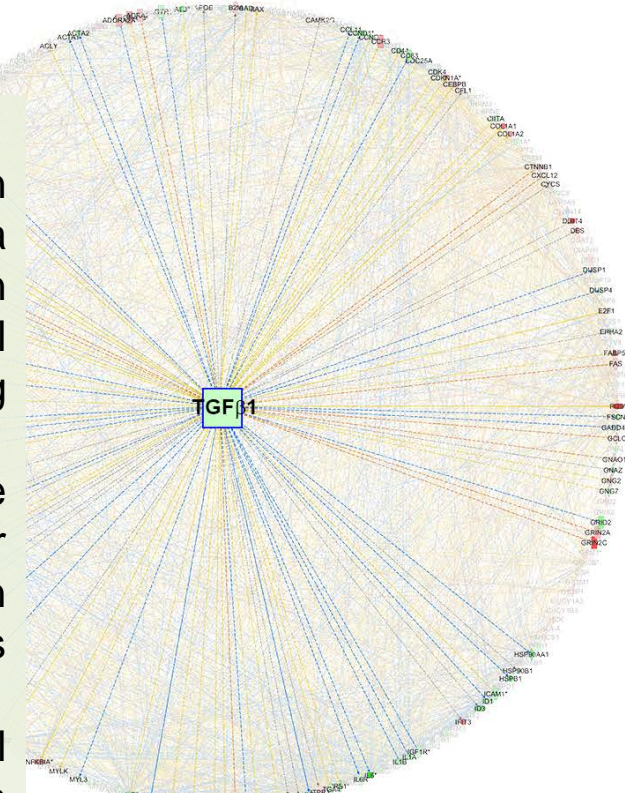
• **TGF β 1 found to be central regulator of key genes**

- TGF β is known to play a context specific role in sustaining tissue homeostasis predominantly via transcriptional regulation of genes involved in differentiation, cell motility, proliferation, cell survival along with regulating immune responses during homeostasis and infection.
- Previous Studies found reduction in gravitational force to diminish TGF- β expression and apoptosis with higher carcinoembryonic antigen expression in 3D human colorectal carcinoma cells, as compared to 3D cultures in unit gravity.
- In another study, differential regulation of blood vessel growth using basic fibroblast growth factor was identified in modeled microgravity with induction early and late apoptosis, extracellular matrix proteins, endothelin-1 and TGFb1 expression



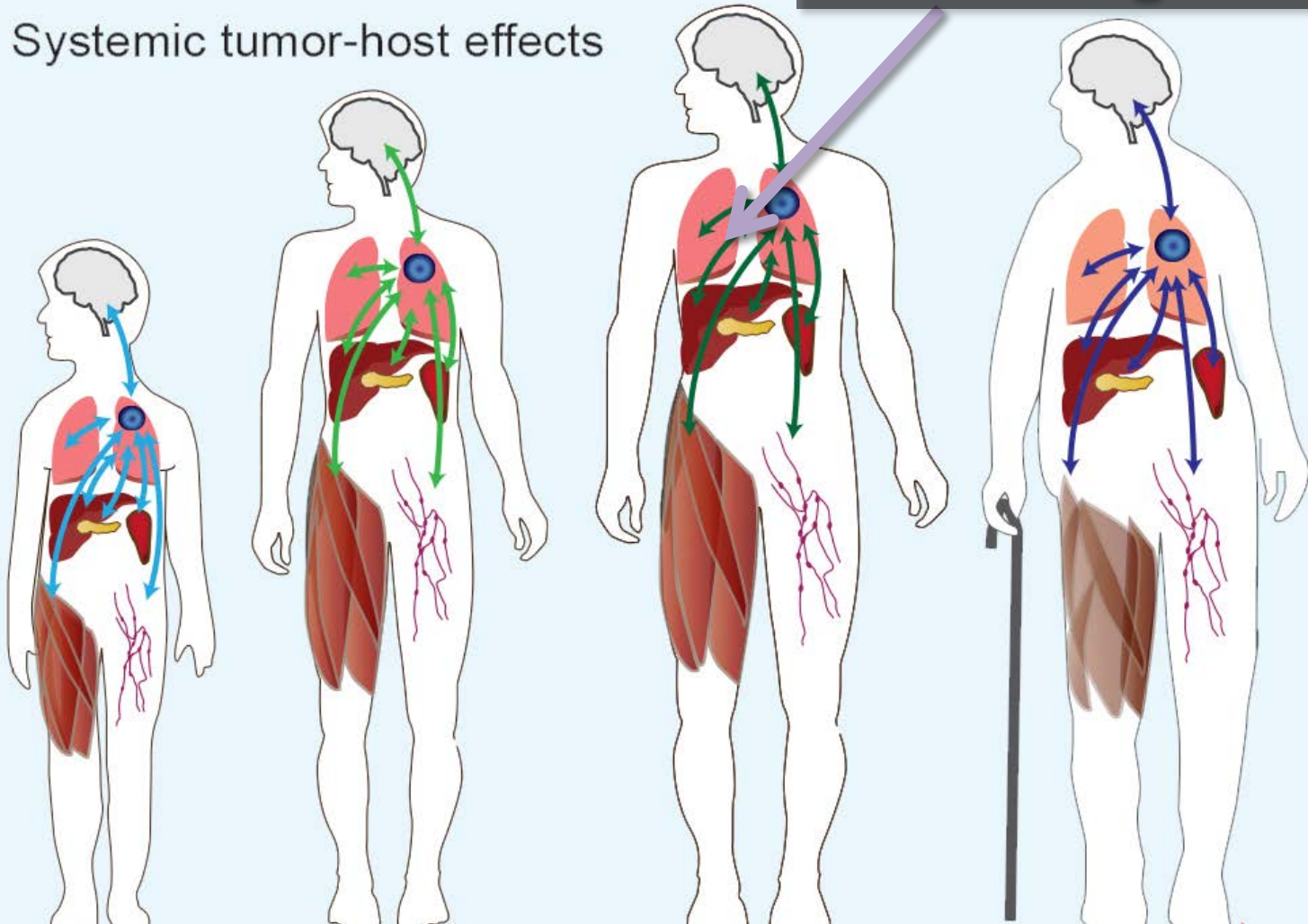
- GLDS-48: ISS, Quad
- GLDS-61: ISS, Skin
- GLDS-48: ISS, Tibialis Anterior (TA)
- GLDS-48: ISS, Liver
- GLDS-48: ISS, Longus (RDL)
- GLDS-111: BF, Extensor Digitorum Longus (EDL)
- GLDS-25: STS135, Liver
- GLDS-21: STS100, Skeletal muscle
- GLDS-4: STS118, Thymus
- GLDS-63: STS70, Mammary Gland (MG)

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

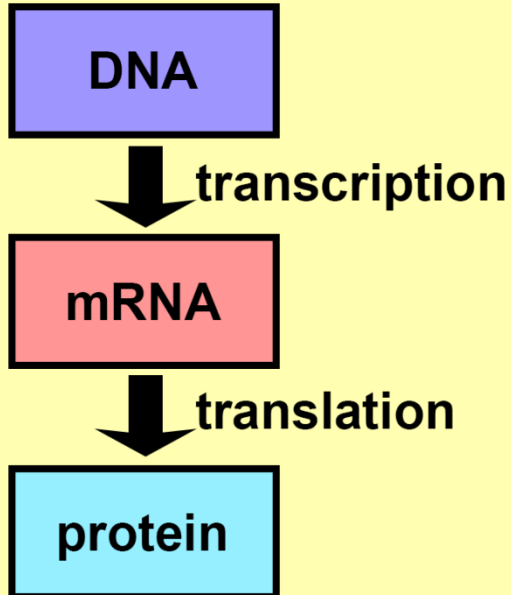


Circulating miRNAs

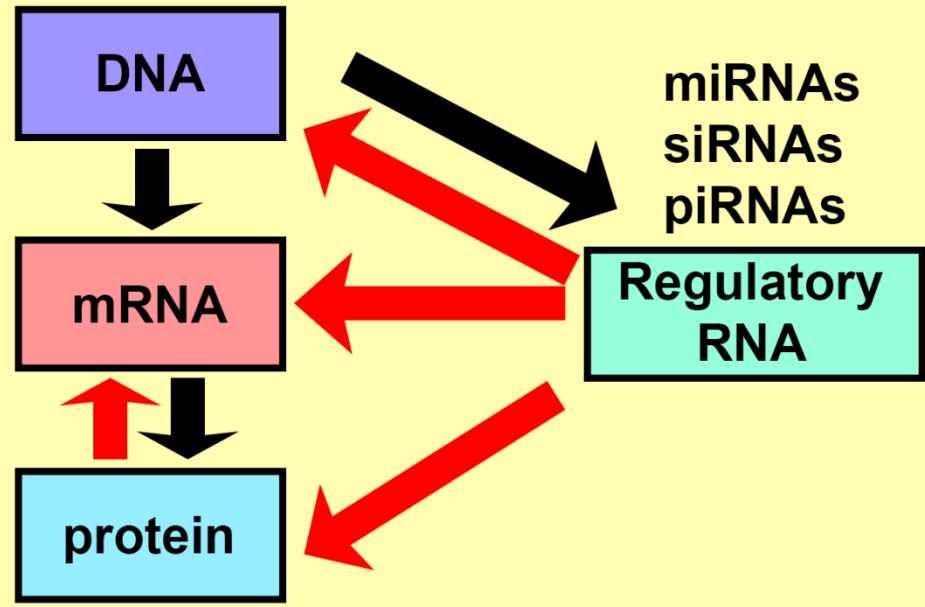
Systemic tumor-host effects



Classical View of Molecular Biology

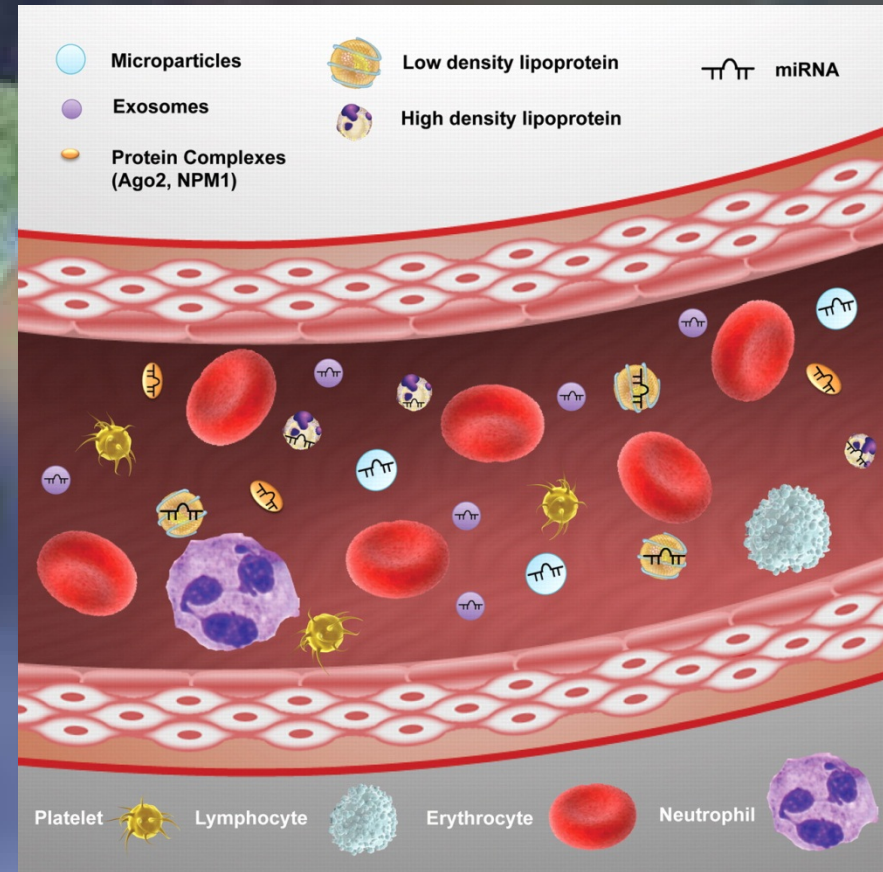


New Understanding of Molecular Biology



- A single miRNA has been estimated to regulate up to 500 mRNAs
- miRNAs are single-stranded RNA sequences, of about 22 nucleotides in length, processed from longer transcripts.
- miRNAs are important regulators that repress the translation of mRNA transcripts

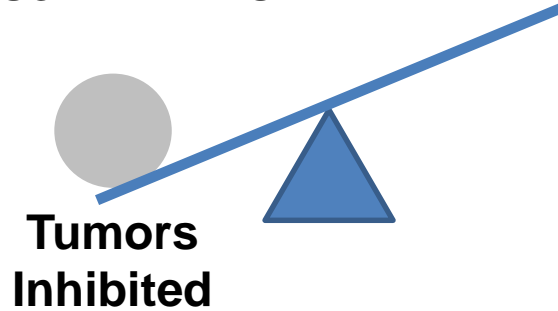
- Circulating miRNAs can carry signals from organs to other various parts of the body through the blood stream.
- The miRNAs can be transported in Exosomes, microparticles, lipoproteins, and outside any type of packaging.
- Our preliminary data shows that a miRNA signature is carried over from the spleen to the tumor with age.
 - Beheshti, et al. *PLoS ONE* 2017



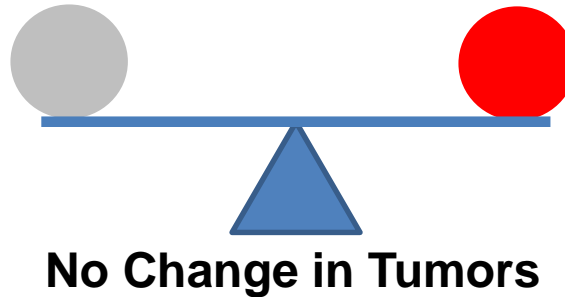
Profiling of circulating microRNAs: from single biomarkers to re-wired networks Anna Zampetaki, Peter Willeit, Ignat Drozdov, Stefan Kiechl, Manuel Mayr. *Cardiovascular Research*, 2011.

● Tumor Suppressor miRNAs

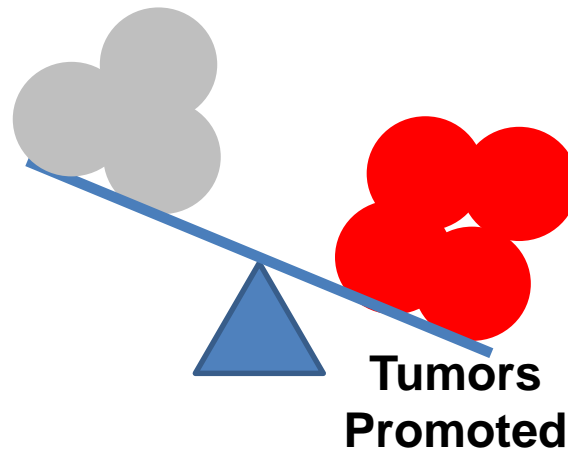
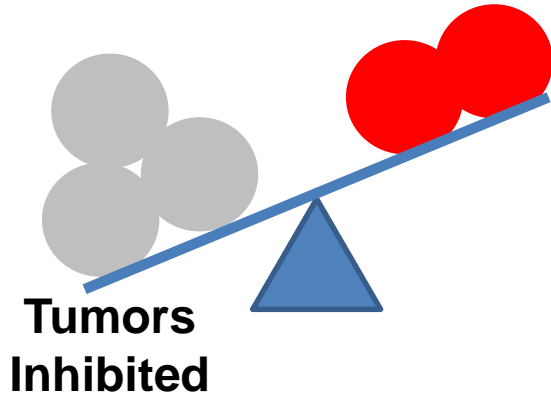
● OncomiRNAs



Only looking at a single miRNA



looking at a pair of miRNAs

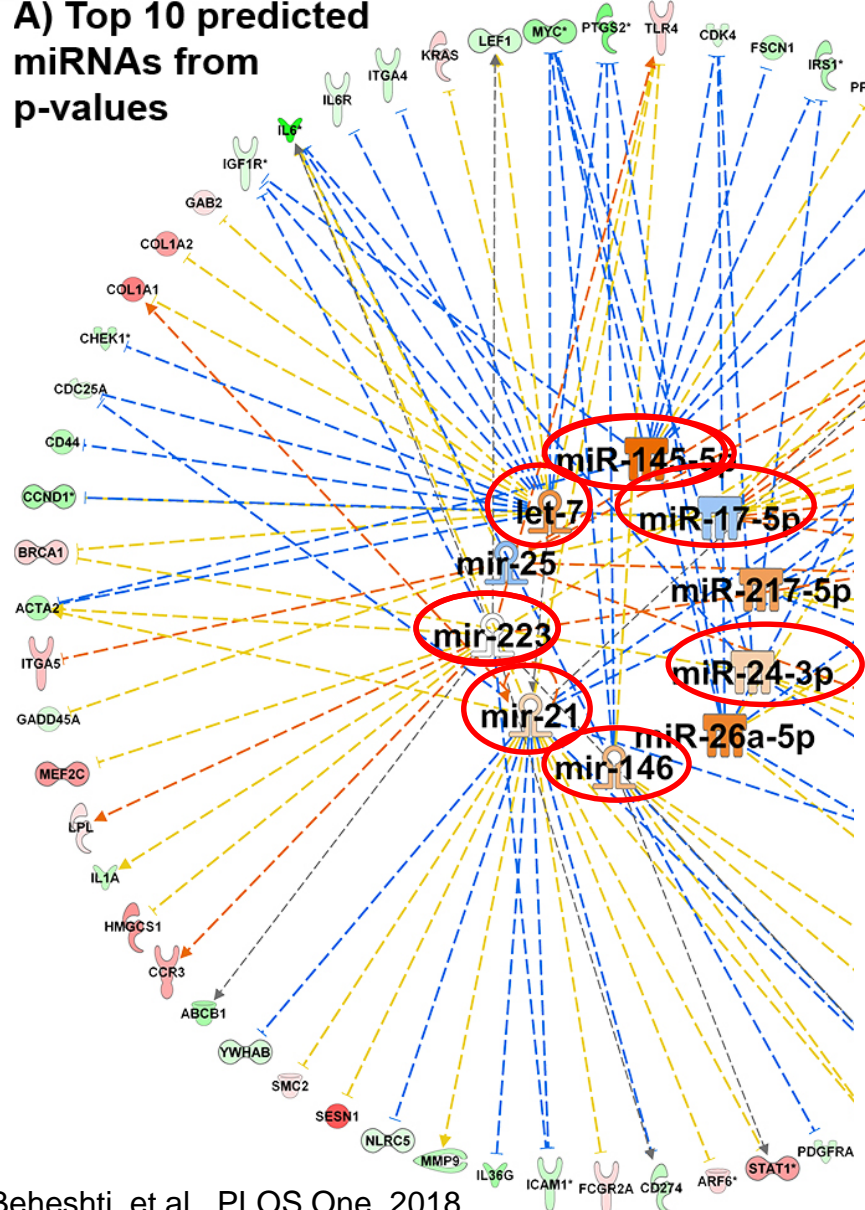


Systems Biology Approach: Looking at how the entire system impacts the most important miRNAs

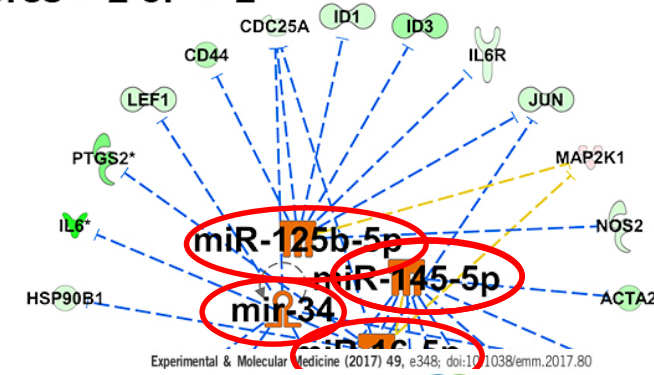
Predicted miRNAs Involved with Microgravity Effects



A) Top 10 predicted miRNAs from p-values



B) All miRNAs with Z-scores > 2 or < -2



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BioMed Research International
Volume 2014, Article ID 296747, 16 pages
<http://dx.doi.org/10.1155/2014/296747>

Experimental & Molecular Medicine (2017) 49, e348; doi:10.1038/emm.2017.80
Hindawi
PLOS one

C
Research Article
Integration Analysis of MicroRNA and mRNA Expression Profiles in Human Peripheral Blood Lymphocytes Cultured in Modeled Microgravity
Chiara, Lucia

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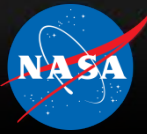
Academic Editor: Mariano Bizzarri

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We analyzed miRNA and mRNA expression profiles in human peripheral blood lymphocytes (PBLs) incubated in microgravity condition, simulated by a ground-based rotating wall vessel (RWV) bioreactor. Our results show that 42 miRNAs were differentially expressed in MMG-incubated PBLs compared with 1 g incubated ones. Among these, miR-9-5p, miR-9-3p, miR-155-5p, miR-150-3p, and miR-378-3p were the most dysregulated. To improve the detection of functional miRNA-mRNA pairs, we performed gene expression profiles on the same samples assayed for miRNA profiling and we integrated miRNA and mRNA expression data. The functional classification of miRNA-correlated genes evidenced significant enrichment in the biological processes of immune/inflammatory response, signal transduction, regulation of response to stress, regulation of programmed cell death, and regulation of cell proliferation. We identified the correlation of miR-9-3p, miR-155-5p, miR-150-3p, and miR-378-3p expression with that of genes involved in immune/inflammatory response (e.g., IFNG and IL17F), apoptosis (e.g., PDCD4 and PTEN), and cell proliferation (e.g., NKX3-1 and GADD45A). Experimental assays of cell viability and apoptosis induction validated the results obtained by bioinformatics analyses demonstrating that in human PBLs the exposure to reduced gravitational force increases the frequency of apoptosis and decreases cell proliferation.

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Predicted miRNAs Involved with Microgravity Effects



Health Risk Due to miRNAs



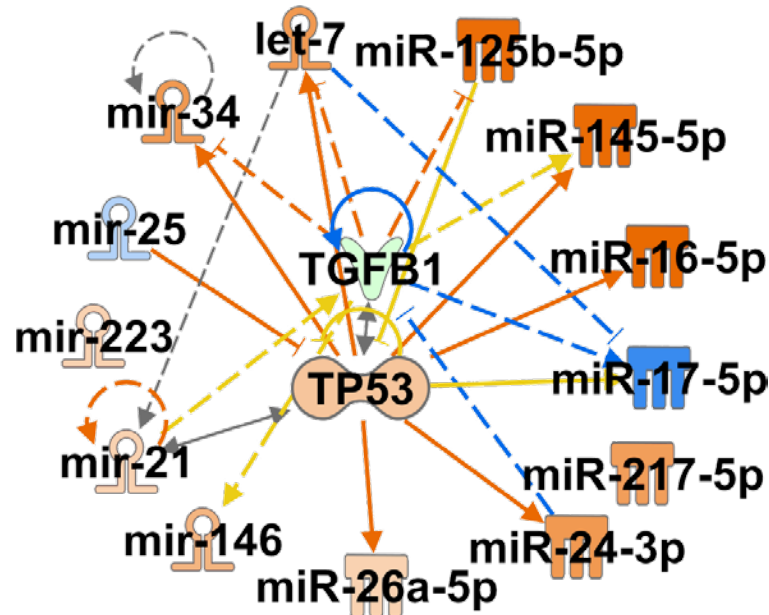
● Predicted Activation

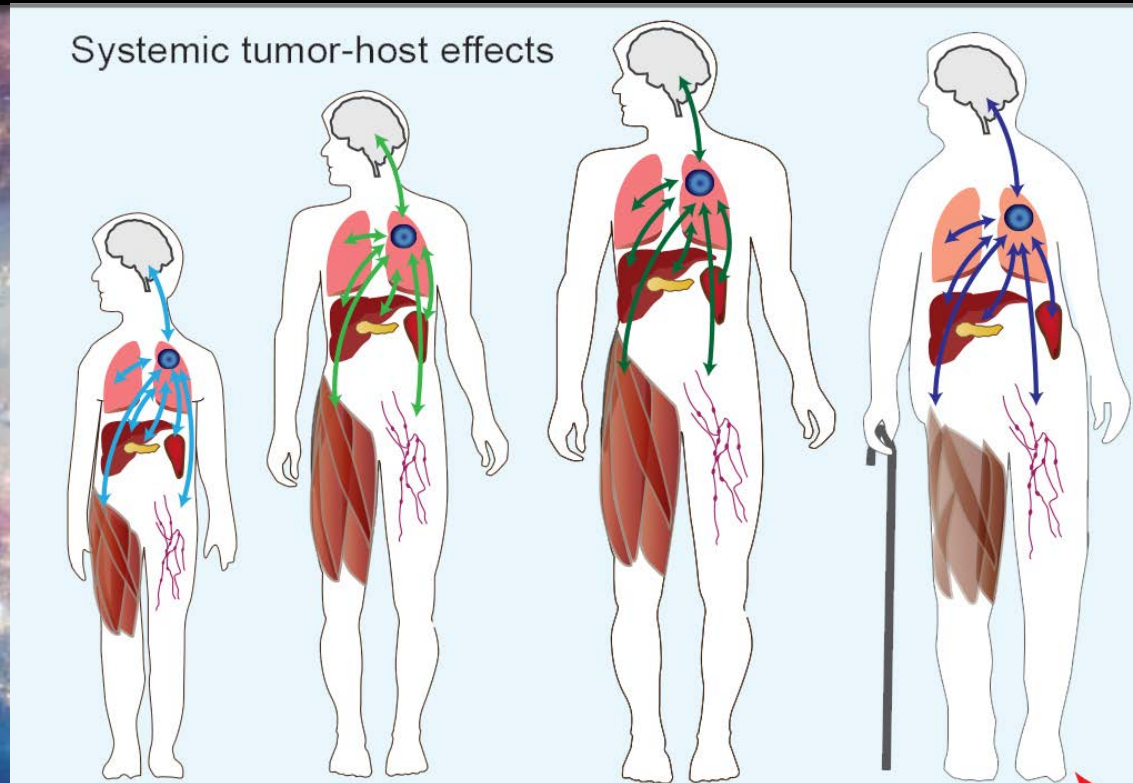
● Predicted Inhibition

○ Negative Impact on Health

- A recent report showed that inactivation of p53 altered TGF- β signaling, which ironically displayed both tumor-suppressive and pro-oncogenic functions. p53 functions to integrate crosstalk between Ras/MAPK and TGF- β signaling via binding to Smad3, dislocating the Smad3/Smad4 complex formation and differentially regulating subsets of TGF- β target genes

*Biological Health
Risk Increased*

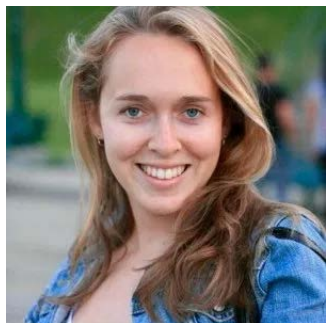




- **Systems biology approach allows for systemic understanding of the impact of Microgravity.**
- **Circulating miRNAs can influence overall progression of health risk to the host.**
- **miRNAs can potentially be used for novel minimally invasive therapeutics and countermeasures**
- **GeneLab (genelab.nasa.gov) is a powerful tool to generate hypotheses and direct future space research**

Analysis Working Group (AWG) Member related work determines novel systemic biological factors causing damage due to spaceflight

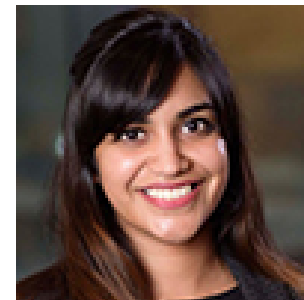
Work in progress



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Helio Costa Kathryn Grabek



STANFORD
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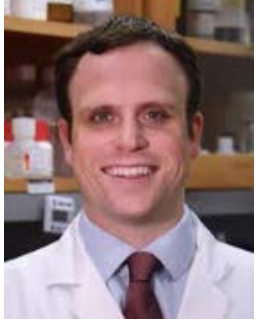


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Gary Hardiman Willian da Silveira





Chris Mason



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Flavia Rius



Cornell University



Yared Kidane



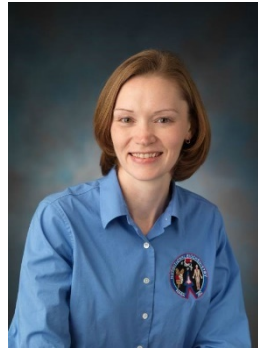
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Scott Smith



Sara Zwart



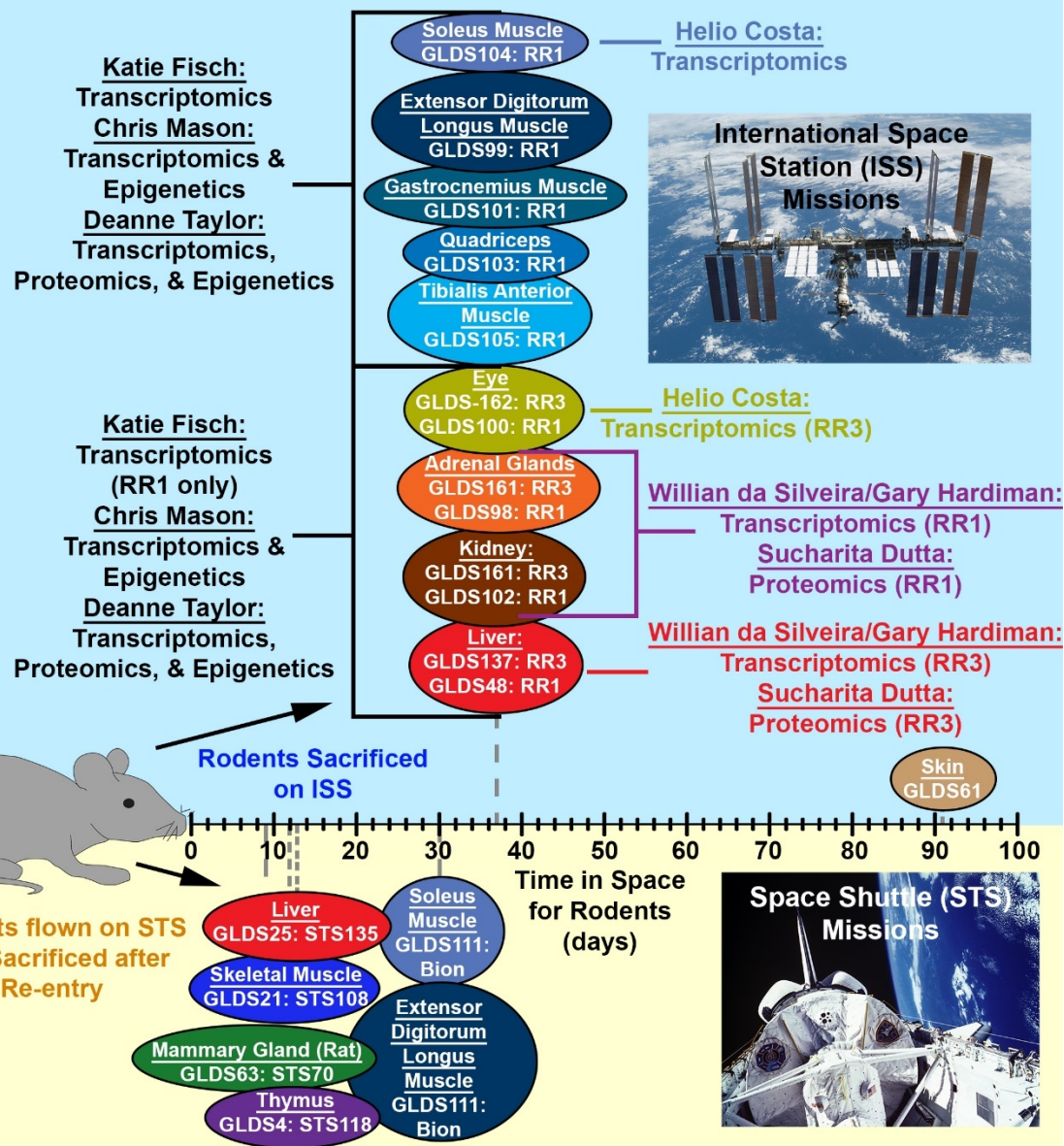
Afshin Beheshti



Sylvain Costes



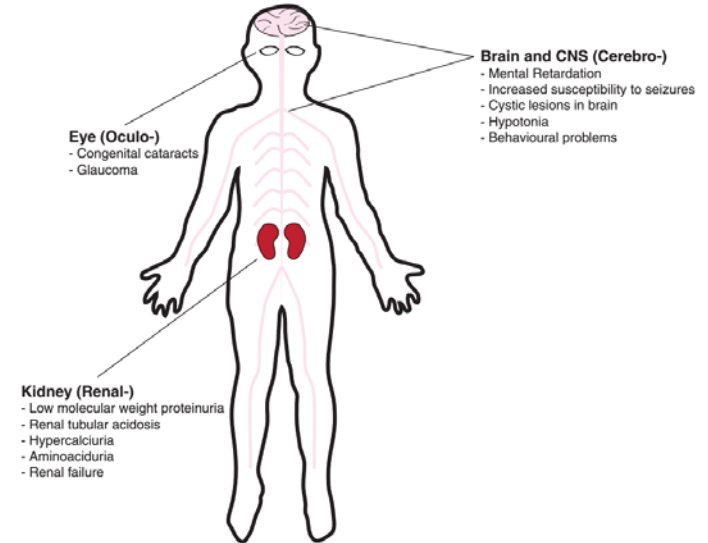
Specific Datasets and Tissues AWG Members Analyzed



- Additional Datasets that are being analyzed:
 - Human datasets
 - GLDS-54, GLDS-174, GLDS-86, GLDS-118, GLDS-53, GLDS-54, GLDS-13, GLDS-52, or GLDS-114 (Tyson McDonald and Yared Kidane)

- Spaceflight changes the physical properties of the cell components impacting from the molecular to the whole body level.
- The Mitochondria are the principal cellular component affect.
- The Liver is the principal organ affected in issues related to the metabolism.
- Possible disease that can be associated with liver damage and pathways is: Oculocerebrorenal Syndrome of Lowe
 - “Extensive research has demonstrated that OCRL-1 is involved in multiple intracellular processes involving endocytic trafficking and actin skeleton dynamics. This explains the multi-organ manifestations of the disease.”
 - “The classic form of the oculocerebrorenal syndrome of Lowe (OMIM #309000), first described by Lowe et al. in 1952 [1], is characterized by the triad of congenital cataracts, severe intellectual impairment, and renal tubular dysfunction with slowly progressive renal failure”
 - Patients with this disease manifest Cataract, Glaucoma and Muscle hypotonia.

Schematic diagram showing the organs affected in Lowe syndrome



<https://genelab.nasa.gov>

Participate in GeneLab Analysis Working Groups

LATEST NEWS
NASA GeneLab Project: Bridging Space Radiation Omics with Ground Studies
Accurate assessment of risks of long-term space missions is critical for human space exploration. It is essential to have a detailed understanding of the biological effects on humans living and working in deep space. Ionizing radiation from galactic cosmic rays (GCR) is a major health risk factor for astronauts on extended missions outside the protective effects of the Earth's magnetic field. Currently, there are gaps in our knowledge of the health risks associated with chronic low-dose, low-dose-rate ionizing radiation, specifically ions associated with high (H) atomic number (Z) and energy (E). The NASA GeneLab project aims to provide a detailed library of omics datasets associated with biological samples exposed to HZE... [Read more](#)

Access GeneLab Omics Data
Home Repository Data Data Mining Tools Submit Data Help Workspace
Search Data
GeneLab NH GEO EB PRIDE ANL US-MSST

SPOTLIGHT ON RADIATION
Radiation Dosimetry Measurements Added to Data Repository
Low-Earth Orbit (LEO) International Space Station (ISS) Mission
Spacecraft, Orbit 6000
ISS & Station
Typical Dosimetry
10,000 hrs

ANALYSIS WORKING GROUPS
Analysis Working Groups Reach Consensus on Pipelines Needed to Generate Higher-order Data
Transcriptomic Pipelines: RNA-Seq

RESEARCH ANNOUNCEMENT
NASA Research Announcement: Topics in Human Health Countermeasures, Human Factors, and Behavioral Performance

LabRoots: A Conversation with Sigrid Reinsch – Public Access to Spaceflight Omics Data
Marianne Sowa and Jack Miller Discuss Radiation Science Using GeneLab

- Social media :
 - @NASA Ames **Facebook**
 - **Twitter** #GeneLab
 - **ResearchGate**: <https://www.researchgate.net/project/Omics-for-Space-Biology-The-GeneLab-project>

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