NASA GeneLab platform utilized for space radiation dosimetry biological response compared to radiation ground studies

National Aeronautics and Space Administration

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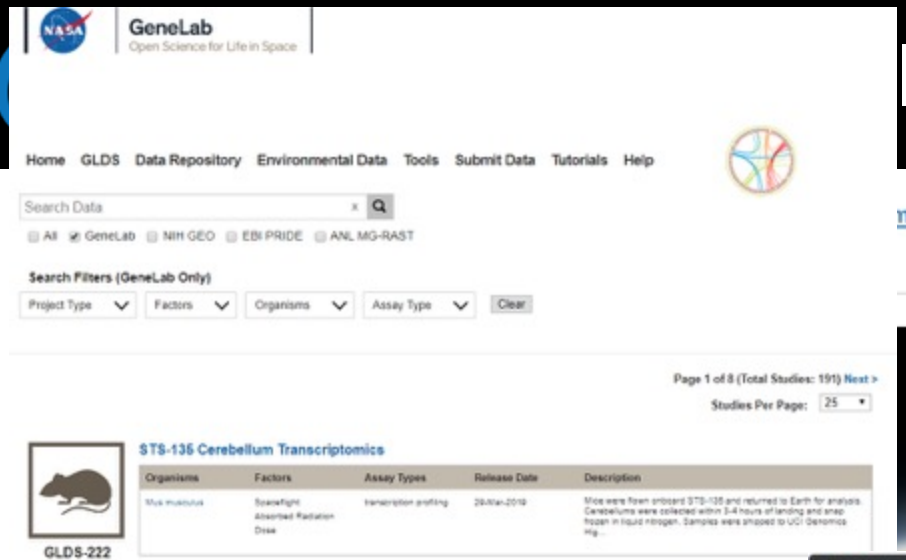
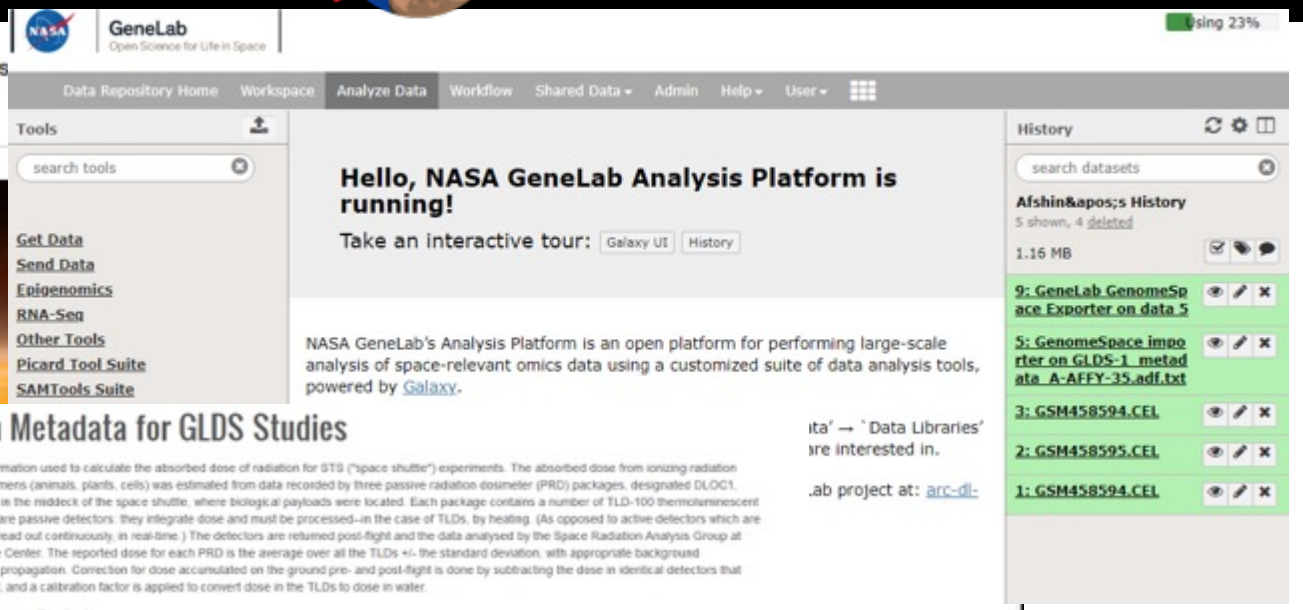
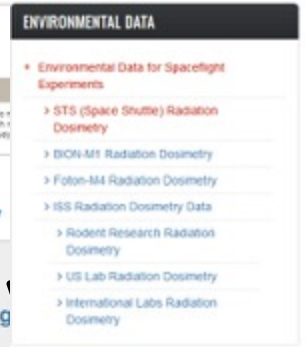
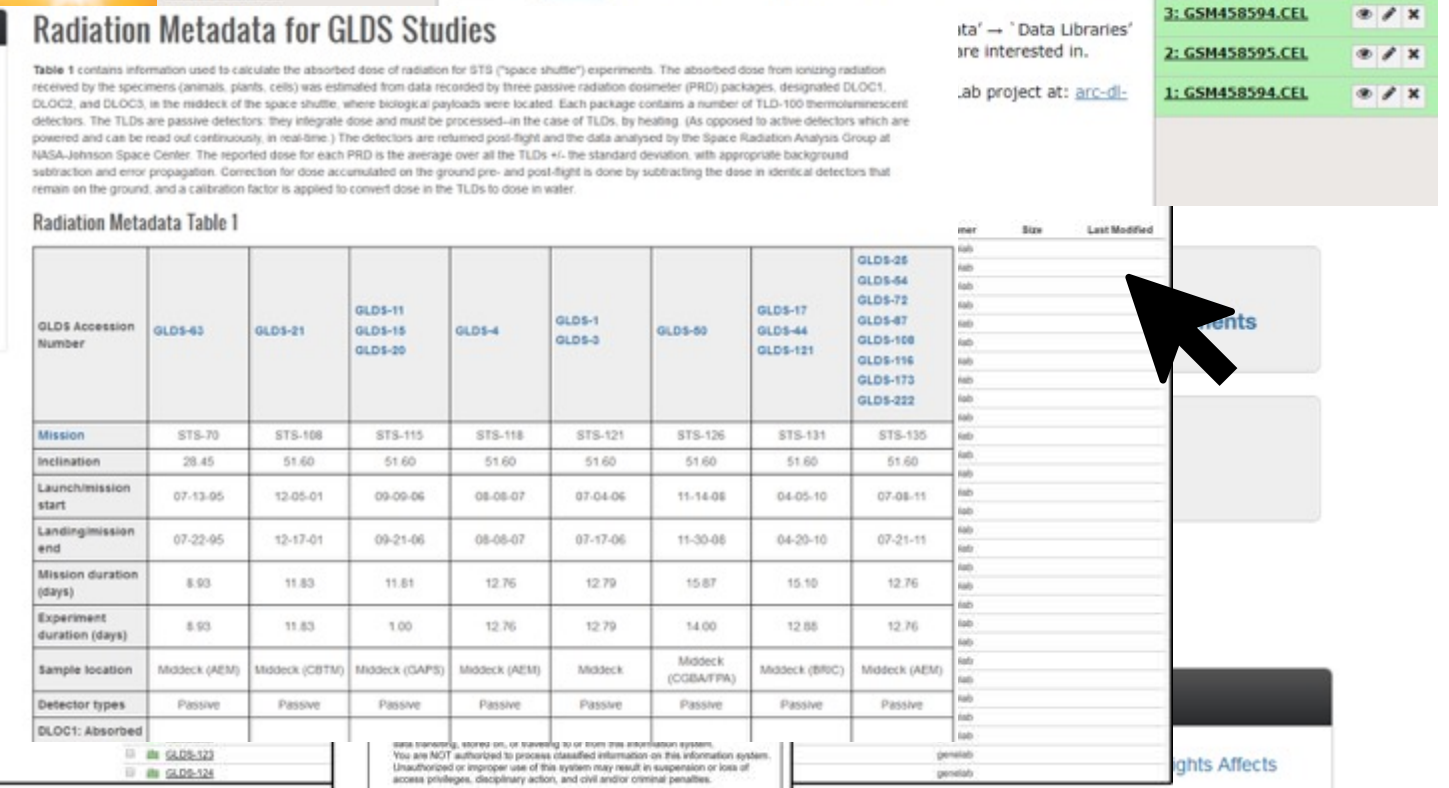
GeneLab Open Science for Life in Space



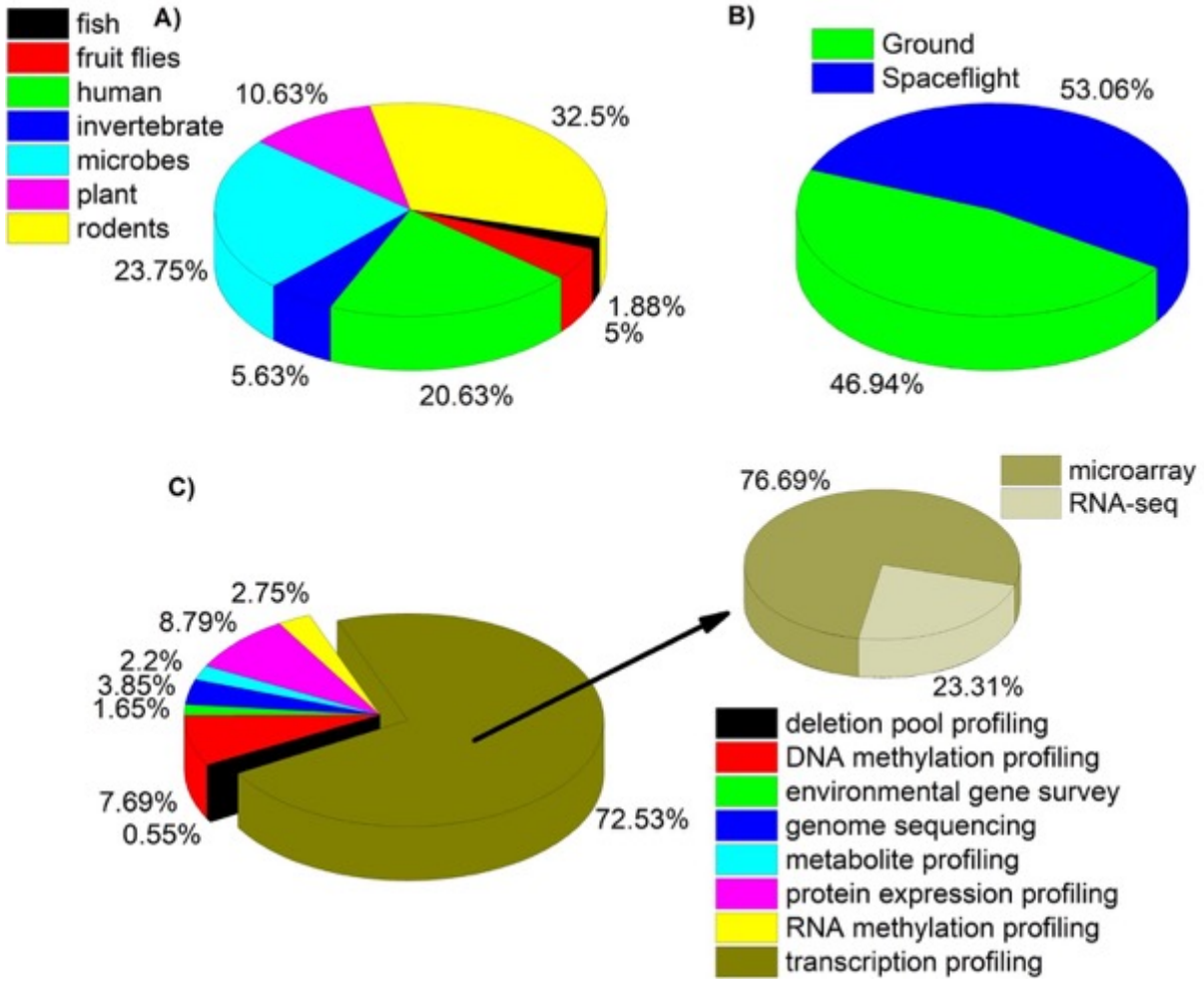




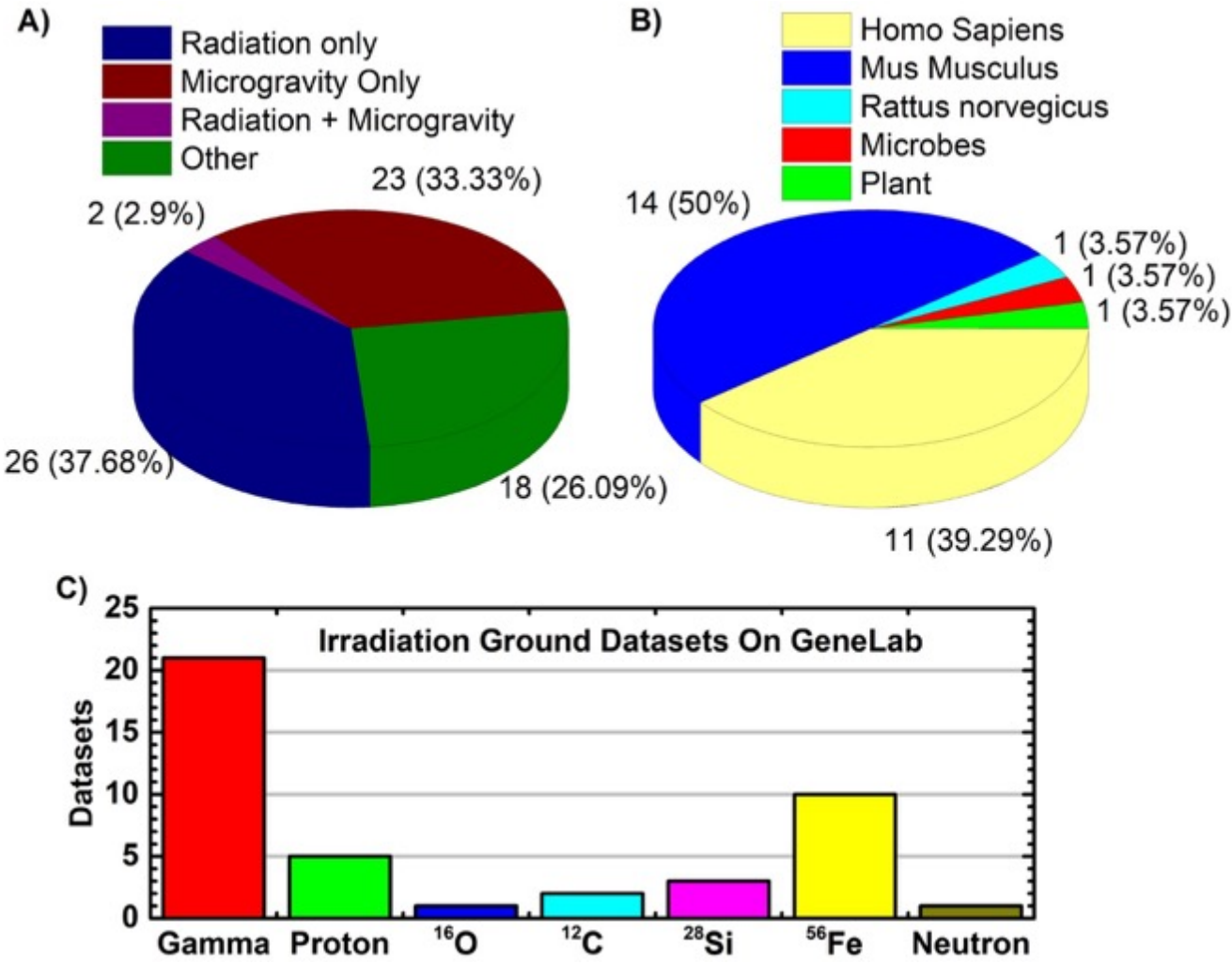


GeneLab Database (>200 data sets)

All GeneLab Datasets

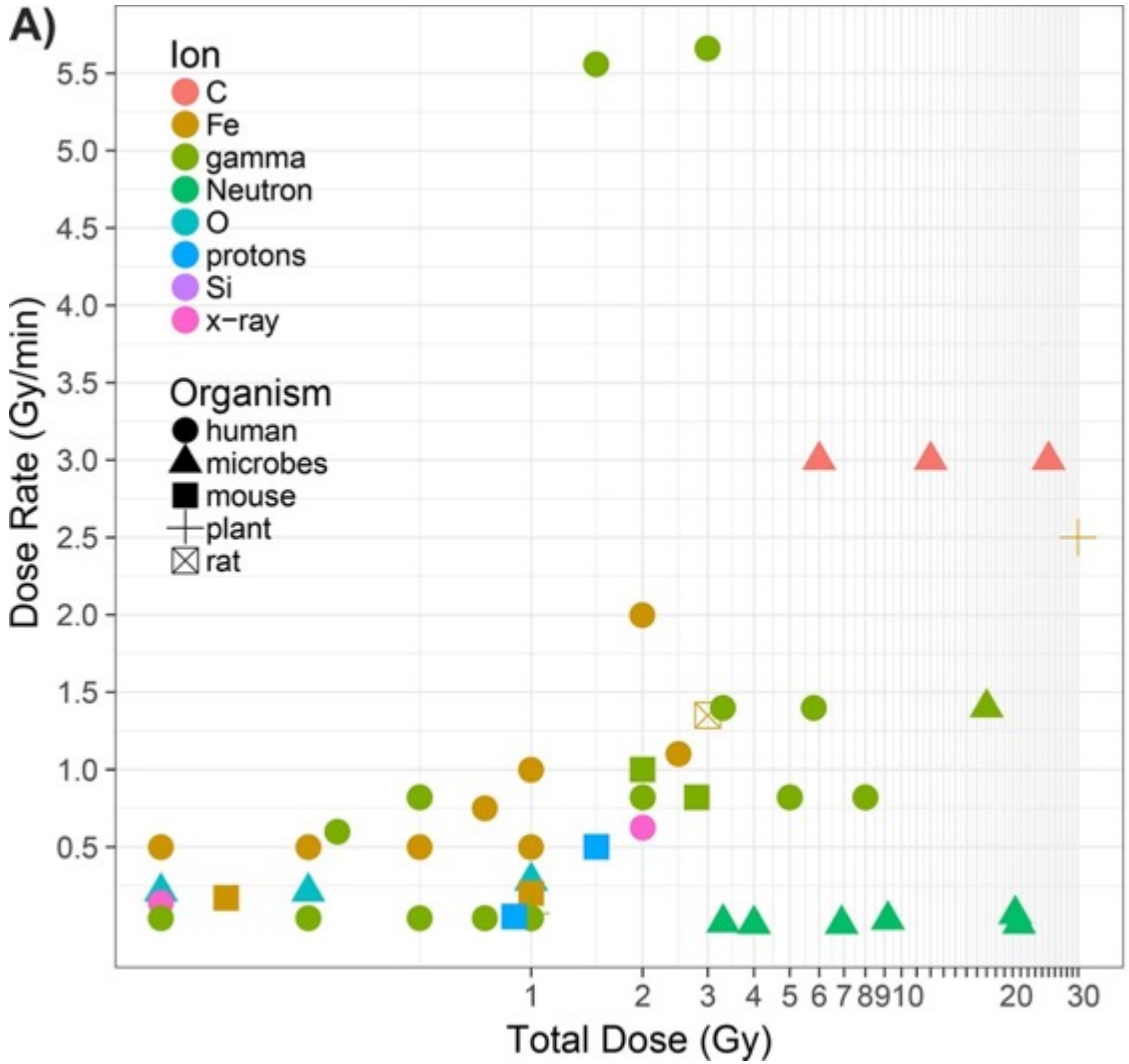


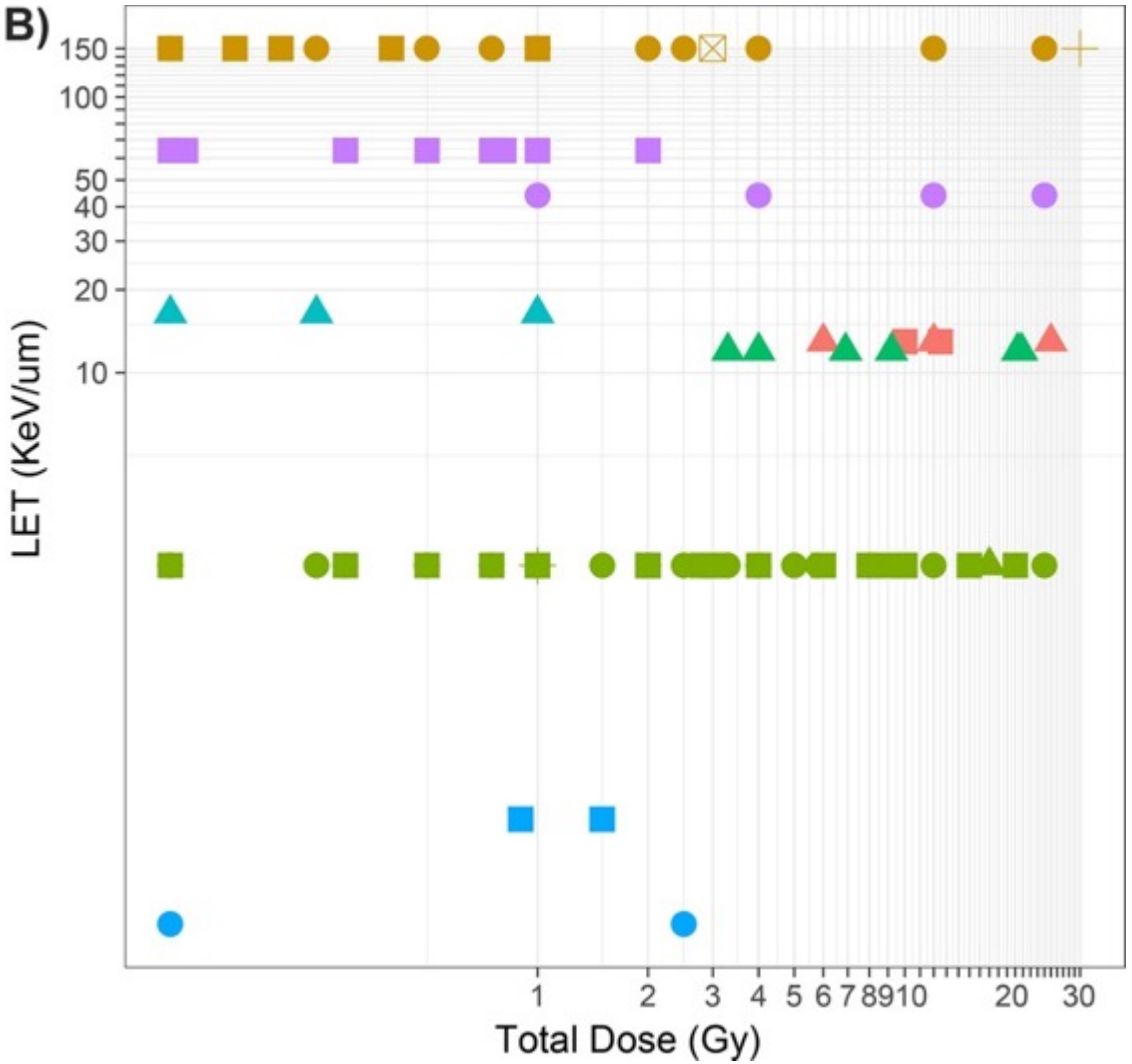
Specific Ground Radiation GeneLab Datasets



Beheshti et al., Radiation Research 2018

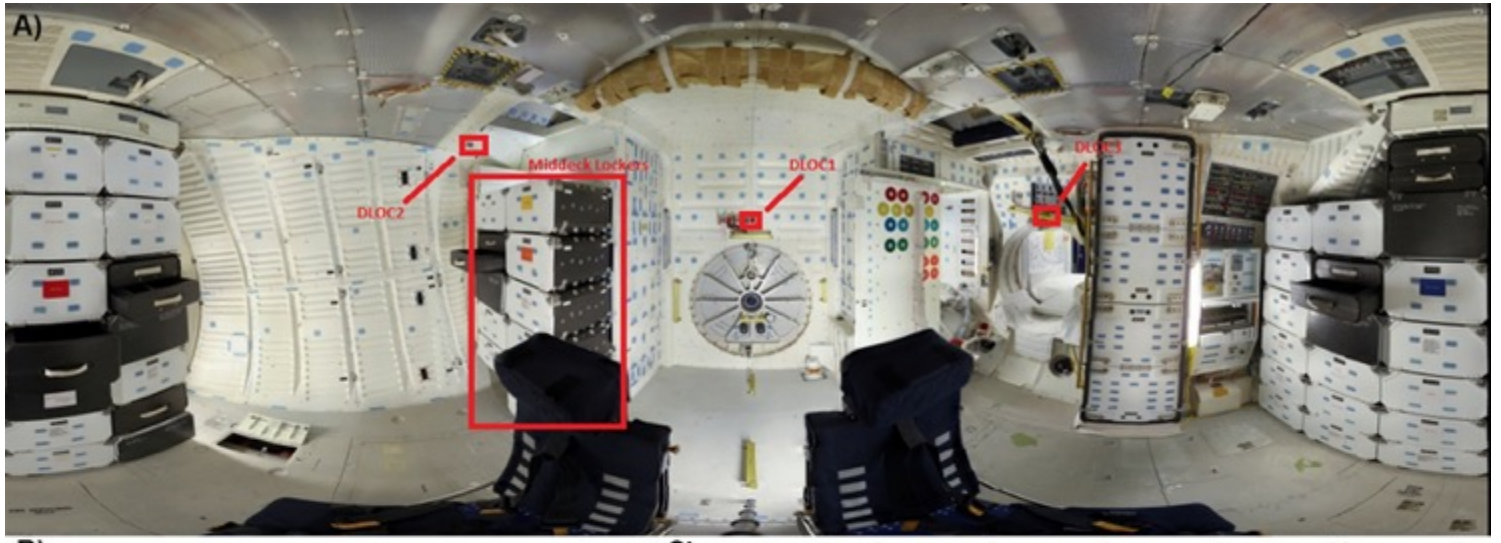
Radiation Ground Studies

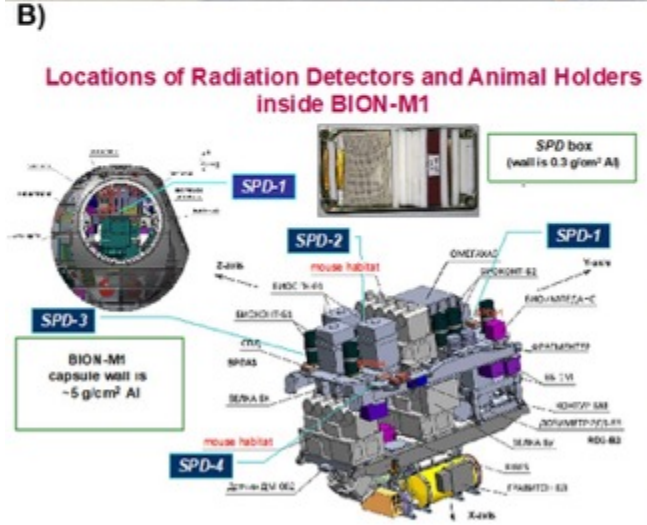


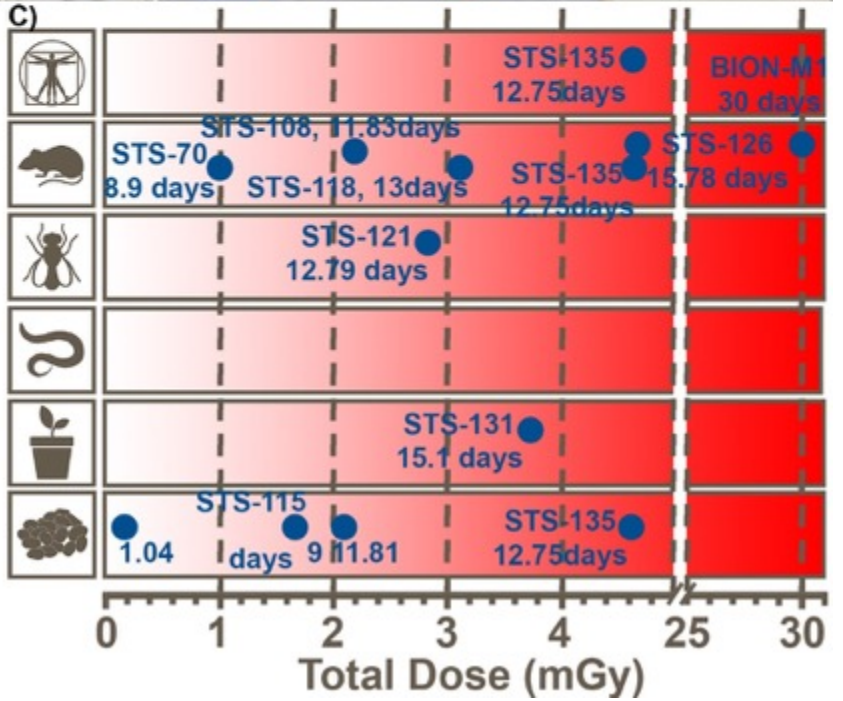


Beheshti et al., Radiation Research 2018

Radiation Dosimetry for STS samples (ISS to follow)







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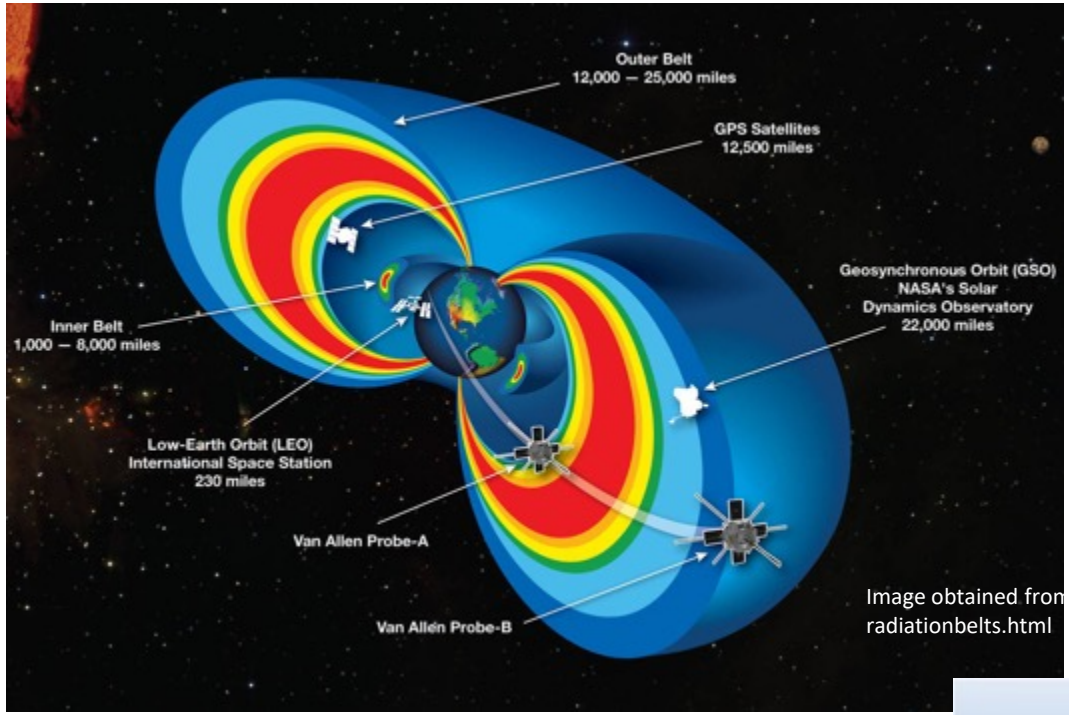
Space Environment

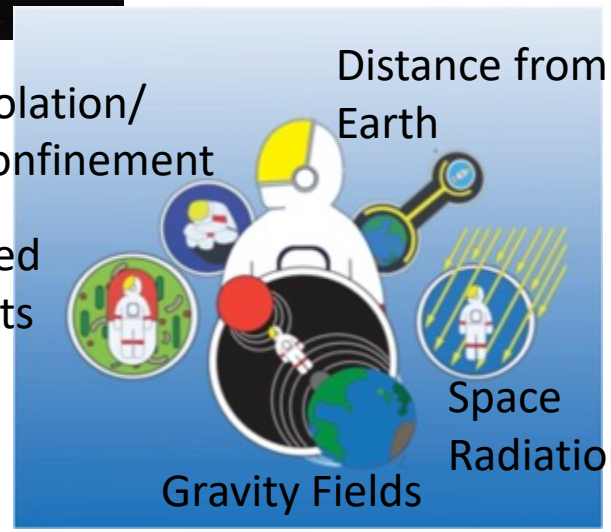


NASA

Isolation/
Confinement

Distance from
Earth

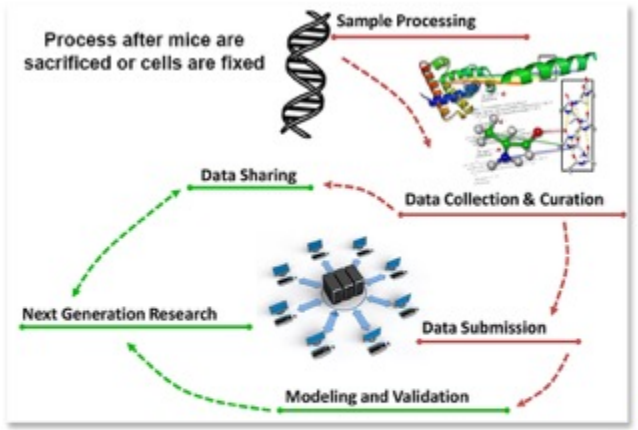
Hostile/closed
environments

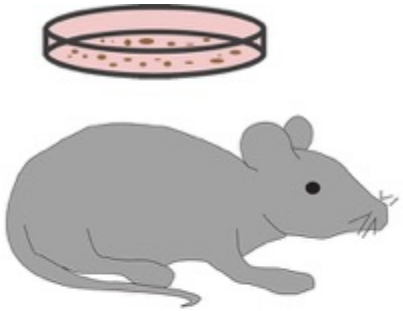


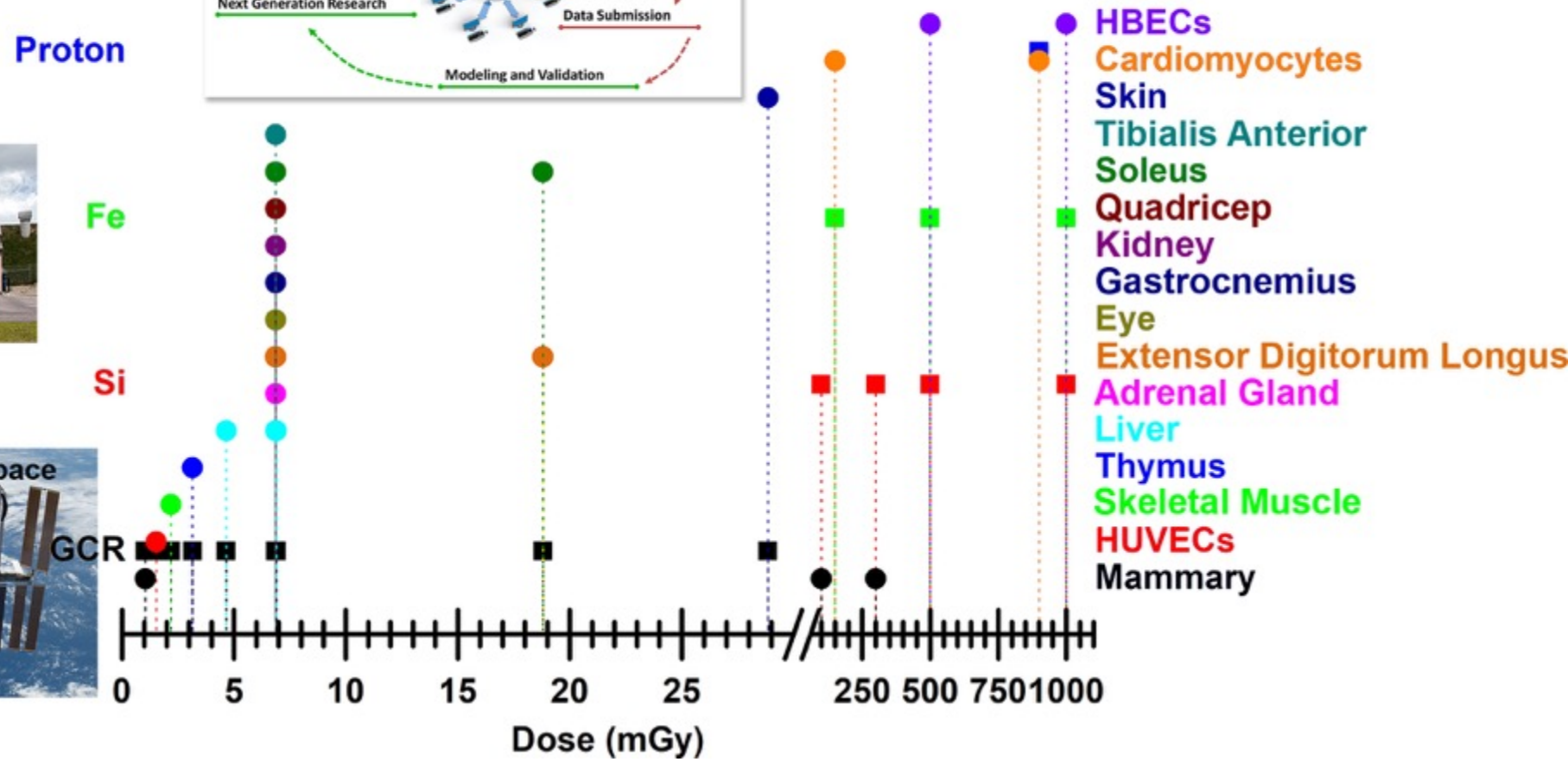
Credits: NASA

The Goal of this work and GeneLab Datasets Utilized for Analysis

- Ground datasets will are compared to both *in vivo* and *in vitro* datasets from samples flown to the ISS and on shorter shuttle missions.
- From this analysis we will be able to associate distinct biological signatures associating specific ions to specific biological response to radiation exposure in space.

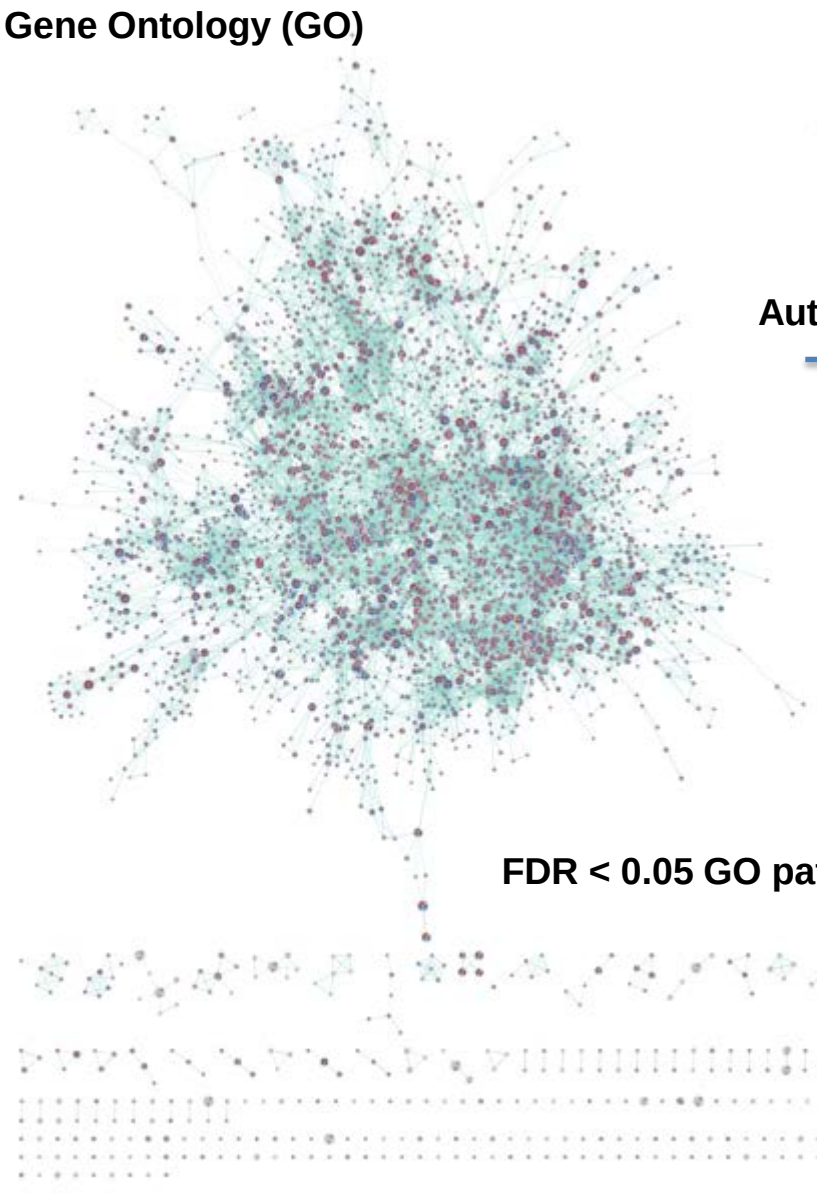




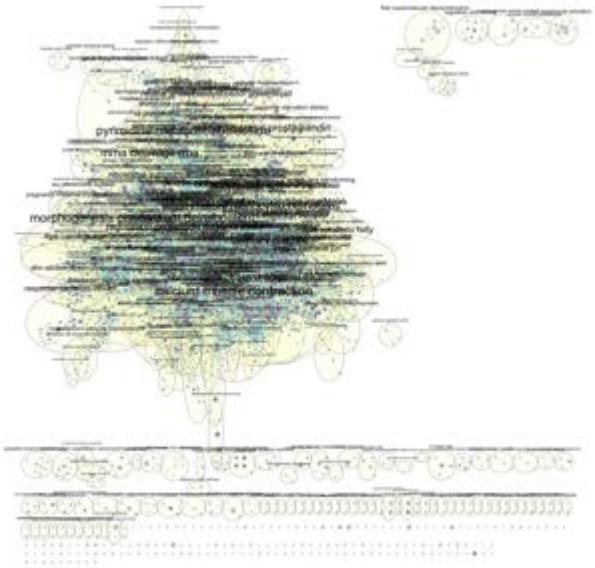


Gene Set Enrichment Analysis to Compare all Datasets

Gene Ontology (GO)



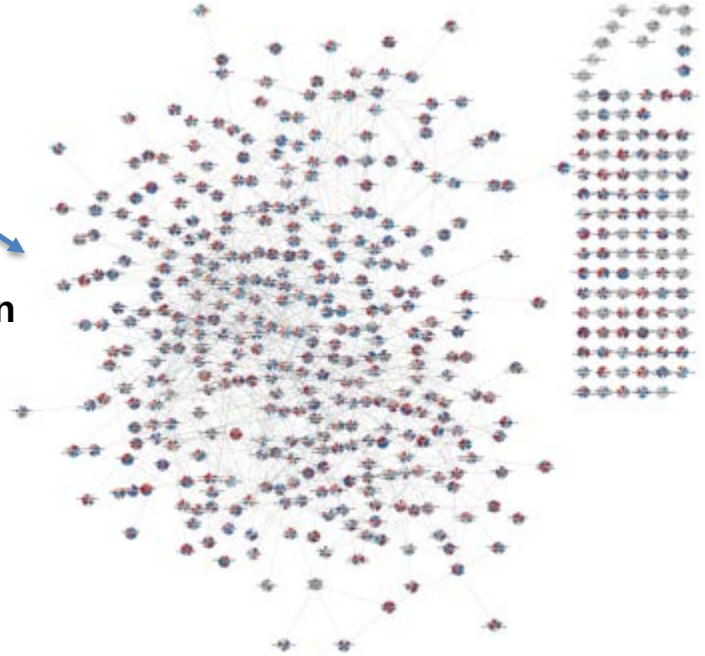
Auto-Annotate GO Clusters



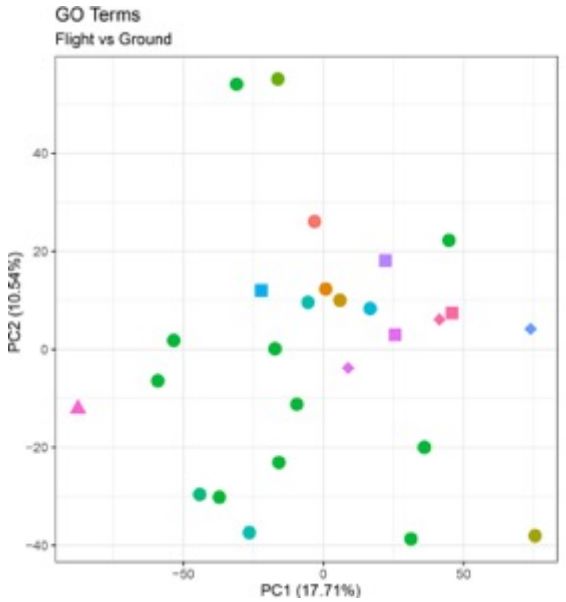
Use Normalized Enrichment Scores (NES) for downstream analysis

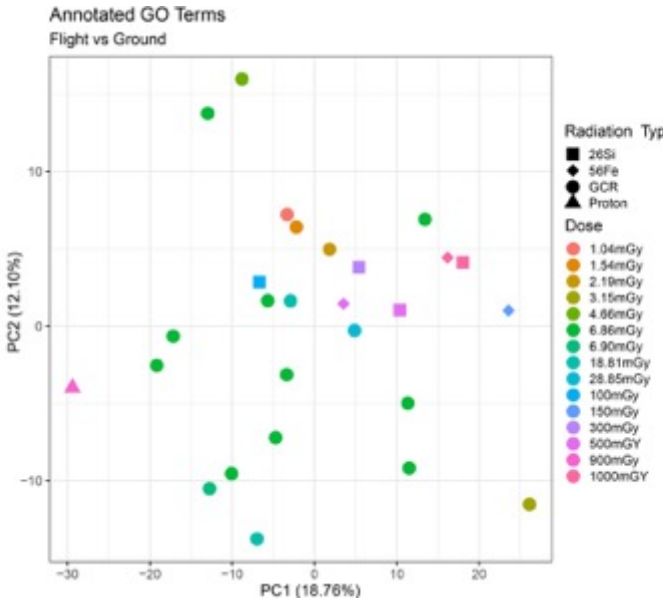
FDR < 0.05 GO pathways utilized

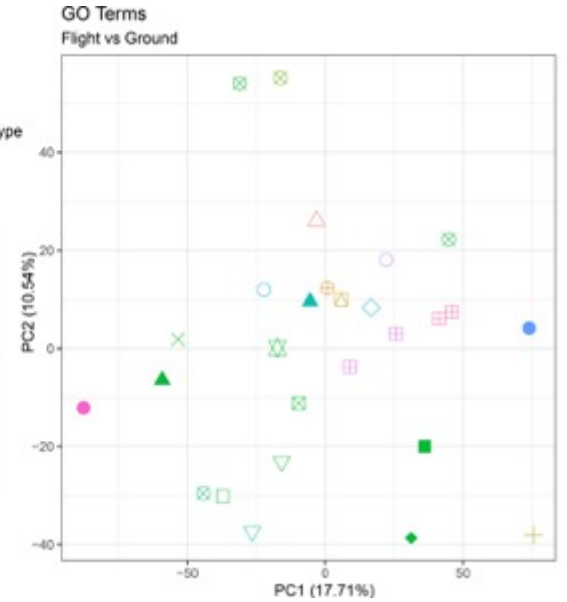
Create new GO network based on Annotated GO Clusters

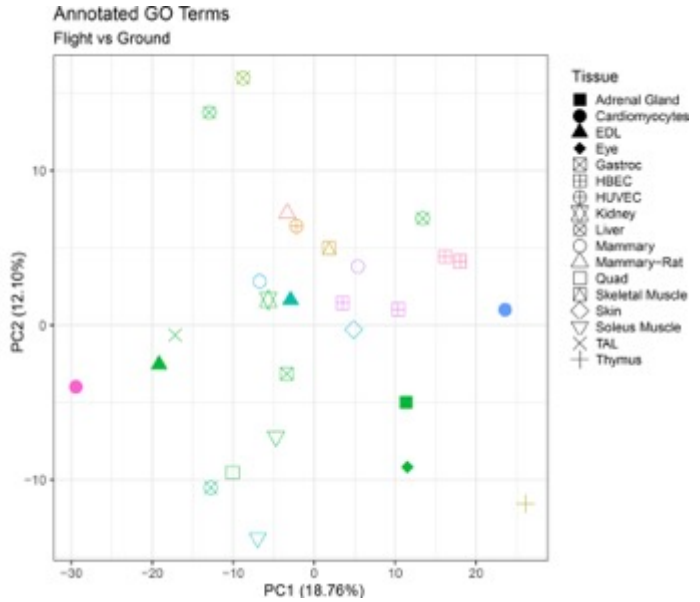


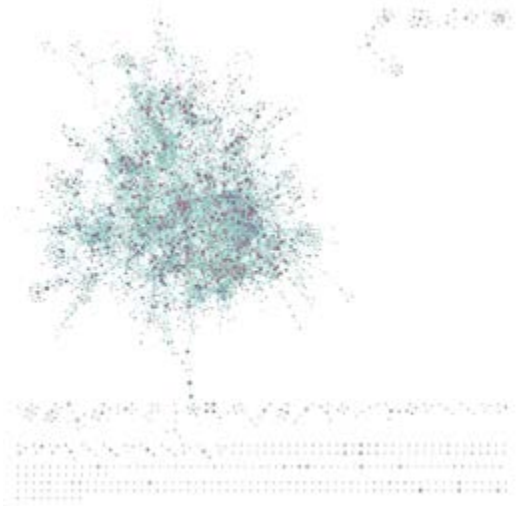
Clustering of GO GSEA Terms Based on Normalized Enrichment Scores (NES)

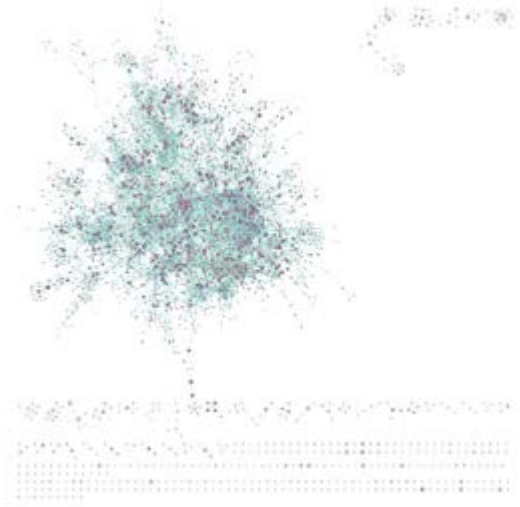






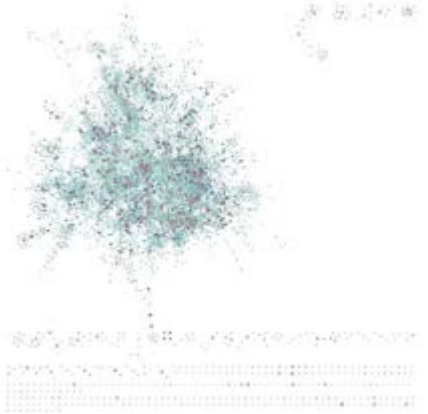


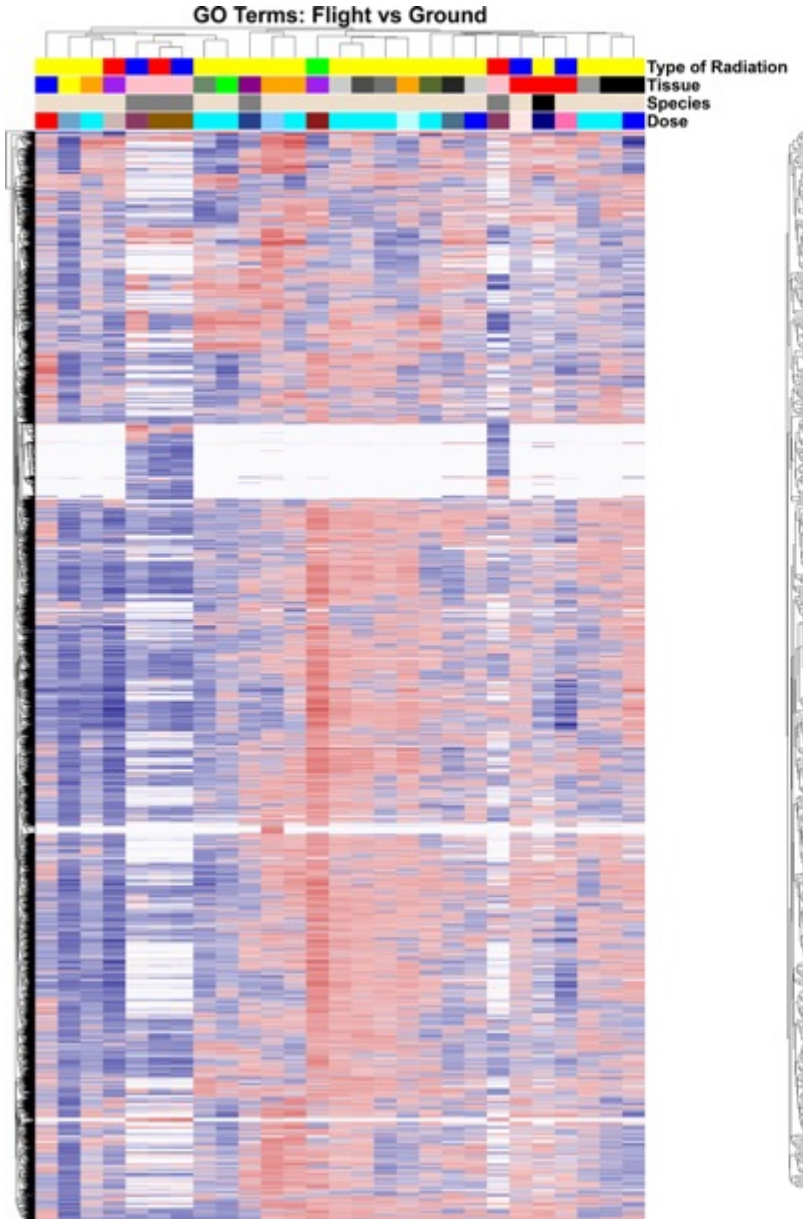


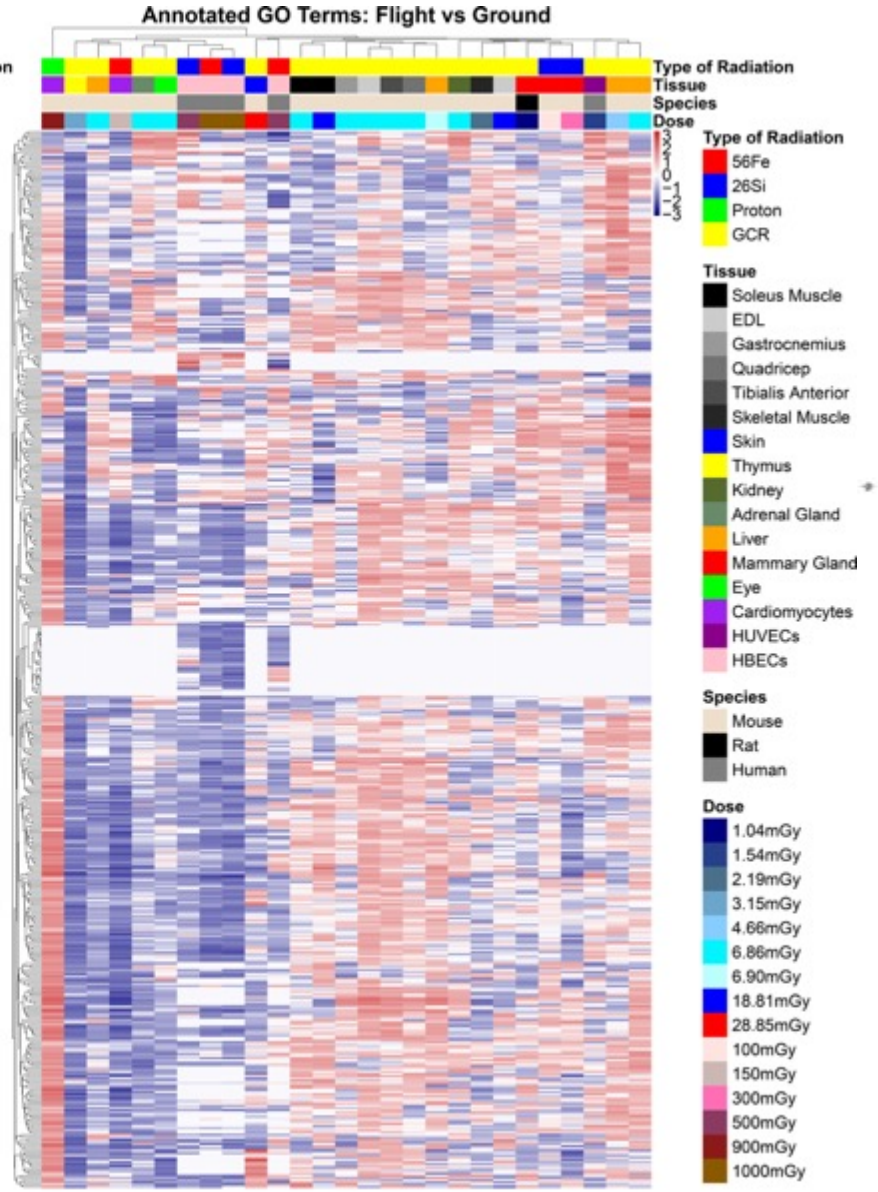


Clustering of Pathways with Dose

All Go Terms

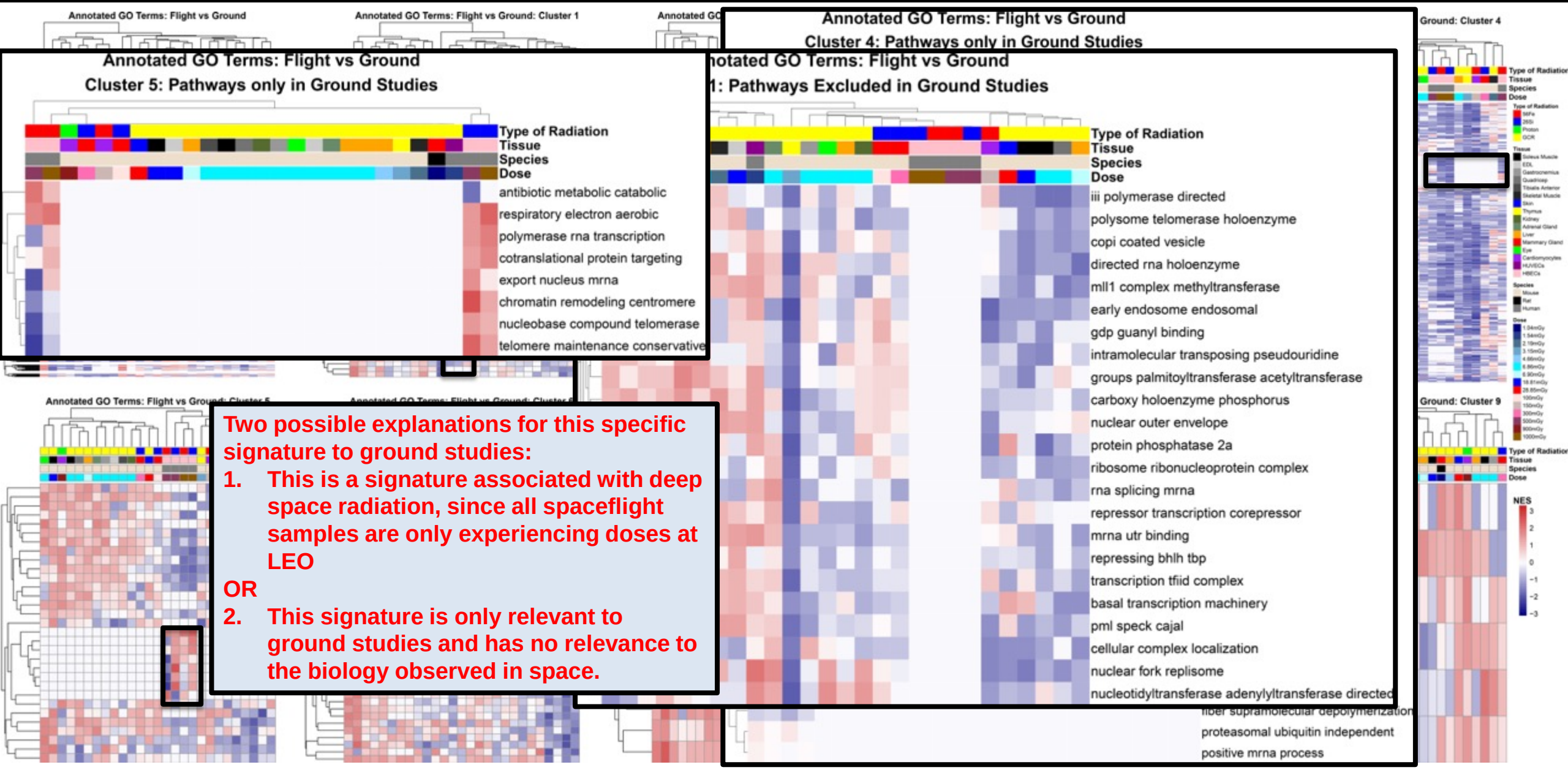






Annotated Go Terms

The Annotated GO Pathways will Subcluster into Logical Groups



Two possible explanations for this specific signature to ground studies:

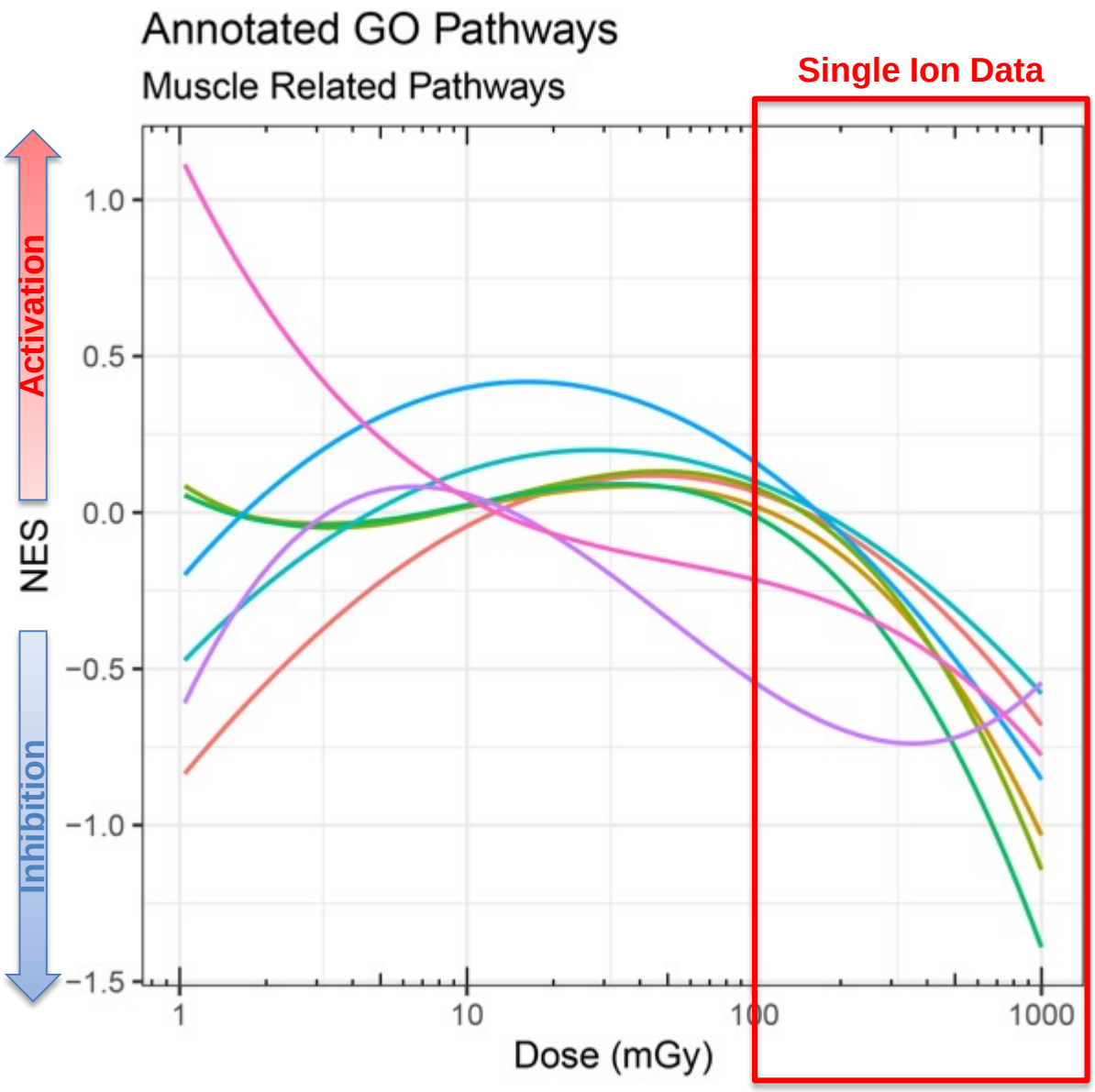
1. **This is a signature associated with deep space radiation, since all spaceflight samples are only experiencing doses at LEO**

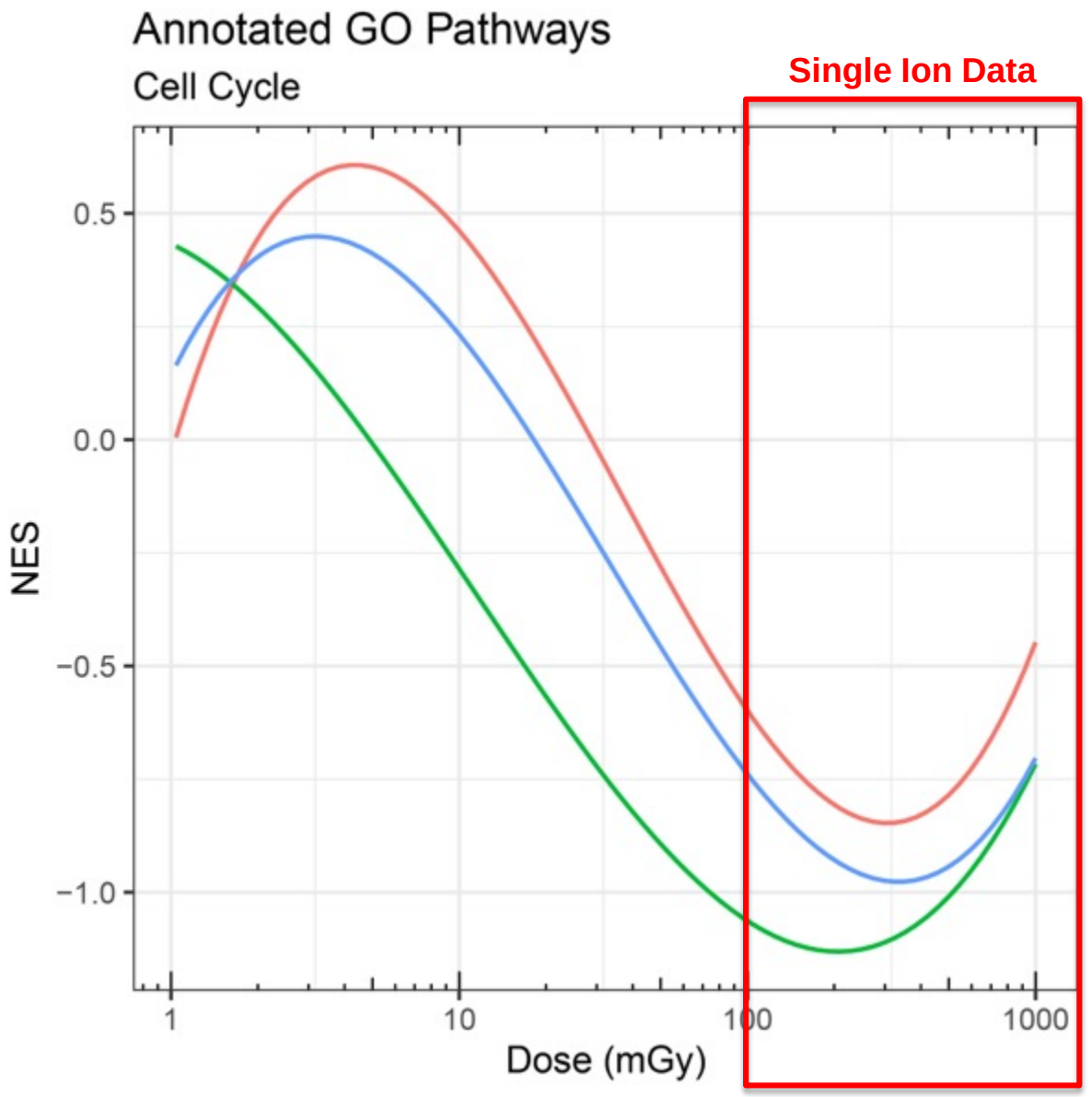
OR

2. **This signature is only relevant to ground studies and has no relevance to the biology observed in space.**

Example Annotated Pathways Known to be Impacted by Space Irradiation

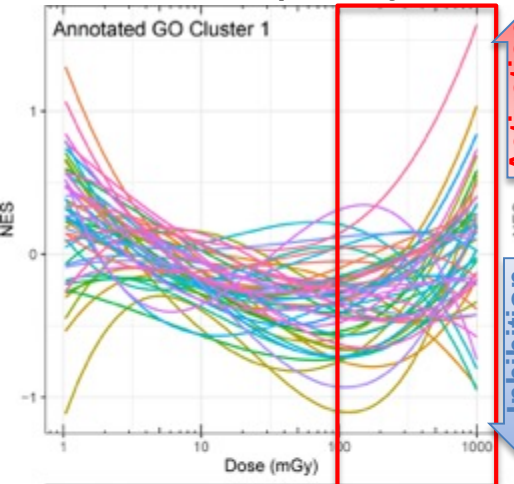
Regression Splines



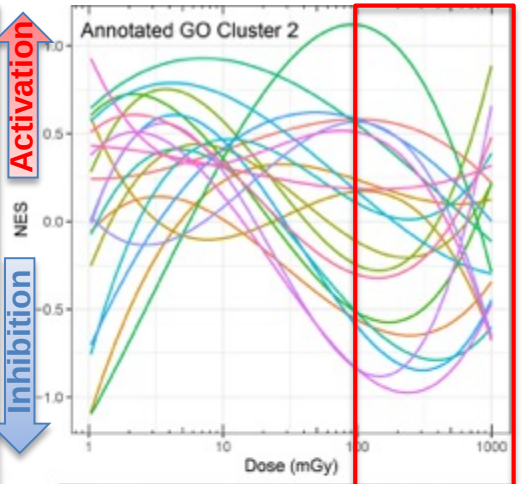


Trends as a function of dose with annotated GO pathways

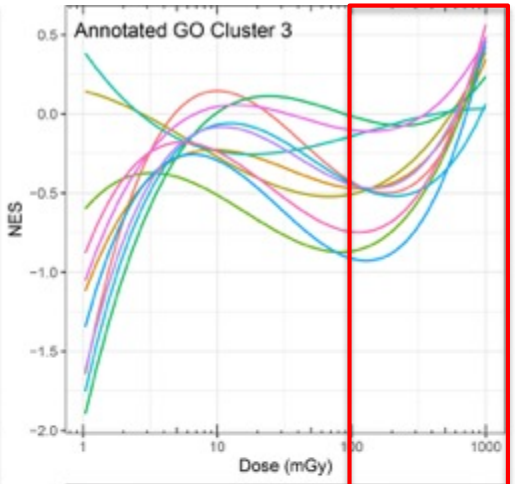
Cluster 1: RNA processing, telomere lengthening, and mitochondrial pathways



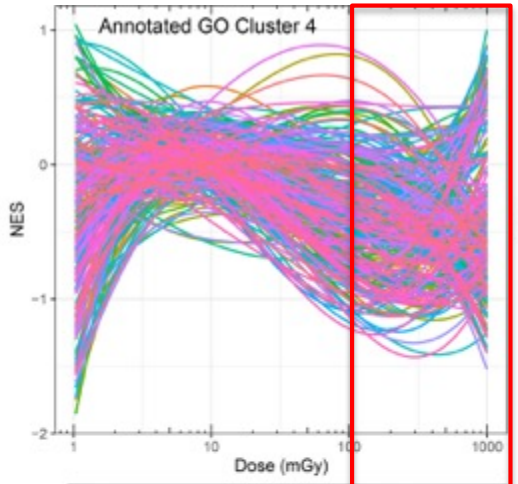
Cluster 2: Developmental Pathways



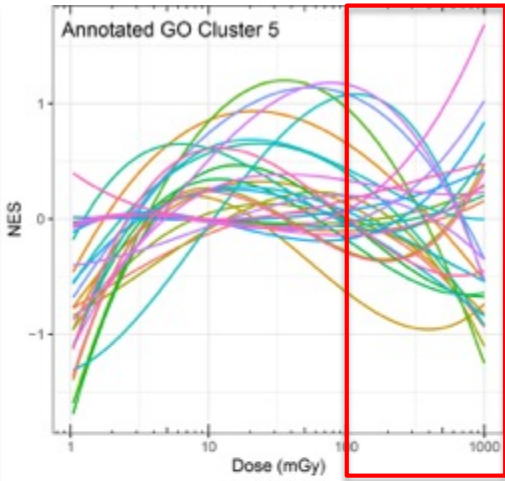
Cluster 3: Calcium Signaling and Actin Binding



Cluster 4: Immune, Inflammation, muscle, and lipid related pathways



Cluster 5: photoreceptor and synapse pathways

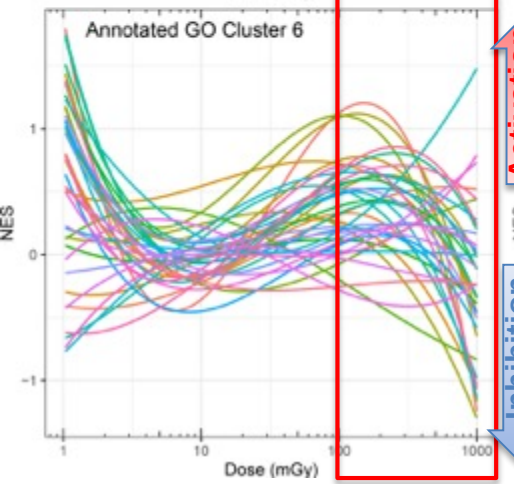


Activation

Inhibition

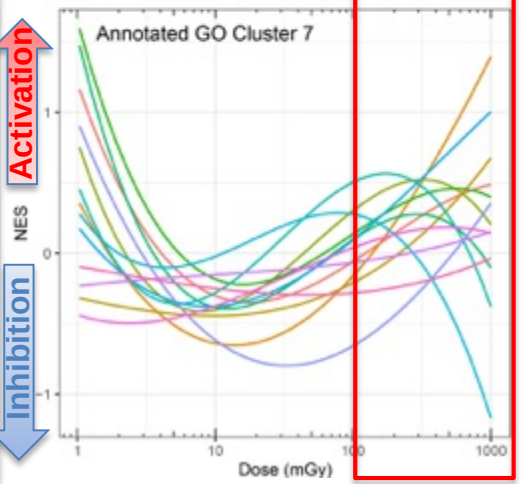
Single Ion Data

Cluster 6: amino acid and ribosomal pathways



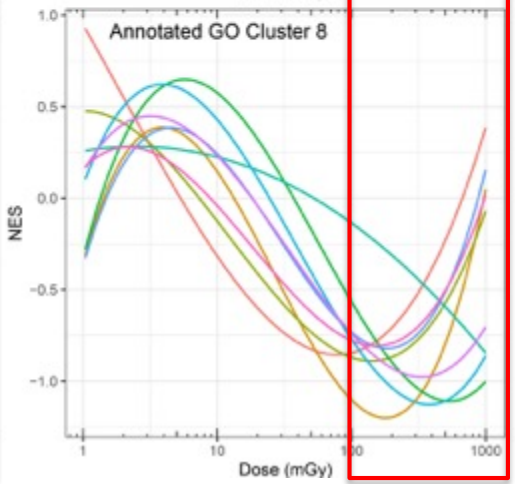
Single Ion Data

Cluster 7: drug response and catabolic process pathways



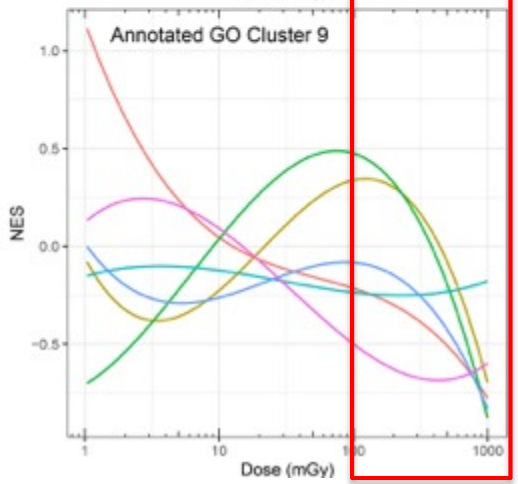
Single Ion Data

Cluster 8: Mitotic and Cell Cycle Related Pathways

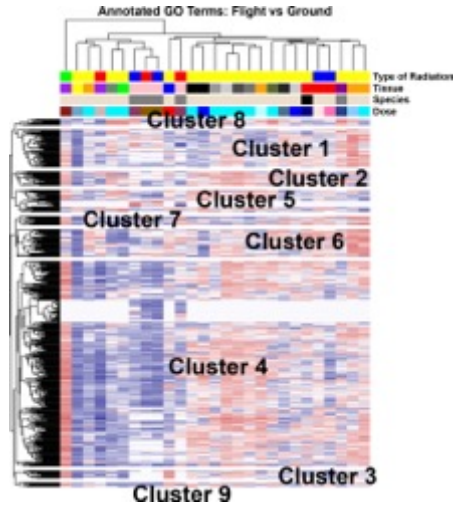


Single Ion Data

Cluster 9: hydration related pathways



Single Ion Data



Regression Splines

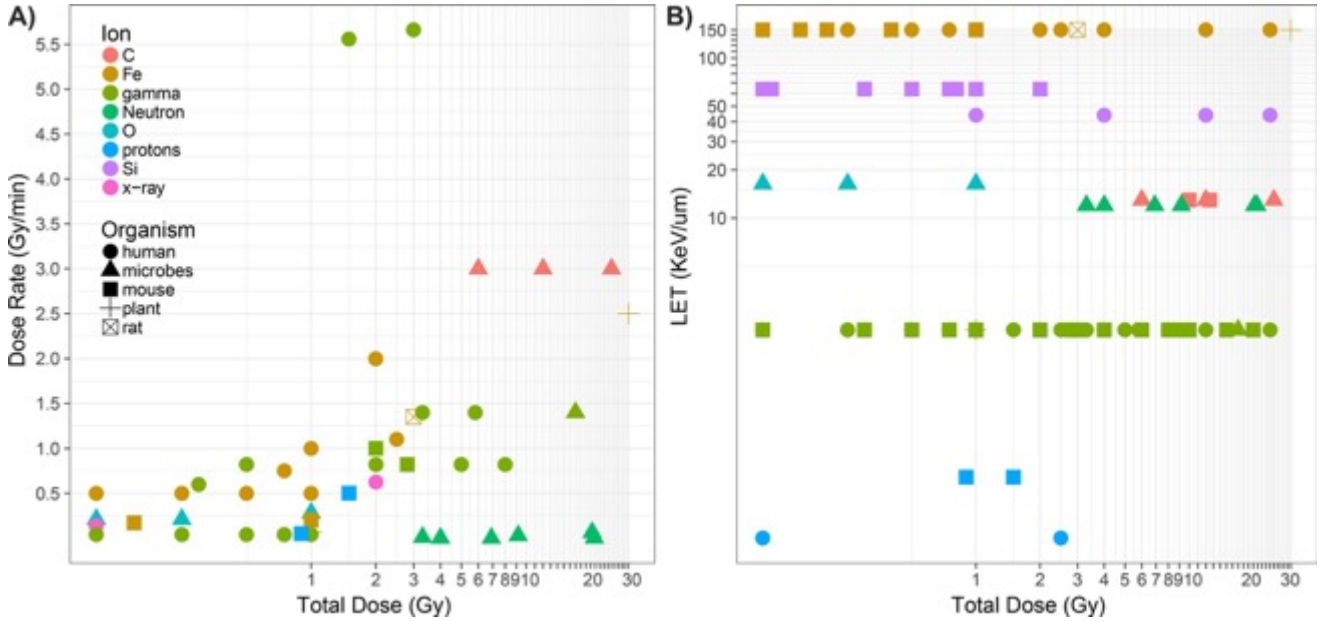
Summary and Future Work

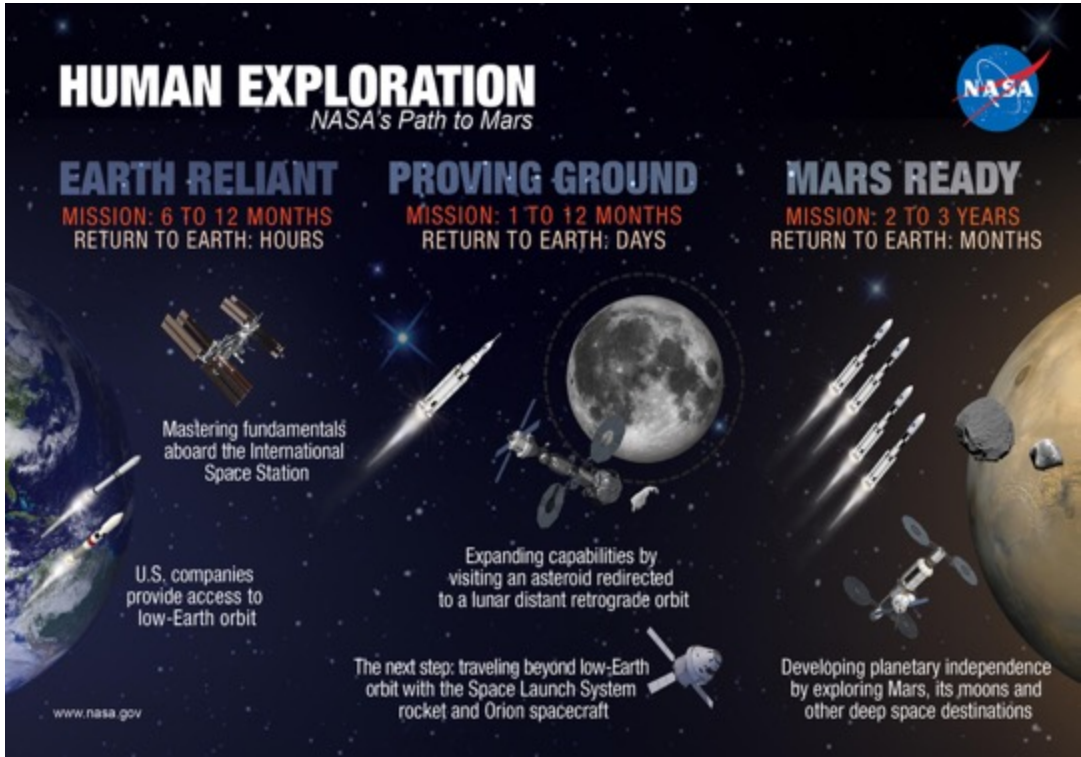
Summary:

- **This technique and results can be used to determine what pathways to filter out from ground experiments to provide relevance to actual space radiation exposure**
- **Help identify unique signatures associated with spaceflight**

Analysis left to do:

- **Add predictions and potentially modeling to predict impact on pathway regulation in deep space**
- **Add LET, Energy, and Dose Rate information to analysis**





Acknowledgements

GeneLab Open Science for Life in Space

https://genelab.nasa.gov/

Gary Hardiman

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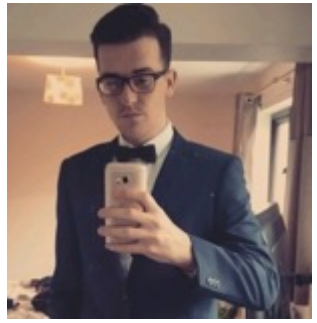

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