

Supplementary Material

**Global transcriptomic analysis suggests carbon dioxide as an environmental stressor in
spaceflight: A systems biology GeneLab case study**

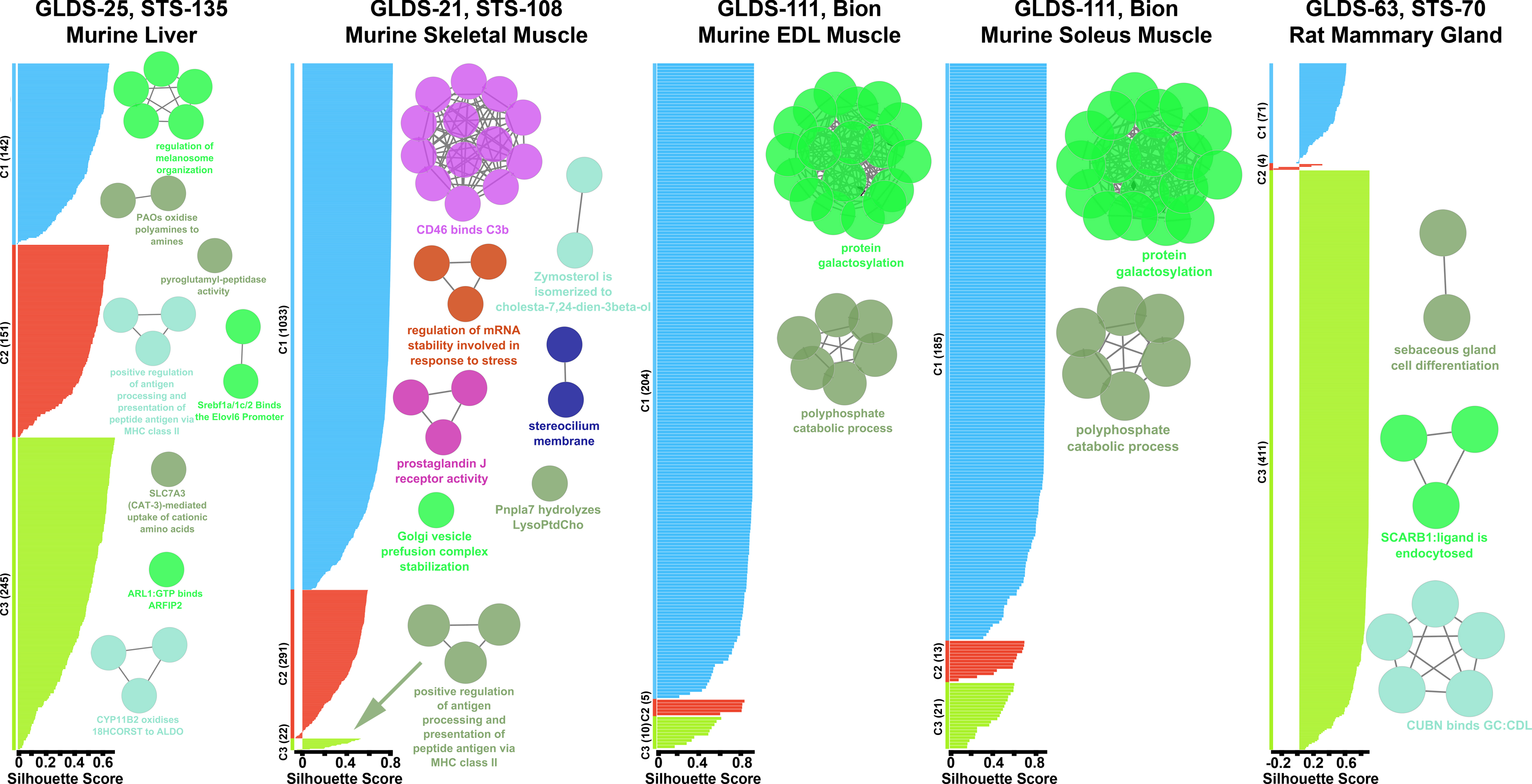
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***share equal first authorship**

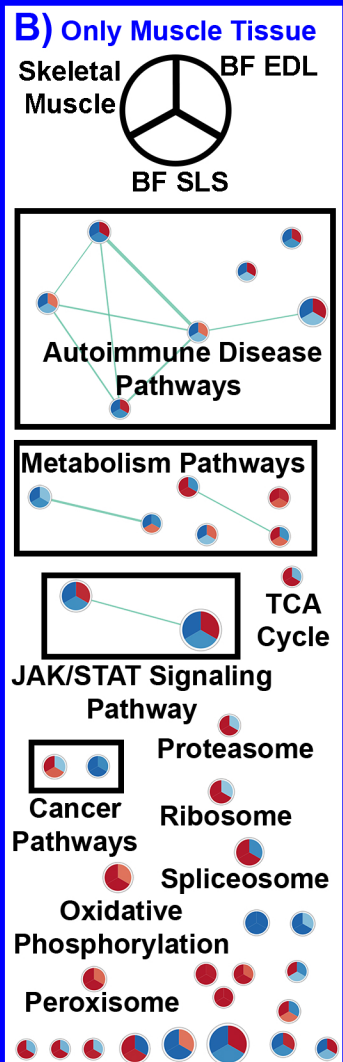
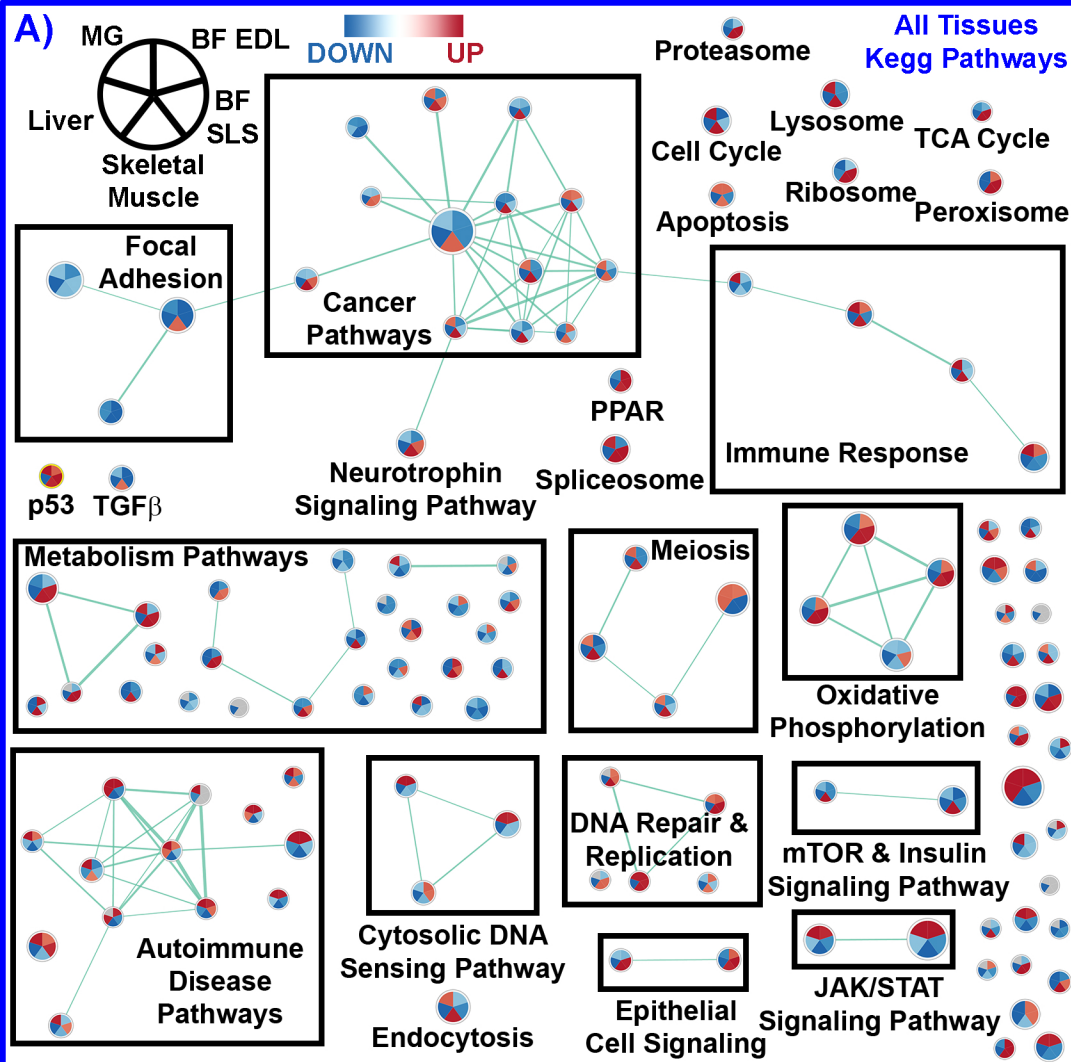
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Supplemental Fig 1. Silhouette plots through K-Mean Statistics for statistically regulated genes for each dataset. Generation of Silhouette plots with K-mean statistics was performed on each dataset for genes that were statistically relevant ($p\text{-value} < 0.05$) (genes from heatmaps in **Fig. 2**). Next to each cluster of genes the functional impact was determined using ClueGO.



Supplemental Fig 2. Full Network representation of gene sets listed in the KEGG pathway database from GSEA C2 gene set annotations. The full GSEA network that was shown in **Fig 4. A)** The statistically significant gene sets and the overlapping regulation of each gene set for all datasets and tissues. **B)** The statistically significant gene sets and the overlapping regulation for only muscle related tissues. Leading edge analysis with an $FDR < 0.05$ determined significant gene sets enriched for each group. The size of each node reflects the amount of molecules involved in each gene set. The edge (green lines) represents the number of genes associated with the overlap of two gene sets (or nodes) that the edge connects. Clusters were named according to common function in each grouping. Upregulated gene sets were denoted with red color and downregulated gene sets were denoted by blue color. The grey color represents no change in regulation for that dataset. The legends on the top show which quadrant in the node is associated with a specific tissue with BF EDL = Bion, Extensor Digitorum Longus, BF SLS = Bion Soleus Muscle, and MG = Mammary Gland. The labels for the majority of single nodes without connections were not shown.

GO Term	Term P-Value
positive regulation of glucocorticoid metabolic process	4.73E-05
positive regulation of glucocorticoid biosynthetic process	4.73E-05
positive regulation of aldosterone metabolic process	9.46E-05
positive regulation of aldosterone biosynthetic process	9.46E-05
negative regulation of testicular blood vessel morphogenesis	4.73E-05
negative regulation of male gonad development	4.73E-05
positive regulation of cortisol biosynthetic process	4.73E-05
regulation of testosterone biosynthetic process	9.46E-05

Supplemental Table 1. Specific Gene Ontology (GO) terms for the nodes shown in Fig. 3D determined from the 3 common genes. The p-values used to determine these GO Terms are also shown.