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Title: Molecular Responses in Mouse Brain Regions to Spaceflight: A Secondary RNA-Seq Analysis

Abstract: Spaceflight presents unique stressors, such as microgravity and cosmic radiation, that deeply impact brain physiology. In this study, we re-analyzed publicly available RNA-seq datasets from NASA's OSD projects, focusing on three mouse brain regions—the cerebellum, hippocampus, and left cerebral hemisphere—to investigate the molecular effects of spaceflight. Our bioinformatics pipeline incorporated quality control with fastp, alignment using STAR, and quantification via Salmon, followed by differential expression analysis with DESeq2. Functional enrichment analyses, including GO and KEGG pathway assessments with clusterProfiler, revealed a consistent enrichment of the "Protein processing in the endoplasmic reticulum" pathway across all datasets. Additionally, pairwise comparisons uncovered region-specific transcriptional responses, such as alterations in RNA splicing, ribosome biogenesis, and phosphorylation regulation. These findings increase our understanding of neural adaptations to spaceflight and may inform future strategies to mitigate the adverse effects of space travel on brain health.