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Spaceflight causes strain-dependent gene expression changes in the kidneys of mice



Rebecca H. Finch¹, Geraldine Vitry^{1,2,3}, Keith Siew⁴, Stephen B. Walsh⁴, Afshin Beheshti^{5,6}, Gary Hardiman^{7,8} & Willian A. da Silveira^{1,2,9} ✉

Incidence of kidney stones in astronauts is a major risk factor associated with long-term missions, caused by increased blood calcium levels due to bone demineralisation triggered by microgravity and space radiation. Transcriptomic changes have been observed in tissues during spaceflight, including the kidney. We analysed kidney transcriptome patterns in two different strains of mice flown on the International Space Station, C57BL/6J and BALB/c. Here we show a link between spaceflight and transcriptome patterns associated with dysregulation of lipid and extracellular matrix metabolism and altered transforming growth factor-beta signalling. A stronger response was seen in C57BL/6J mice than BALB/c. Genetic differences in hyaluronan metabolism between strains may confer protection against extracellular matrix remodelling through the downregulation of epithelial-mesenchymal transition. We intend for our findings to contribute to the development of new countermeasures against kidney disease in astronauts and people here on Earth.

Renal health risks are one of the key risk factors facing astronauts on long-term missions due to the increased incidence of kidney stones after missions¹, but current mitigation strategies are insufficient to fully protect against the damage caused by the space environment¹.

One of the main causes of such damage is space radiation, exposure to which causes increased levels of reactive oxygen species, which leads to oxidative stress, inflammation, genetic and epigenetic alterations, and mitochondrial dysfunction^{2,3}. The kidney is particularly vulnerable to the stresses of spaceflight due to its large number of mitochondria, playing an important part in the regulation of oxidative stress in the body and being severely affected by oxidative stress itself. This organ is affected in a multifactorial way, and disruption of its oxidative stress regulation functions acts as a positive feedback mechanism for continuous kidney damage².

A second source of spaceflight damage derives from microgravity itself. The combination of radiation and microgravity exposure results in loss of bone mass, with the consequence of increased calcium levels leading to

build-up of calcium oxalate². This, linked with dietary constraints and decreased fluid intake in space, can contribute to the formation of kidney stones via supersaturated urine, caused by increased oxalate and uric acid, decreased citrate, and lowered pH levels⁴. Kidney stones, or renal calculi, form from the build-up and crystallisation of calcium oxalate, leading to severe pain and blockages, and can require surgery to remove. The potential risk of formation of kidney stones was first raised by Cockett, Beehler and Roberts⁵ due to weightlessness and lack of physical activity in spaceflight. Increased incidence of kidney stones has been seen in spaceflight, with reported cases of 12 NASA astronauts developing the condition after missions. One cosmonaut has been reported to have developed a kidney stone during a mission⁶. Potential issues from kidney stones on long-term missions include impacting the health and well-being of astronauts and limiting their abilities to carry out their duties. The cosmonaut who developed a kidney stone during a mission did not require intervention to remove the stone⁶, but future cases have the potential to necessitate a decision to abort a

¹ University of Staffordshire, Department of Sports and Science, School of Health, Education, Policing and Sciences, Science Centre, Leek Road, Stoke-on-Trent, ST4 2DF, UK. ² International Space University, 1 Rue Jean-Dominique Cassini, 67400 Illkirch-Graffenstaden, France. ³ Georgetown University Medical Center, Lombardi Comprehensive Cancer Center, Department of Oncology, 3970 Reservoir Rd, NW, New Research Building EP11, Washington, DC, 20057, USA. ⁴ London Tubular Centre, Department of Renal Medicine, University College London, London, UK. ⁵ Center for Space Biomedicine, McGowan Institute for Regenerative Medicine, Department of Surgery, University of Pittsburgh, Pittsburgh, PA, 15219, USA. ⁶ Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard, Cambridge, MA, 02142, USA. ⁷ Faculty of Medicine, Health and Life Sciences, Institute for Global Food Security (IGFS), School of Biological Sciences, Queen's University Belfast, 19 Chlorine Gardens, Belfast, BT9 5DL, UK. ⁸ Department of Medicine, Medical University of South Carolina, MSC 403, 171 Ashley Ave Suite 419, Charleston, SC, 29425, USA. ⁹ School of Science, Engineering and Environment, University of Salford, Manchester, M5 4WT, UK.

✉ e-mail: w.a.dasilveira@salford.ac.uk

mission and return to Earth for surgery, and the longer the mission, the more this risk increases.

Adding to that, previous research has shown downregulated expression of nuclear oxidative phosphorylation genes and upregulated expression of mitochondrial oxidative phosphorylation genes in space in multiple tissues, including the kidney; this switch is thought to be caused by reactive oxygen species causing damage to transcripts from nuclear DNA³. The kidney is particularly sensitive to oxidative stress due to its large number of mitochondria. Other effects that space has been observed to exert on the kidneys include changes to endothelial cells and the cytoskeleton, vascular senescence, altered fluid distribution and neurohormonal balance².

Not all astronauts develop kidney stones after spaceflight exposure and it is still not clear to what extent the increased risk of renal calculi could derive from differences in genetic background⁷. Although studying this with human subjects presents a plethora of ethical and logistic issues, we can - fortunately - initially use animal models to explore the question. Animals have been used as models to assess the ability of humans to survive in space for the last seventy years, and the first mouse was launched into space in 1950⁸. Previous studies have shown that different strains of mice have different reactions to kidney injury. C57BL/6 mice showed more profound inflammation, intrinsic injury responses and renal architecture disruption than BALB/c mice in response to reversible unilateral ureteral obstruction, a model of renal fibrosis⁹. The two strains also show different sensitivities to radiation, C57BL/6 are more radioresistant, while BALB/c are more radiosensitive^{10,11} and BALB/c have lower ratios of mitochondrial DNA to nuclear DNA, which has been associated with sensitivity to mitochondrial calcium overload¹¹.

C57BL/6 mice have also been shown to be more sensitive to the effects of streptozotocin-induced diabetes than BALB/c mice¹². Induction of kidney stones experimentally in mice has been found to be significantly more difficult than in rats, leading to the hypothesis that mice have species-specific protective mechanisms against kidney stones. A model of calcium oxalate crystal deposition in the mouse kidney was induced by injection of glyoxylate but began to decrease 12 days after administration¹³. Another method of promoting calcium oxalate crystal deposition in mice is the introduction of an oxalate-rich diet. Such diets have been shown to induce calcium oxalate crystal-related nephropathy and chronic kidney disease in other strains, but this has not been seen in C57BL/6J or BALB/c mice¹⁴.

Interestingly, we have reported in the past unexpected differences in the intensity of transcriptomic changes in tissues, including the kidney, in

mice of the C57BL/6J and BALB/c lineages when exposed to spaceflight. BALB/c presented subtle alterations in gene expression, whereas C57BL/6J presented major alterations³.

For the first time in this study, we focus on renal transcriptome alterations in space and how they could be impacted by genetic background.

Results

Lipid metabolism, ECM and TGF- β signalling gene expression

Differential expression analysis of kidney transcriptome data from C57BL/6J (RR-1 mission) and BALB/c mice (RR-3 mission) was carried out to determine the differences in their responses to spaceflight. Differential expression analysis of C57BL/6J was determined by comparison of Spaceflight versus Ground Control groups and found 638 differentially expressed genes (Supplementary Data 1). The same analysis identified zero differentially expressed genes in RR-3, and an alternative approach to isolate specific genes altered by spaceflight on BALB/c kidney was used, i.e., both Spaceflight and Ground Control groups were compared to basal levels of gene expression at the beginning of the experiment and genes that were altered only by spaceflight were selected, a total of 671 genes (Supplementary Data 2). The gene signature of the differentially expressed genes in C57BL/6J had a stronger and clearer separation between the Spaceflight and Ground Control groups than in BALB/c (Supplementary Fig. 3).

By focusing on a subset of genes exhibiting a twofold increase or decrease in expression following exposure to spaceflight, we pinpointed alterations in genes involved in lipid metabolic pathways, extracellular matrix degradation, and TGF- β signalling within the kidneys of both lineages (Fig. 1). Interestingly, the *Ccl28* gene—belonging to the TGF- β signalling pathway—was the most differentially expressed gene in the C57BL/6J samples with a log2 fold change of 2.05 (adjusted p -value ≤ 0.1) (Fig. 1a, Supplementary Table 1).

Genes involved in lipid metabolism were differentially expressed in C57BL/6J. *Slc10a1*, *Npas2* and *Arntl*, were upregulated, while *Hmgcs2* was downregulated with a log2 fold change of -1.68 (Fig. 1).

Genes involved in lipid metabolism were also differentially expressed in BALB/c, including *Egr1*, which was positively differentially expressed (log2 fold change 1.59), and *Hmgcr*, which was negatively differentially expressed (log2 fold change -1.13).

Both strains exhibited differential expression in genes involved in extracellular matrix degradation. *Adamts8* was upregulated in C57BL/6J, while expression of *Ncam1* and *Aspn* were altered in BALB/c (Fig. 1).

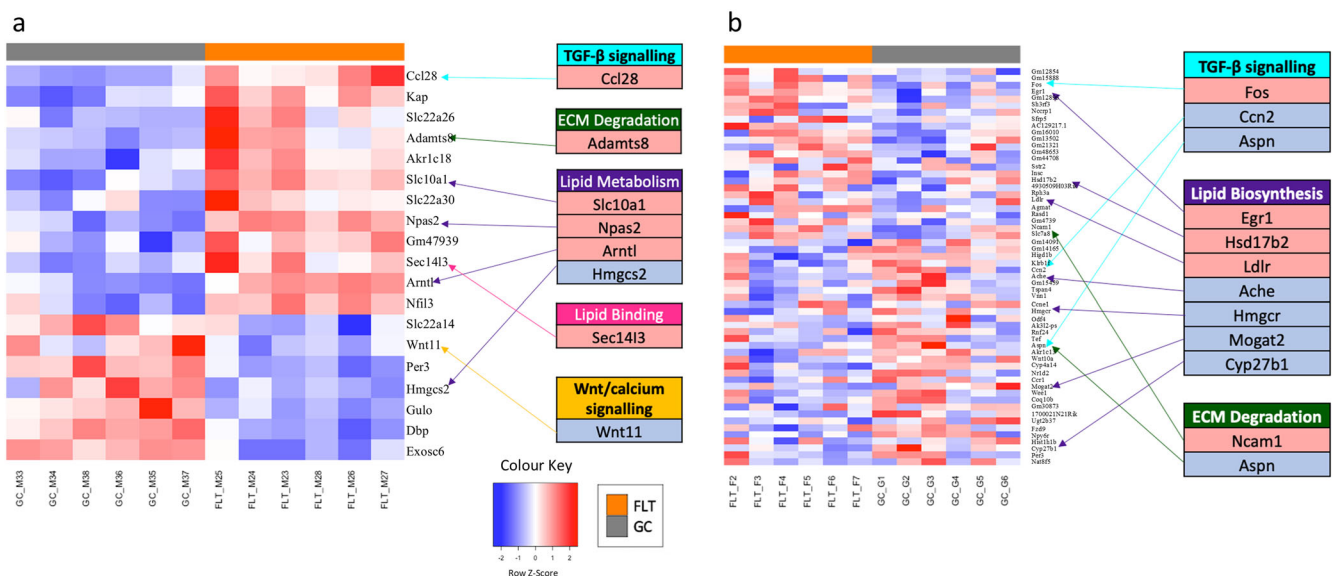


Fig. 1 | Gene expression signature of mouse kidneys exposed to spaceflight shows genes of TGF- β and Lipid Metabolism altered in C57BL/6J and BALB/c mice lineages. Differentially expressed genes in spaceflight in kidney tissue from (a) the

C57BL/6J mice on the RR-1 mission and (b) the BALB/c mice on the RR-3 mission (adjusted p -value ≤ 0.1) with a minimum of twice the expected log2 fold change ($>1/ <-1$). FLT spaceflight samples, GC ground control samples.

Table 1 | Spaceflight-exposed kidney shows cholesterol and protein synthesis pathways up and downregulated, respectively, in both lineages, while extracellular matrix pathways show downregulation in C57BL/6J and upregulation in BALB/c mice

	Upregulated in C57BL/6J	Downregulated in C57BL/6J
BALB/c up	Cholesterol Biosynthesis Pathway Cholesterol biosynthetic Cholesterol biosynthesis Superpathway of cholesterol biosynthesis Cholesterol Biosynthesis with Skeletal Dysplasias Cholesterol metabolism (includes both Bloch and Kandutsch-Russell pathways) Steroid biosynthetic Regulation of cholesterol biosynthesis by SREBP (SREBF) Cholesterol biosynthesis, squalene 2,3-epoxide → cholesterol Cholesterol biosynthesis II (via 24,25-dihydrolanosterol)	Genes encoding secreted soluble factors Ensemble of genes encoding ECM-associated proteins, including ECM-affiliated proteins, ECM regulators and secreted factors Kisspeptin/Kisspeptin Receptor System in the Ovary E3 ubiquitin ligases ubiquitinate target proteins Ovarian steroidogenesis Protein ubiquitination Ensemble genes encoding extracellular matrix and extracellular matrix-associated proteins TGF-beta signalling pathway
BALB/c down	N/A	Peptide chain elongation Eukaryotic Translation Elongation metabolism Ribosome Cytoplasmic Ribosomal Proteins Viral mRNA Translation Selenocysteine synthesis Translation Eukaryotic Translation Termination Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)

Biological process pathways enriched by overrepresentation of differentially expressed genes in kidney transcriptomic data from C57BL/6J (RR-1) and BALB/c (RR-3) mice (FDR < 0.05).

Enrichment of pathways related to TGF- β signalling was seen in genes upregulated in BALB/c (RR-3) and downregulated in C57BL/6J (RR-1) in response to spaceflight (Fig. 1). As previously mentioned, both strains showed increased cholesterol biosynthesis, and BALB/c exhibited enrichment in hallmark Myc targets, both of which affect TGF- β signalling. Both strains exhibited differential expression in genes involved in TGF- β signalling. This included *Ccl28*, the most differentially expressed gene in C57BL/6J (log2 fold change 2.05). In BALB/c *Fos* was upregulated (log2 fold change 1.60), while *Ccn2* and *Aspn* were downregulated (Fig. 1).

In C57BL/6J mice, the *Wnt11* gene shows downregulation in the spaceflight group compared to the control group, with a log2 fold change of -1.15 (adjusted *p*-value ≤ 0.1). This gene is involved in Wnt signalling, a pathway which is involved in crosstalk with TGF- β signalling.

Overrepresentation analysis of both datasets showed upregulation in genes linked with cholesterol-related pathways.

Genes connected with extracellular matrix and TGF- β signalling pathways were upregulated in BALB/c (RR-3) and downregulated in C57BL/6J (RR-1) (Table 1, Supplementary Fig. 2). A GSEA analysis carried out using the Gene Ontology biological process database, Supplementary Table 1, showed that pathways related to increased lipid and fat metabolism were enriched in both datasets. In BALB/c, there was an enrichment in several hallmark pathways connected with dysregulated extracellular matrix metabolism, including Myc targets, adipogenesis and epithelial-mesenchymal transition (Supplementary Data 4).

Lipid and protein synthesis and circadian rhythm patterns

Overrepresentation analysis on both C57BL/6J (RR-1) and BALB/c (RR-3) using the hallmarks database indicated increased enrichment of pathways associated with epithelial cell remodelling, but different pathways were identified in each dataset (Supplementary Data 3 and 4).

Comparison of statistically relevant GSEA results of biological processes for C57BL/6J (RR-1) and BALB/c (RR-3) datasets identified clusters of gene sets, including clusters with opposite patterns between datasets (Fig. 2). Notably, cholesterol biosynthesis and fatty acyl coA biosynthesis were positively correlated with spaceflight in C57BL/6J and negatively correlated in BALB/c. The opposite pattern was seen in hallmarks related to translation, protein folding and circadian rhythm. Lipid metabolism and storage, cell cycle processes and immune response were positively correlated with spaceflight in both C57BL/6J and BALB/c (Supplementary Fig. 3).

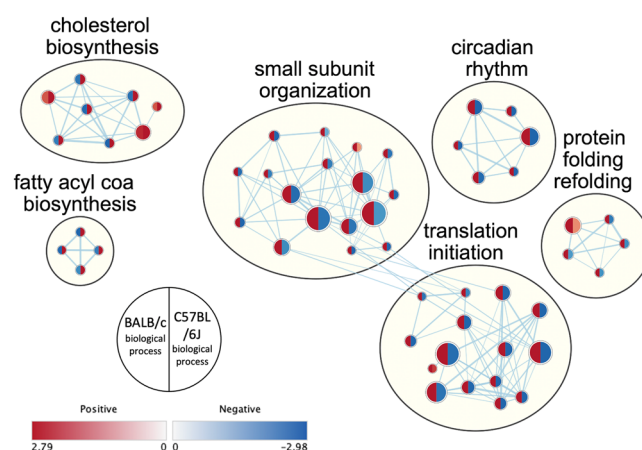


Fig. 2 | Network analysis showing clusters with opposite expression patterns in spaceflight in gene ontology biological process comparison between mice kidney tissue data from C57BL/6J (RR-1) and BALB/c (RR-3) datasets.

Effect of genetic background differences on mice lineages

While mice in both missions were affected by the space environment, the C57BL/6J mice appeared to experience more severe effects than the BALB/c mice. The BALB/c mouse strain has previously been found to have a distinct set of genes with protein-inactivating mutations¹⁵ compared to the C57BL/6J mouse strain. These genetic differences were assessed to provide insight into their different reactions to spaceflight, (Fig. 3, supplementary Fig. 4, and Supplementary Data 5). The hyaluronan metabolic pathway had the highest enrichment ratio, and genes in this pathway were differentially expressed by BALB/c mice in spaceflight. Other pathways containing protein inactivating mutations between the two strains which contained genes differentially expressed in BALB/c in spaceflight related to cytoskeleton and the innate immune system. Pathways containing protein-inactivating mutations between the two strains, which contained genes differentially expressed in C57BL/6J in spaceflight, were connected to organic acid metabolism and negative regulation of intracellular signalling.

Comparison between genes with protein-inactivating mutations in BALB/c compared to C57BL/6J and differentially expressed genes in C57BL/6J (RR-1) and BALB/c (RR-3) (Fig. 4) showed upregulation of genes related to fatty acid metabolism and downregulation of genes related to cell

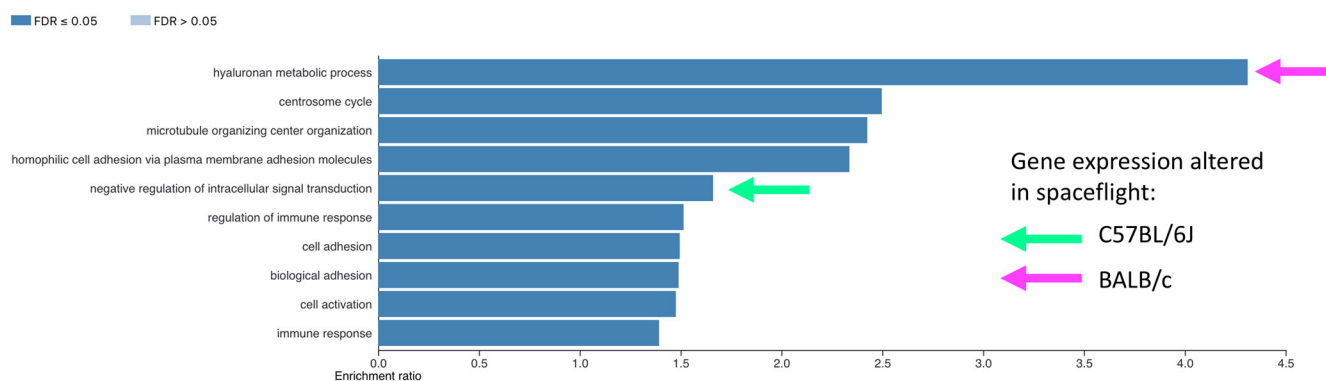


Fig. 3 | Enriched biological process pathways of protein inactivating mutations in BALB/c mice compared to C57BL/6J mice strain reveal connections with expression of genes involved in pathways related to hyaluronan metabolism in BALB/c and intracellular signalling in C57BL/6J. Top 10 enriched biological

process pathways in the genetics of protein inactivating mutations in BALB/c strain of mice compared to C57BL/6J strain 15 and their connections with enriched pathways in the transcriptomic data of kidneys obtained from C57BL/6J mice (RR-1) (green arrow) and BALB/c (RR-3) (pink arrow).

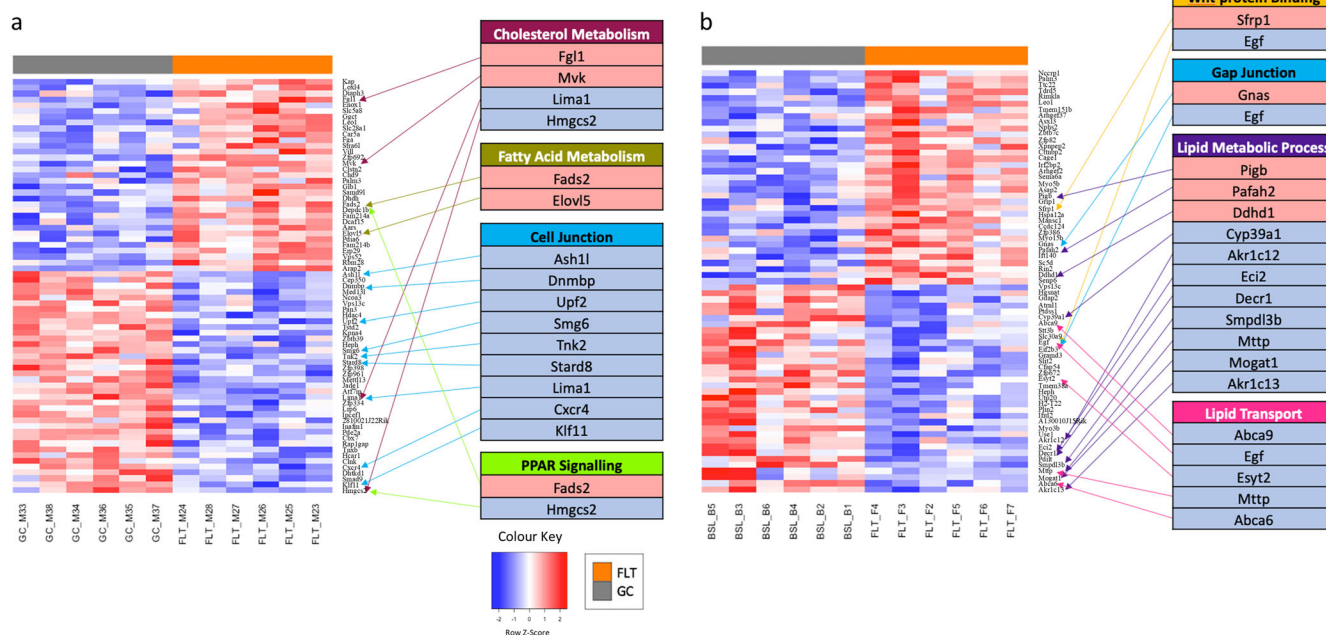


Fig. 4 | Gene expression signatures of mice kidneys exposed to spaceflight limited by protein-inactivating mutations between the BALB/c and C57BL/6J genes show genes involved in lipid metabolism and cell junction altered in C57BL/6J and BALB/c mouse lineages. Differentially expressed genes in kidney

transcriptomic data from **a** C57BL/6J mice on the RR-1 mission and **b** BALB/c mice on the RR-3 mission (adjusted p -value ≤ 0.1). FLT spaceflight samples, GC ground control samples.

junction, and expression of genes related to cholesterol metabolism and PPAR signalling were altered in the comparison with differentially expressed genes in C57BL/6J. In comparison with differentially expressed genes in BALB/c, regulation of genes related to lipid transport was identified, as well as altered expression of genes involved in Wnt-protein binding, gap junction and lipid metabolism. In general, a pattern of upregulation of genes involved in lipid processes was seen in C57BL/6J and downregulation of genes involved in lipid processes was seen in BALB/c in response to spaceflight.

Discussion

With progressions in the space era and the advent of space tourism¹⁶, it will be increasingly common for larger numbers of people with different genetic backgrounds to have access to space. Taking into account the limited amount of people who have been exposed to space so far, it is unknown how the genetic backgrounds of people could affect their responses to the space

environment and how they may differ from the responses to stress on Earth¹⁷, so it is of crucial importance for us to explore this area. In this work, for the first time, we show that not only do the kidneys of BALB/c and C57BL/6J mice have distinct responses to spaceflight, but these can be linked back to their genetic differences.

Mice in both the C57BL/6J and BALB/c lineages—RR-1 and RR-3 missions, respectively—showed transcriptomic alterations associated with their exposure to space. However, their responses were different. Different sets of genes were differentially expressed in each lineage, with extracellular matrix metabolism and TGF- β signalling pathways upregulated and downregulated in BALB/c and C57BL/6J, respectively.

Common alterations in pathways, including lipid metabolism, extracellular matrix degradation and TGF- β signalling, were found. Disruption of lipid metabolism can impair extracellular matrix degradation, via increased levels of TGF- β and PAI1, leading to a build-up of extracellular matrix and promoting fibrosis¹⁸. The strong expression of the *Ccl28* gene suggests an

inflammatory environment in the C57BL/6J spaceflight-exposed kidney as its expression is mediated by proinflammatory cytokines, and causes regulatory T cells to migrate to mucosal surfaces and increase TGF- β production¹⁹.

Mice are commonly used as subjects in unilateral ureteral obstruction, which is a model for chronic kidney disease and renal fibrosis²⁰ both of which are diseases correlated with ageing. Spaceflight is known to promote accelerated ageing, and microgravity, in particular, has been used as a model for ageing due to the similarities in physiological changes observed in both, including insulin resistance, decreased protein breakdown after meals, decreased immune function and dysregulation of cytokine production²¹.

One of the changes associated with ageing in the kidney is nephrosclerosis, which consists of glomerulosclerosis, interstitial fibrosis, and arteriosclerosis²². The incidence of chronic kidney disease development is higher in patients with kidney stones, and therefore, kidney stones are a predictor and risk factor for chronic kidney disease^{23,24}. Tissue injury initiates renal fibrosis, and this injury may be caused by kidney stones. The formation of kidney stones in the papilla involves the activation of inflammatory cascades, leading to the accumulation of calcium, phosphate, and oxalate ions in the interstitial space, forming Randall's plaque. The plaque can erode into the renal pelvis leading to loss of cells and exposing it to urine supersaturated with calcium phosphate, which both contribute to renal stone formation²⁵. High levels of reactive oxygen species associated with the formation of kidney stones can also cause lipid peroxidation, which can damage cell membranes²⁵, which is another mechanism by which fibrotic tissue injury may occur.

Fibrosis is a pathological build-up of extracellular matrix caused by trauma or injury, for instance, a kidney stone, and is driven by disruption of transforming growth factor- β (TGF- β) signalling. Increased levels of TGF- β and PAI1 cause an increased production and decreased degradation of the extracellular matrix, which leads to fibrotic build-up of its components¹⁸. Previous studies have shown an association between dysregulation of lipid metabolism, a decline in kidney function and the development of chronic kidney disease²⁶.

In spaceflight, profibrotic markers have been observed in mouse lung tissue²⁷ and lipid dysregulation has been observed in mouse liver tissue²⁸. TGF- β has also been identified as an important regulator of response to spaceflight²⁹.

Alterations in the expression of genes and enrichment of pathways connected with lipid metabolism were seen in both C57BL/6J (RR-1) and BALB/c (RR-3) mice when exposed to spaceflight. Lipid storage and fatty acid metabolism were enriched in network analysis of biological processes for both C57BL/6J and BALB/c (Supplementary Fig. 3), and GSEA analysis showed enrichment of pathways related to lipid metabolism and synthesis in genes upregulated in both datasets (Table 1). This could indicate increased lipid accumulation which can cause impairment of extracellular matrix degradation¹⁸.

Cholesterol biosynthesis and fatty acyl Co-A biosynthesis were positively correlated with spaceflight in C57BL/6J, with the opposite pattern seen in BALB/c (Fig. 2), potentially affected by the *Hmgcr* gene which plays a role in cholesterol biosynthesis³⁰ which we have shown is downregulated in spaceflight exposed BALB/c (Fig. 1). Accumulation of cholesterol increases TGF- β levels and disrupts extracellular matrix degradation through inhibition of PAI1, which controls normal degradation of the extracellular matrix³¹. Decreased lipid synthesis may be an adaptive response against contribution to fibrotic damage in the BALB/c mice or may be indicative that they are less affected by oxidative stress.

Maintaining homeostasis in lipid metabolism is important to maintain normal kidney function, which is essential for blood pressure and cardiovascular system regulation. Disrupted lipid metabolism can lead to chronic kidney disease and atherosclerosis, which can, in turn, lead to cardiovascular disease, the leading cause of death in chronic kidney disease³². Interestingly, BALB/c appears to exhibit an adaptive response to lipid dysfunction in spaceflight, whereas C57BL/6J does not.

Statistically significantly differentially expressed genes in BALB/c indicate that the strain is affected by spaceflight, but exhibits an adaptive response, protecting it from lipid dysfunction. Upregulation of *Egr1* in BALB/c (Fig. 1) indicates that the strain is affected by spaceflight, as *Egr1* has been shown to play a role in lipid metabolism³², and also in an increase of extracellular matrix components and epithelial-mesenchymal transition, both profibrotic processes which can contribute to kidney disease³³.

The negative differential expression of *Hmgcr* in BALB/c (Fig. 1) could represent an adaptive response. *Hmgcr* encodes HMG-CoA reductase, which is an enzyme involved in the ketogenesis pathway, as is *Hmgcs2*, which was negatively differentially expressed in C57BL/6J. HMG-CoA reductase is also involved in the mevalonate pathway which synthesises cholesterol, catalysing the conversion of HMG-CoA to mevalonate³⁰. HMG-CoA reductase inhibitors are used to reduce the risk of death from cardiovascular disease in chronic kidney disease patients, as the inhibition of mevalonate production reduces total cholesterol and low-density lipoprotein cholesterol³⁴. Therefore, downregulation of *Hmgcr* in BALB/c may indicate increased lipid metabolism, as shown in a previous study²⁸, which could act as a protective mechanism against kidney injury during spaceflight. Together these results suggest that BALB/c mice exhibit an adaptive response to lipid dysfunction in spaceflight.

C57BL/6J, however, did not exhibit an adaptive response to the stresses of spaceflight, and gene expression indicates activated mechanisms related to increased inflammation. The *Hmgcs2* gene, downregulated in C57BL/6J (Fig. 1), encodes the protein 3-hydroxy-3-methylglutaryl-CoA (HMG-CoA synthase) which catalyses the conversion of acetyl-CoA and acetoacetyl-CoA to HMG-CoA and CoA, a which is a rate-limiting step in ketogenesis³⁵. Impairment of ketogenesis causes hepatic injury and inflammation³⁶, and downregulation of HMG-CoA synthase has been identified as a marker for kidney stone disease in a model of induced urolithiasis in rats³⁷, suggesting that the downregulation of HMG-CoA synthase in our data may be a marker for kidney injury.

Although a physiological examination was not carried out as part of this study to confirm signs of lipid dysfunction in mouse kidneys exposed to spaceflight, previous studies have found both transcriptomic and physiological changes associated with this condition in other organs. Abnormal lipid accumulation was detected in liver tissue from mice exposed to spaceflight by Oil Red O staining, supporting the transcriptomic data on lipid dysfunction pathways in the liver²⁸. In another study, increased numbers of lipid droplets were also observed in the liver of spaceflight mice by CARS microscopy and Oil Red O staining along with upregulation of triglyceride biosynthetic pathways seen in multi-omics analysis³⁸.

Maintaining normal levels of turnover in the extracellular matrix is important for normal kidney function, as a fibrotic build-up of its components can cause scarring and impair function, leading to kidney disease³⁹.

BALB/c exposed to spaceflight showed enrichment in pathways connected with dysregulated extracellular matrix metabolism (Supplementary Data 4), including Myc targets, adipogenesis and epithelial-mesenchymal transition. In the kidney, gene targets of the Myc group of proteins have been linked to an activation of glycolytic metabolism, which increases production and deposition of extracellular matrix⁴⁰ and promotion of TGF- β signalling via transcriptional activation of integrin α ⁴¹. Adipogenesis and disruption of fatty acid metabolism can impair extracellular matrix degradation via intracellular accumulation of lipids and lipotoxicity⁴². Mesenchymal cells such as fibroblasts produce the components of the extracellular matrix, so increased levels due to epithelial-mesenchymal transition can cause a potentially fibrotic build-up of these components⁴³.

Lipid accumulation—signs of which were observed in the liver of both strains of mice—can also lead to the impairment of normal extracellular matrix degradation. A build up in extracellular matrix components can lead to kidney disease as disrupted wound repair mechanisms are unable to restore kidney function^{28,44}. Future works need to evaluate lipid levels in the kidney, by histology or other means.

Genes in pathways related to TGF- β signalling were upregulated in BALB/c and downregulated in C57BL/6J (Fig. 1). TGF- β is a cytokine which

increases the production of extracellular matrix components and can lead to kidney dysfunction via glomerulosclerosis and tubulointerstitial fibrosis, leading to renal dysfunction⁴⁵. TGF- β has been previously identified as a master regulator of both response to spaceflight through microRNA signatures²⁹ and fibrosis⁴⁶.

Downregulation of the *Wnt11* gene was associated with spaceflight in C57BL/6J. Its expression is essential for normal development of the glomeruli and for uretic epithelial branching in the kidney, and knockout of the gene has been shown to be lethal to mice *in utero*⁴⁷. *Wnt11* deficiency in older mice has been found to result in tubular abnormalities, glomerular cysts, and interstitial fibrosis⁴⁸. *Wnt11* is involved in Wnt/calcium signalling, and dysregulation of this pathway has been associated with cellular senescence and diseases related to ageing, including renal fibrosis⁴⁹. Wnt signalling is involved in crosstalk with other profibrotic signalling pathways, including the renin-angiotensin system, TGF- β , Notch and Hedgehog⁴⁹. Inhibitors of Wnt signalling have been explored as treatments for fibrosis but have resulted in off-target effects⁴⁹, perhaps in part due to the profibrotic effects of *Wnt11* downregulation.

In C57BL/6J there was enrichment in TNF- α signalling (Supplementary Data 3), which causes intense temporary inflammation and fibrosis⁵⁰, and mTORC signalling (Supplementary Data 3), which increases fibroblast activation and interstitial fibrosis⁵¹. Interferon alpha response, interferon-gamma response and JAK-STAT signalling indicate an increase in adaptive immune response, which may be in response to increased inflammation caused by oxidative stress. Also enriched was angiogenesis (Supplementary Data 3), the formation of new blood vessels as a part of wound healing⁵², and overactivation of the wound healing process is a profibrotic process which can lead to kidney injury.

Both C57BL/6J and BALB/c showed enrichment of the hallmark E2F targets (Supplementary Table 3, Supplementary Data 4), which are involved in DNA repair, and BALB/c also shows enrichment of the DNA repair pathway (Supplementary Data 4). The DNA damage response has been found to contribute to the progression of fibrosis in systemic sclerosis⁵³. The JAK-STAT signalling pathway is also enriched in BALB/c, indicating increased inflammation in both lineages.

Clusters of biological processes related to cell cycle and immune response (Supplementary Fig. 3) were positively correlated with spaceflight in both datasets, which could represent responses to cellular damage by oxidative stress. The circadian rhythm was affected, negatively correlated with spaceflight in C57BL/6J and positively in BALB/c (Supplementary Fig. 3). Mitochondrial gene expression and function are affected by the circadian clock⁵⁴, which has also been seen to be dysregulated in astronauts¹. Protein re-folding pathways were negatively correlated with spaceflight in C57BL/6J and positively in BALB/c (Supplementary Fig. 3). Oxidative stress can lead to protein unfolding, and if unfolded proteins are not re-folded or destroyed, they can accumulate and cause loss of proteostasis, which is associated with ageing⁵⁵. Ribosome activity and translation initiation were also negatively correlated with spaceflight in C57BL/6J and positively in BALB/c (Supplementary Fig. 3), which has been observed previously to be disrupted in spaceflight studies and is linked to loss of proteostasis³.

Photoreceptor development and light perception were correlated negatively with spaceflight in both datasets (Supplementary Fig. 3); many genetic diseases affect both the kidney and the retina due to the presence of common developmental pathways⁵⁶, so these enrichment patterns likely represent expression of genes common to both the retina and the kidney with different functions in each.

To seek explanations for the difference in responses to spaceflight from C57BL/6J and BALB/c mice, we determined enriched pathways for the protein inactivating mutations found previously between these lineages¹⁵ and hyaluronan metabolism was the pathway found to be most enriched (Fig. 3). Hyaluronan is a component of the extracellular matrix which plays important roles in wound healing and inflammation and is upregulated during these processes⁵⁷.

No genes involved in the metabolism of hyaluronan were differentially expressed in C57BL/6J, but one gene involved in hyaluronan metabolism,

Egf, was downregulated in BALB/c (Fig. 3). EGF treatment in rat mesothelial tissue was shown to result in the increase of hyaluronan synthesis and epithelial-mesenchymal transition⁵⁸. The hyaluronan synthesis process is linked with morphological changes such as mitosis and anchorage-independent growth seen in epithelial-mesenchymal transition, by inducing de-adhesion and budding of extracellular vesicles⁵⁸. Increased EGF protein in the urine has been identified as a hallmark of renal interstitial fibrosis and is correlated with increased transcription of the *Egf* gene⁵⁹. Downregulation of *Egf* in the BALB/c mice could potentially confer resistance to extracellular matrix remodelling via reduced hyaluronan synthesis (Fig. 5).

Previous studies have shown similar, milder effects on BALB/c mice compared to C57BL/6J in response to injury and stress. A study on retinal ischaemia/reperfusion injury, a model for diabetic retinopathy, caused increased inflammation and damage due to oxidative stress in C57BL/6J compared to BALB/c mice⁶⁰. BALB/c has also been shown to have milder reactions to UVB exposure than C57BL/6J⁶¹, despite their lack of protective pigmentation. In this study, higher hyaluronan levels and lower collagen levels were measured in C57BL/6J mice. Hyaluronan is a component of the extracellular matrix, plays an important role in the wound repair process, and has been shown to contribute to the development of fibrosis⁶². Increased metabolism of hyaluronan showed the highest enrichment in a functional enrichment analysis of the genetic differences in BALB/c compared to C57BL/6J mice.

Genes with protein inactivating mutations between the strains were also differentially expressed in BALB/c (Supplementary Data 2 and 5), including genes with links to lipid transport which were downregulated, and genes linked to lipid metabolism, gap junction and Wnt-protein binding were also affected. For example, *Mogat1*, which is a lipid precursor which usually has high levels of expression in the kidney⁶³ is downregulated in BALB/c during spaceflight.

In C57BL/6J, genes with protein inactivating mutations between the strains were differentially expressed (Supplementary Data 1 and 5), including alterations in the expression of genes involved in cholesterol metabolism and PPAR signalling, upregulation of genes related to fatty acid metabolism, and downregulation of genes related to cell junction. *Fads2* and *Elovl5* are both involved in fatty acid synthesis, potentially contributing to the impairment of the extracellular matrix via increasing build-up of lipids and lipotoxicity⁴². These genes are not differentially expressed in BALB/c (RR-3), so the differences in these genes between the two mouse strains may confer some resistance to extracellular matrix remodelling. Variation in the *Hmgcs2* gene in BALB/c compared to C57BL/6J may also confer some fibrotic resistance to BALB/c as its downregulation as seen in C57BL/6J (RR-1) promotes proinflammatory ketogenesis^{35,36}. Genes related to cell junction were downregulated, potentially contributing to de-adhesion, which is a part of epithelial-mesenchymal transition.

We would expect that mice exposed to the same length of spaceflight would have similar responses to the stress, nonetheless we encountered a very different response between strains. Their different genetic background is potentially a factor for explaining this difference.

While the C57BL/6J (RR-1) and BALB/c (RR-3) mice showed profibrotic hallmarks they did not develop kidney stones, as seen in astronauts. Nonetheless, a recent work performed a multi-omics analysis of mice exposed to spaceflight on different missions or to ionising radiation and found a signature of renal fibrosis and increased risk of kidney stone formation⁷. Mice on Earth have previously proven to be poor experimental models of kidney stones¹³ but good models of renal fibrosis²⁰ and this research indicates that the same may be true in space. Kidney stones and fibrosis can both result from metabolic disturbances, which have been seen both in these data and in previous studies. A better understanding of the metabolic effects of spaceflight could lead to the development of new treatments and protective measures, and to inform risk assessments for astronauts.

A current countermeasure against bone loss on the ISS since 2008 is the advanced resistive exercise device, which has been shown to prevent bone

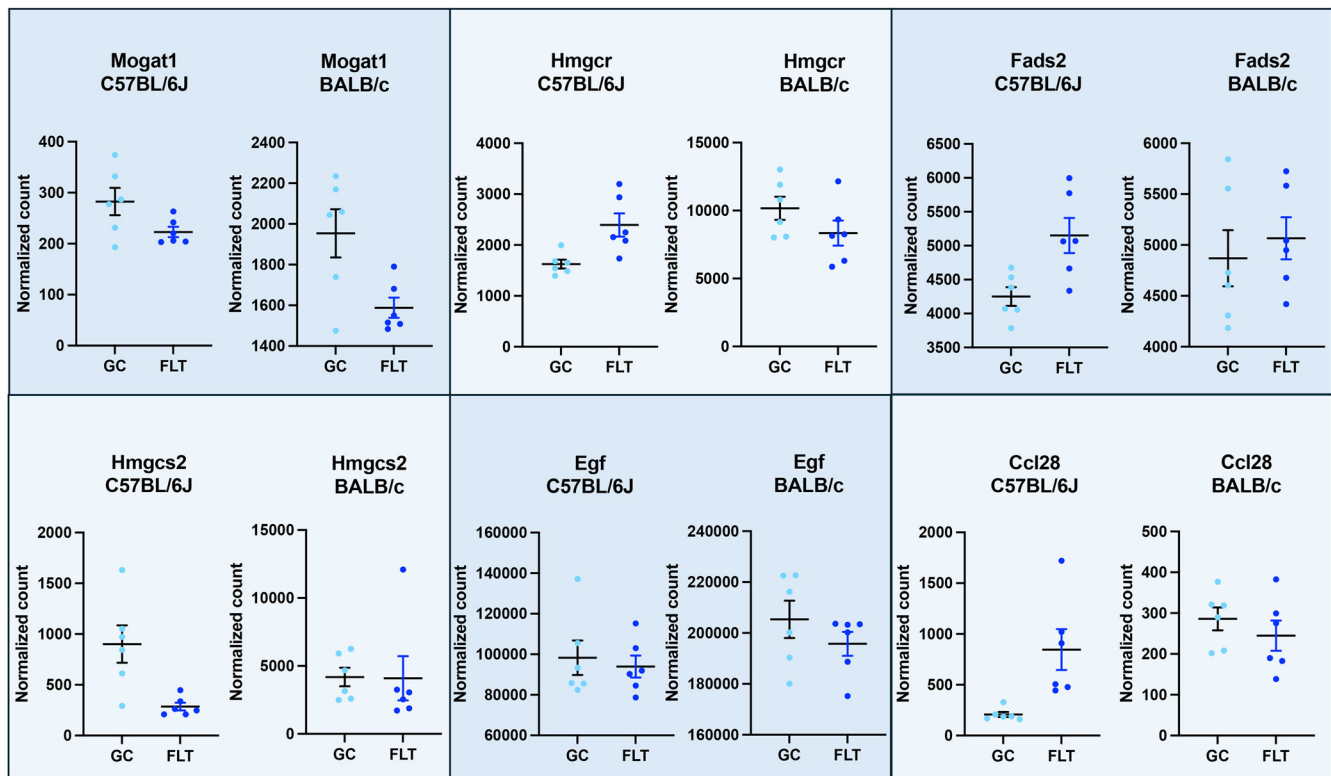


Fig. 5 | Expression profile of targeted genes in the BALB/c and C57BL/6J mouse strains during spaceflight. Normalised counts of Ccl28, Hmgcs2, Hmgcr, Egf, Mogat1, and Fads2 genes in both C57BL/6J (RR1 protocol) and RR3 BALB/c (RR3

protocol) ground control mice (GC) and inflight mice (FLT). Data were plotted on GraphPad Prism software.

mineral density loss while increasing lean mass and decreasing fat mass. The increased blood levels of calcium originating from bone loss can contribute to and exacerbate kidney stone formation⁷. Vitamin D supplementation is necessary as due to the shielding of the ISS from radiation, there is a lower production of endogenous Vitamin D by the astronauts and this vitamin is essential for bone health and calcium metabolism⁶⁴. Nonetheless, the supplementation of Vitamin D needs to be taken carefully as this component is involved in the homeostasis of Calcemia⁶⁵. The long-term effects of bone loss due to extended and repeated exposure to microgravity remains an unresolved issue, and recommendations from the 2010 NASA bone summit included improving pre-flight risk assessment and post-flight monitoring of bone health, continuing implementation of current countermeasures and development of pharmacological interventions with strong links to kidney function⁶⁶.

Countermeasures against the increased risk of kidney stones were first suggested by Cockett, Beehler and Roberts⁵, including a physical exercise regimen and increased fluid intake for astronauts. However, the current mitigations in place are not sufficient to bring the risk of kidney issues on long-term space missions to within acceptable levels¹. In the present study, we show that gene expression related to extracellular matrix dysregulation and fibrosis in the kidney are upregulated during spaceflight, which are two factors known to promote kidney stone formation. As such, considering treatments for fibrosis may be of relevance in the future as a countermeasure.

Although our findings can potentially be of importance to human research we have to bring attention to some limitations of the study. The mice in the study were part of different, non-identical missions. This work claims that the genetic background of mice can influence their response to spaceflight conditions, but it is not possible to infer how strong, if any, the genetic background component of the human response would be to spaceflight.

In conclusion, kidney stones are considered the primary risk to the renal health of astronauts, but because of the link between the development

of kidney stones and renal fibrosis, and observations of profibrotic markers in this and other studies, fibrosis should be considered as an additional serious potential risk on long term space missions.

Further study into the influences of genetic background on the response to spaceflight should be conducted to discover potential protective genes.

Methods

Subjects

Transcriptomic data related to kidney tissue obtained in the missions Rodent Research-1 (RR-1) version 3⁶⁷, Rodent Research-3 (RR-3) version 4⁶⁸ were obtained from NASA's GeneLab Platform (<https://genelab.nasa.gov/>) from dataset identifiers. OSD-102 and OSD-163 respectively. On the RR-1 mission, six C57BL/6J 16-week-old female mice (Jackson Lab) were flown to ISS for 37 days⁶⁷. On the RR-3 mission, 10 BALB/c 12-week-old female mice (Jackson Lab) were flown to ISS for 39 - 42 days⁶⁸. At the end of the mission, the animals were euthanized by the ISS crew and stored at -80 °C until fully dissected on Earth. For both missions, the Ground Control group was composed of mice of similar age, sex and strain and was housed using identical hardware, matching ISS conditions and were euthanized using similar methods.

Differential expression analysis

R Studio (version 1.4.1717)⁶⁹ and the package DESeq2 (version 1.32.0)⁷⁰ were used to perform differential gene expression analysis by fitting a generalised linear model to each gene following a negative binomial distribution. Differentially expressed genes were identified by Flight to Ground Control comparison on C57BL/6J mice in the OSD-102 dataset with an adjusted p value of 0.1. For OSD-163, the Basal group was used as a common control, and differential expression analysis was carried out between Spaceflight versus Basal, and Ground Control versus Basal groups. Genes differentially expressed in the Ground Control group were excluded to leave only genes differentially expressed in Spaceflight compared to Basal. An

adjusted p value of 0.1 was used for the threshold. p -Values were adjusted for multiple testing by the DESeq2 R Package using the procedure of Benjamini and Hochberg⁷⁰.

Heatmaps were created using threshold adjusted p -value ≤ 0.1 and log2 fold change (>1 / <-1) with the addition of manual annotation of genes of interest. The R package gplots version 3.1.1⁷¹ was used.

Pathway level analysis

Overrepresentation analysis was done using WebGestalt⁷² for datasets OSD-102 and OSD-163 from the analysis performed using Deseq2. Venny⁷³ was used to determine common and different pathways between strains.

Gene set enrichment analysis was performed using GSEA (version 4.1.0)^{74,75} using datasets OSD-102 and OSD-163 independent from the analysis performed using Deseq2.

Pathway network visualisation

EnrichmentMap (versions 3.3.2 and 3.3.3) and AutoAnnotate (versions 1.3.4 and 1.3.5) applications in Cytoscape (versions 3.8.2 and 3.9.0) were used to visualise networks of enriched pathways using FDR q -value cut off value 0.1^{76,77}.

Comparison between strains

The set of proteins inactivating genetic differences between C57BL/6J and BALB/c was taken from Timmermans and collaborators, 2017¹⁵. WebGestalt biological processes gene ontology database⁷² was used to assess the effect of the genetic differences between the two strains of mice on their responses to spaceflight. Venny⁷³ was used to determine genes with protein-inactivating mutations between C57BL/6J and BALB/c, compared to differentially expressed genes (adjusted p -value ≤ 0.1) in the RR-1 and RR-3 datasets. R Studio (version 1.4.1717)⁶⁹ and package gplots⁷¹ were used to generate supervised heatmaps of the genes identified by these two comparisons.

Heatmaps were constructed as described above.

Targeted gene expression between the two strains

According to the differential expression analysis results, 6 genes of interest, e.g., Ccl28, Hmgcs2, Hmgcr, Egf, Mogat1, and Fads2, were selected for targeted expression analysis pattern in C57BL/6J (RR-1 mission) and BALB/c (RR-3 mission), using data of the selected genes extracted from normalised count from the NASA's GeneLab Platform (<https://genelab.nasa.gov/>). For each gene, normalised counts were plotted on the GraphPad Prism (version 10.3.1) software (<https://www.graphpad.com>).

Data availability

The datasets used in this work are publicly available at the database NASA Genelab (<https://genelab.nasa.gov/>) under the classification: OSD-102 and OSD-163.

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Author contributions

R.H.F. and G.V. analysed data. RHF and G.V. wrote the paper and prepared the figures. K.S. and S.B.W. contributed to the writing and editing of the paper, A.B. participated in the exchange of ideas, edited the paper and gave feedback on the draft. G.H. designed the study and edited the paper. WAdS funding acquisition, designed the study, supervised the project and wrote and edited the paper.

Competing interests

The authors declare no competing interests.

Additional information

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Correspondence and requests for materials should be addressed to Willian A. da Silveira.

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