Figure 1.

Workflow of the 'Endothelial Cells' (ENDO) study. The centrifuge (circled in yellow) within KUBIK could accommodate 8 EUs maximum. Blue: samples prepared for nucleic acid extraction. They were fixed in RNAprotect Cell Reagent (Qiagen, Germantown MD, USA) 1:6 in 1X PBS. Yellow: samples prepared for cell imaging analysis, fixed in NOTOXHisto (EarthSafe Industries, IL USA) 1:2 in 1X PBS. Diagonal stripes: samples to be exposed to 1g in space. Squares: GCs.

Figure 2.

A: Light-microscopy inspection of cell cultures returned from space. Microscope: Leica DM IL Led. Magnification: 10X.

B: Representative case of gel electrophoresis of gDNA from GC and g samples.

C: Statistics for STAR alignment of the eight samples used for whole-transcriptome RNASeq analysis. Plot generated using MultiQC 18.

D: HMEC-1 stained for F-actin (red, phalloidin Atto 550, Sigma-Aldrich, USA) and nuclei (blue, DAPI, Sigma-Aldrich, USA). Confocal laser scanning microscope Nikon C2s, 40X. Scale bar: 20 µm. Yellow arrow: putative stress granules.

D': Analysis of intensity of fluorescent peaks (ImageJ 1.50i software).

E: HMEC-1 stained with beta-catenin Monoclonal Antibody (Thermo Scientific) and DAPI (Sigma-Aldrich, USA). Microscope: Zeiss PALM MicroBeam, 100x objective. Scale bar: 10 µm.

F: To gain quantitative data about cell morphology, cell area and cell-shape descriptors (circularity, roundness and solidity) were calculated with ImageJ 1.50i software as in 19. We analyzed cells stained for beta-catenin. There were not statistically significant changes in cell area between GC and g samples. However, circularity, roundness and solidity were significantly higher in g cells than in GCs. At least 20 cells were analyzed by three independent operators.

Table 1.

Listing of names and use of the different samples prepared for the study and either sent into space and exposed to g or in the centrifuge at 1g, or kept as ground controls (GCs).