

# Epigenomics



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## Specific Aims

**Aim 1.** We will measure DNA methylation and chromatin at a genome-wide level in biological samples obtained from the space traveler at quarterly intervals, pre- and post-flight, and at times of unexpected exposures such as radiation events, or spacecraft environmental contamination. We also obtain measurements of the ground-based twin.

**Aim 2.** We will integrate epigenomic data with exposure to spaceflight conditions, looking for exposure-linked changes, and by comparison to the ground-based twin, determine whether these are transient or long-lived effects. We will also determine whether DNA mutations arise secondarily to these epigenetic changes.

## Sample Collection and Analysis



- Whole genome sequencing prior to launch and post-recovery
- Whole genome bisulfite sequencing at several time points, 450K between
- ChIP-seq at all time points
- RNAseq at several time points, arrays between

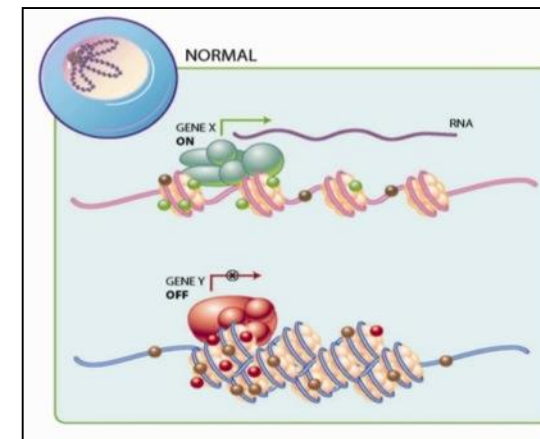
## Implications of the Research for Space & Earth



**Space:** Identify reversible causes of genomic damage in space, e.g. radiation or toxin induced epigenomics change; quantify aging and genomic exposure.



**Earth:** First human study of the epigenome over time in a defined/controlled environment.



- DNA methylation
- Histone modifications (>200 known)
- Chromatin factor complexes
- Chromatin structure