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Supplemental Information

Clonal Hematopoiesis Before, During, and After Human Spaceflight

Nuria Mencia-Trinchant, Matthew J. MacKay, Christopher Chin, Ebrahim Afshinnekoo, Jonathan Foox, Cem Meydan, Daniel Butler, Christopher Mozsary, Nicholas A. Vernice, Charlotte Darby, Michael C. Schatz, Susan M. Bailey, Ari M. Melnick, Monica L. Guzman, Kelly Bolton, Lior Z. Braunstein, Francine Garrett-Bakelman, Ross L. Levine, Duane C. Hassane, and Christopher E. Mason

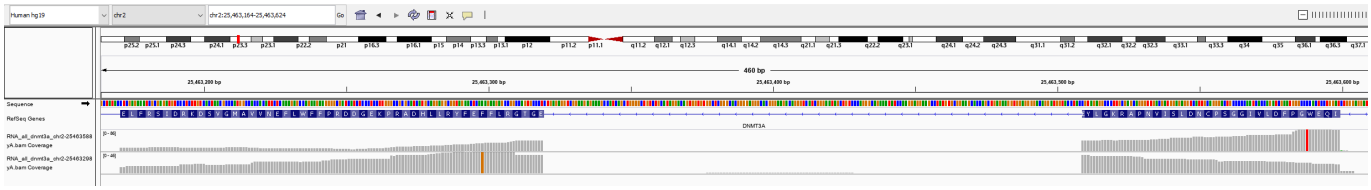

Figure S1. Distinct expression of each mutation DNMT3A allele. Related to Figure 1. RNA-sequencing data was mapped to the DNMT3A locus, and the two mutations found in the CH data from bulk DNA, Trp698Ter and Phe732Ser, were intersected with the variants found in the RNA-seq data. Integrated Genome Viewer (IGV) plots show the chromosomal location (top), the amino acids for each codon (purple), and the coverage for each strand of the RNA-seq libraries (top row, depth=86X, bottom row, depth=46x) on this locus. Variants such as Trp698Ter (orange, left on the bottom track) and Phe732Ser (red, right on the top track) are colored within the grey, wild-type alleles that were mapped from the paired-end 150nt reads.

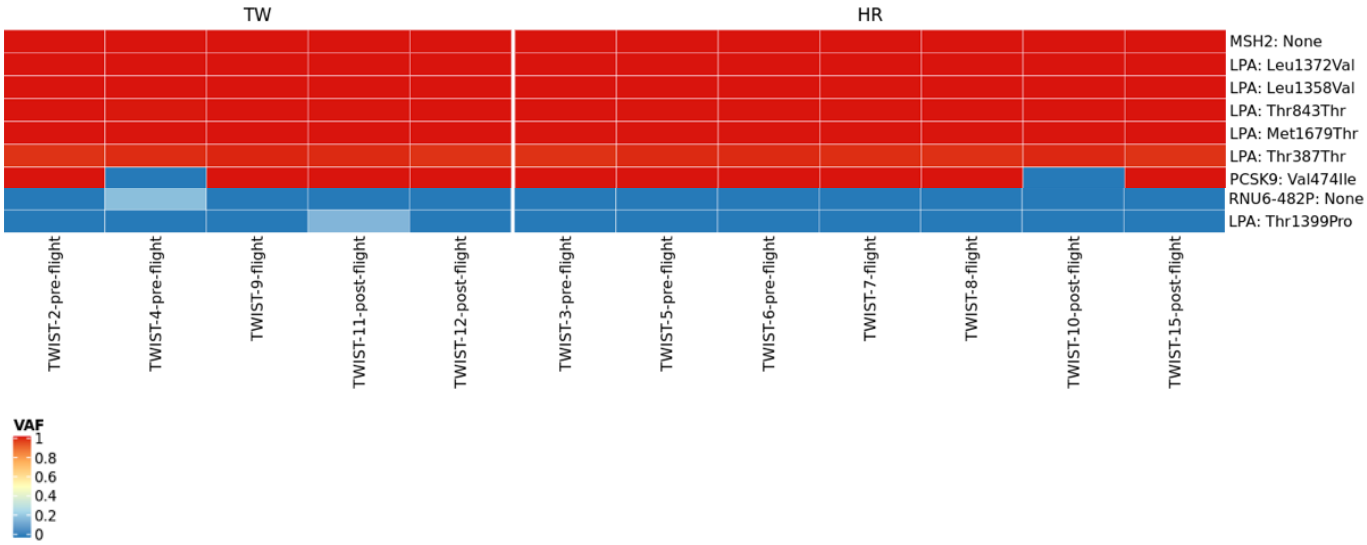

Figure S2. Alternate alleles from the Twist Panel. Related to Figure 2. Other non-reference alleles were usually stable or transient, whereas the robust CH mutations (Figure 1) persisted and were detected at all time points. Variant allele fraction (VAF) is shown from highest (red) to lowest (blue). Cells are sorted CD4+ fractions and sequenced with the Twist capture panel.