Cell Reports, Volume 33

## **Supplemental Information**

## **Clonal Hematopoiesis Before, During,**

## and After Human Spaceflight

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Human hg 19	<ul> <li>dr2</li> <li>dr2:25,463,164-25,463,624</li> </ul>	∞ 🗂 • ► 🕸 🗖 x 📁					
	p252 p25.1 p243 p24.1 p233 p23.1 p222	p21 p163 p161 p15 p14 p133	p131 p12 p112 p11.1 q112 q121 q12.	g q14.1 q14.2 q14.3 q21.1 q21.3	q22.2 q23.1 q24.1 q24.2 q24.3	q31.1 q31.2 q32.1 q32.2 q32.3 q33.1	q333 q34 q35 q361 q363 q37.1
	23,463,200 bp	25.46	00 bp	460 bp	1	25,653,500 bp	23,663,660 bp
Sequence 🔿							
RefSeq Genes	ELFRSIDRKDSYGMAVVNEELWFE	PRDDGEXPRADHLLRYFEF		DIMITIA	····	Y L G K R A P N V I S L	D N C P S G G I V L D F P G W E Q I
RNA_all_dnnt3a_oh/2-25463588 yA.barr Coverage	[2- 6]						
RNA_all_drvnt3a_chrl2-25463298 yA.barn Coverage	1 - 2 - 24						

## 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.