

## Figure List

**Figure 1. Heritable Transcriptional States in Expanded Clonal T cells In Vivo** (In\_Vivo dataset Donors A-C)

**Figure 2. Heritable transcriptional states in expanded clonal T cells in vitro** (P1902 dataset)

**Figure 3. Clonal transcriptional signatures are robust and persists through subclonal diversification** (Large In\_Vitro\_Clones dataset)

**Figure 4. Shared transcriptional identities of progeny from sister clones separated in Vivo** (P3128 dataset)

**Figure 5. Clonally heritable gene expression in the mouse central nervous system** (Mouse Brains dataset)

**Figure 6. Clonal maintenance of parental chromatin accessibility patterns and clone-specific chromatin accessibility** (P9855 dataset)

**Figure 7. Heritable differences in chromatin accessibility underlie clonally variable gene expression .** (P9855 dataset)

## Supplemental Figures

**Figure S1.** Summary of clonal size distribution and differentiation state variability in vivo. Related to Figure 1.

**Figure S2.** Copy number variations are uncommon in clonally expanded lymphocytes. Related to Figure 3.

**Figure S3.** Clonally variable gene expression is mirrored in protein expression levels and correlations between each measurement are strengthened by measuring clonal averages. Related to Figure 3.

**Figure S4.** Dissection strategy, replicates and cell type classification for the mouse brain dataset. Related to Figure 4.

**Figure S5.** Clonally variable genes in cell types of the mouse central nervous system grouped by clone size/number. Related to Figure 5.

**Figure S6.** Description of CRE variability metrics and evidence for common patterns of peak variability across T cell clone datasets. Related to Figures 6 and 7.

**Figure S7.** Linking CRE variability to clonal gene expression variability. Related to Figure 7.

## Table List

**Table S1:** Information on the clonality for all single cell transcriptomes for in vivo data from three YFV-vaccine donors (Donors A, B, C). Clones annotated as cloneID: '-1' are clones which are lacking necessary information to accurately assign them to a specific clone (i.e. have only a TRA chain but that chain is found in more than 1 clone in the dataset).

**Table S2:** p-values for top 10 in vivo clones examining clonal gene expression variability using ANOVA test.

**Table S3:** p-values for 9 in vitro clones (figure 2) using Kruskal-Wallis or ANOVA testing.

**Table S4:** p-values for 3 large in vitro clones (figure 3) comparing ANOVA test results from TPM or UMI values (Smart-seq3 data) for each clonal population.

**Table S5:** p-values for 20 in vitro clones (figure 4) using Kruskal-Wallis or ANOVA testing. Nested ANOVA test on sisters (panel 2).

**Table S6:** protein and gene expression values for clones related to Figure S3.

**Table S7:** Genes with highly significant clonal variation among different mouse central nervous system clonal populations related to Figure 5 and Figure S5.

**Table S8:** Phenotypic Information collected about founder cells related to Figure 6.

**Table S9:** RPV values and statistics relating to ATAC-seq data from Figures 6 and 7.

**Table S10:** ANOVA test and p-values relative to bulk RNA-seq datasets on clones for project ID P9855 in Figure 7.