

TCR data analysis using Immunarch

The data generated from Cell Ranger V(D)J software version 5.0.0 was used for downstream analysis using Immunarch (ImmunoMind Team. (2019). Immunarch is a R package used to analyze T-cell receptor (TCR) and B-cell receptor (BCR) repertoires (ImmunoMind Team. (2019). The 10x Single - cell datasets were obtained from Samir.J et al (2020).

The number of clonotypes and their distribution in pre-flu and post-flu vaccination samples were determined using repExplore() function. The relative abundance of the clonotypes in both conditions were determined using repClonality() function based on the frequency of clonotypes. The diversity between the samples were estimated using repDiversity() function.

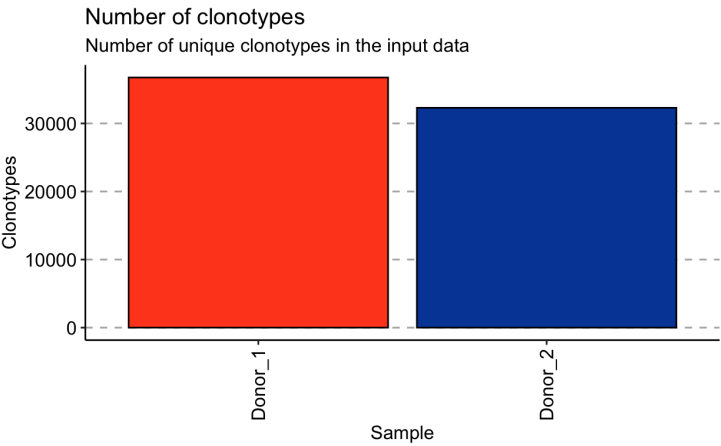
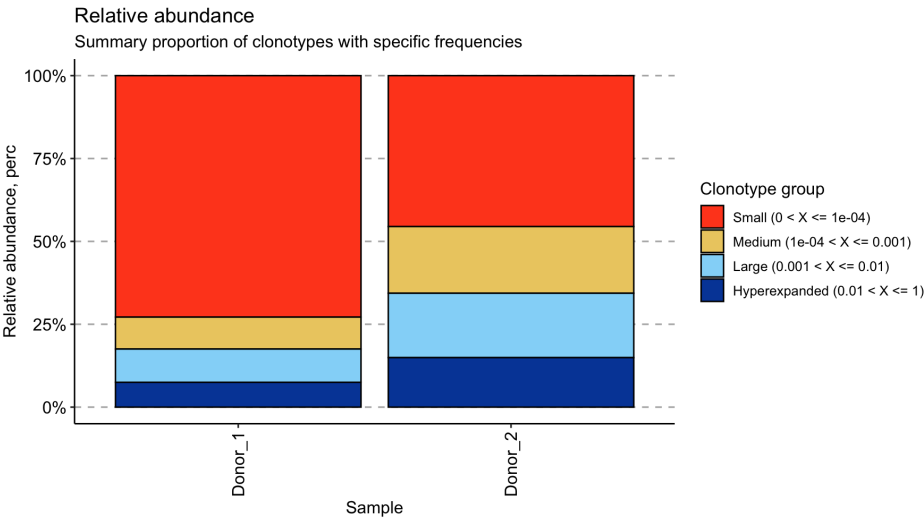


Figure 1. TCR summary statistics in pre-flu and post-flu vaccination samples. Barplot representation of total number of clonotypes per treatment group.

A.



B.

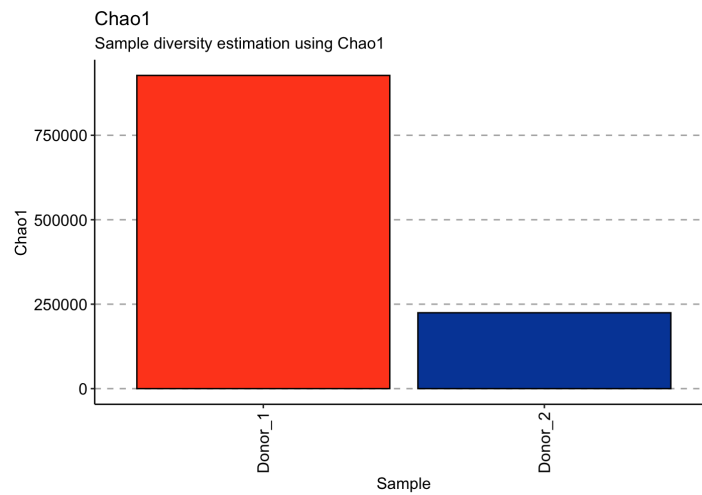


Figure 2. TCR diversity statistics in pre-flu and post-flu vaccination samples. (A) Relative abundance of clonotypes based on their frequencies. (B) Barplot representation of relative abundance metrics.

References:

ImmunoMind Team. (2019). immunarch: An R Package for Painless Bioinformatics Analysis of T-Cell and B-Cell Immune Repertoires. Zenodo. <http://doi.org/10.5281/zenodo.3367200>