

CITE-Seq data analysis was performed on:

R version 4.3.0 (2023-04-21)

Platform: x86_64-pc-linux-gnu (64-bit)

Running under: Ubuntu 20.04.6 LTS

The R packages/software used:

- edgeR (Robinson *et al.*, 2010)
- limma (Ritchie *et al.*, 2015)
- tidyverse (Wickham *et al.*, 2019)
- SingleCellExperiment (Amezquita *et al.*, 2020)
- scran (Lun *et al.*, 2016)
- scater (McCarthy *et al.*, 2017)
- igraph (Csardi & Nepusz, 2006)
- bluster (Lun, 2022)
- aricode (Chiquet *et al.*, 2022)
- Wind (Wu & Wu, 2019)
- ggplot2 (Wickham, 2016)
- pheatmap (Kolde, 2019)
- patchwork (Pedersen, 2022)
- cowplot (Wilke, 2020)
- ggrepel (Slowikowski, 2022)
- ggplotify (Yu, 2021)
- ggpubr (Kassambara, 2022)
- magrittr (Bache & Wickham, 2022)
- scDblFinder (Germain *et al.*, 2021)

The version of all the R packages/software used and *session info* is printed out in the scripts' corresponding *html* files.

All scripts and their *html* and intermediate files are deposited in this public GitHub repository:
https://github.com/AGImkeller/CD33_NK_cells_2022.git