



**Supplementary figure 1: Single cell sorting strategy for haemagglutinin specific B cells and abundance of haemagglutinin specific B cells**

- (A) Example flow sorting gating strategy on B cells. B cells were negatively separated from PBMC using magnetic sorting prior to flow sorting.
- (B) The proportion of haemagglutinin binding B cells (as % of live B cells), is not significantly different between age groups either before, or 6 weeks after TIV immunization. (C-D) The number of haemagglutinin binding B cells per  $10^7$  PBMC analysed by age and days post vaccination.
- (C) The number of haemagglutinin binding B cells is higher in 22-36 year olds at day 42. The number of haemagglutinin binding B cells was calculated as in (C). In (B) and (D), the  $P$  values shown are from an unpaired two-tailed Mann-Whitney test. In (C), samples from the same individual are indicated with a grey line. The  $P$  values shown are from a paired two-tailed Mann-Whitney test.

## SessionInfo

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: CentOS Linux 7 (Core)
##
## Matrix products: default
## BLAS: /bi/apps/R/3.6.1/lib64/R/lib/libRblas.so
## LAPACK: /bi/apps/R/3.6.1/lib64/R/lib/libRlapack.so
##
## locale:
## [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C LC_TIME=C
## [4] LC_COLLATE=C LC_MONETARY=C LC_MESSAGES=C
## [7] LC_PAPER=C LC_NAME=C LC_ADDRESS=C
## [10] LC_TELEPHONE=C LC_MEASUREMENT=C LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats graphics grDevices utils datasets methods base
##
## other attached packages:
## [1] ggpubr_0.2.4 magrittr_1.5 forcats_0.4.0 stringr_1.4.0
## [5] dplyr_1.0.2 purrr_0.3.3 readr_1.3.1 tidyr_1.0.0
## [9] tibble_3.0.4 ggplot2_3.3.2 tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.1.0 xfun_0.11 reshape2_1.4.3 haven_2.2.0
## [5] colorspace_1.4-1 vctrs_0.3.6 generics_0.0.2 htmltools_0.4.0
## [9] yaml_2.2.0 rlang_0.4.10 gridtext_0.1.4 pillar_1.4.7
## [13] glue_1.4.2 withr_2.1.2 DBI_1.1.0 dbplyr_1.4.2
## [17] modelr_0.1.5 readxl_1.3.1 plyr_1.8.5 lifecycle_0.2.0
## [21] munsell_0.5.0 ggsignif_0.6.0 gtable_0.3.0 cellranger_1.1.0
## [25] rvest_0.3.5 evaluate_0.14 labeling_0.3 knitr_1.26
## [29] markdown_1.1 fansi_0.4.0 broom_0.7.3 Rcpp_1.0.3
## [33] scales_1.1.0 backports_1.1.5 jsonlite_1.6 farver_2.0.1
## [37] fs_1.3.1 hms_0.5.2 digest_0.6.23 stringi_1.4.3
## [41] cowplot_1.0.0 grid_3.6.1 cli_2.0.0 tools_3.6.1
## [45] crayon_1.3.4 pkgconfig_2.0.3 ellipsis_0.3.0 xml2_1.2.2
## [49] reprex_0.3.0 lubridate_1.7.4 assertthat_0.2.1 rmarkdown_2.0
## [53] http_1.4.1 rstudioapi_0.10 R6_2.4.1 ggtext_0.1.1
## [57] compiler_3.6.1
```