



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

- (B) Example flow sorting gating strategy on B cells. B cells were negatively separated from PBMC using magnetic sorting prior to flow sorting.
- (C) 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. (D-E) The number of haemagglutinin binding B cells per 10^7 PBMC analysed by age and days post vaccination.
- (D) 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 (C) and (E), the P values shown are from an unpaired two-tailed Mann-Whitney test. In (D), 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_GB.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8      LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8  LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel stats4 stats graphics grDevices utils datasets
## [8] methods base
##
## other attached packages:
##  [1] ggpubr_0.2.4             magrittr_1.5
##  [3] forcats_0.4.0            stringr_1.4.0
##  [5] dplyr_1.0.2              purrr_0.3.3
##  [7] readr_1.3.1              tidyr_1.0.0
##  [9] tibble_3.0.4             ggplot2_3.3.2
## [11] tidyverse_1.3.0          SingleCellExperiment_1.8.0
## [13] MultiAssayExperiment_1.12.1 SummarizedExperiment_1.16.0
## [15] DelayedArray_0.12.0      BiocParallel_1.20.0
## [17] matrixStats_0.55.0       Biobase_2.46.0
## [19] GenomicRanges_1.38.0     GenomeInfoDb_1.22.0
## [21] IRanges_2.20.1           S4Vectors_0.24.1
## [23] BiocGenerics_0.32.0
##
## loaded via a namespace (and not attached):
##  [1] httr_1.4.1               jsonlite_1.6             modelr_0.1.5
##  [4] assertthat_0.2.1         GenomeInfoDbData_1.2.2   cellranger_1.1.0
##  [7] yaml_2.2.0               pillar_1.4.7             backports_1.1.5
## [10] lattice_0.20-38          glue_1.4.2               digest_0.6.29
## [13] gridtext_0.1.4           XVector_0.26.0           ggsignif_0.6.0
## [16] rvest_0.3.5              colorspace_1.4-1         cowplot_1.0.0
## [19] htmltools_0.5.2          Matrix_1.2-17            plyr_1.8.5
## [22] pkgconfig_2.0.3          broom_0.7.3              haven_2.2.0
## [25] zlibbioc_1.32.0          scales_1.1.0             farver_2.0.1
## [28] generics_0.0.2           ellipsis_0.3.0          withr_2.1.2
## [31] cli_2.0.0                crayon_1.3.4             readxl_1.3.1
## [34] ggtext_0.1.1             evaluate_0.14            fs_1.3.1
## [37] fansi_0.4.0              xml2_1.2.2              tools_3.6.1
## [40] hms_0.5.2                lifecycle_0.2.0          munsell_0.5.0
## [43] reprex_0.3.0             compiler_3.6.1           rlang_0.4.10
## [46] grid_3.6.1              RCurl_1.95-4.12         rstudioapi_0.10
## [49] labeling_0.3             bitops_1.0-6            rmarkdown_2.14
```

## [52]	gtable_0.3.0	DBI_1.1.0	markdown_1.1
## [55]	reshape2_1.4.3	R6_2.4.1	lubridate_1.7.4
## [58]	knitr_1.26	fastmap_1.1.0	stringi_1.4.3
## [61]	Rcpp_1.0.3	vctrs_0.3.6	dbplyr_1.4.2
## [64]	tidyselect_1.1.0	xfun_0.31	