Supplementary Figure 8 – Somatic hypermutation is reduced in haemagglutinin specific memory B cells from aged individuals after TIV immunisation

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] scater_1.14.5             ggplot2_3.3.2
##  [5] SingleCellExperiment_1.8.0  stringr_1.4.0
##  [7] readr_1.3.1               MultiAssayExperiment_1.12.1
##  [9] SummarizedExperiment_1.16.0 DelayedArray_0.12.0
## [11] BiocParallel_1.20.0       matrixStats_0.55.0
## [13] Biobase_2.46.0            GenomicRanges_1.38.0
## [15] GenomeInfoDb_1.22.0       IRanges_2.20.1
## [17] S4Vectors_0.24.1          BiocGenerics_0.32.0
## [19] dplyr_1.0.2
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.3              rsvd_1.0.2            lattice_0.20-38
##  [4] digest_0.6.29          R6_2.4.1             plyr_1.8.5
##  [7] evaluate_0.14          pillar_1.4.7        zlibbioc_1.32.0
## [10] rlang_0.4.10           irlba_2.3.3          Matrix_1.2-17
## [13] rmarkdown_2.14         labeling_0.3         BiocNeighbors_1.4.1
## [16] gridtext_0.1.4         RCurl_1.95-4.12      munsell_0.5.0
## [19] compiler_3.6.1         vipor_0.4.5          BiocSingular_1.2.0
## [22] xfun_0.31              pkgconfig_2.0.3      ggbeeswarm_0.6.0
## [25] htmltools_0.5.2        ggtext_0.1.1         tidyselect_1.1.0
## [28] tibble_3.0.4           gridExtra_2.3        GenomeInfoDbData_1.2.2
## [31] viridisLite_0.3.0      crayon_1.3.4         withr_2.1.2
## [34] bitops_1.0-6           grid_3.6.1           gtable_0.3.0
## [37] lifecycle_0.2.0        scales_1.1.0         stringi_1.4.3
## [40] farver_2.0.1           ggsignif_0.6.0       XVector_0.26.0
## [43] reshape2_1.4.3         viridis_0.5.1        xml2_1.2.2
## [46] DelayedMatrixStats_1.8.0 ellipsis_0.3.0      generics_0.0.2
## [49] vctrs_0.3.6            cowplot_1.0.0        tools_3.6.1
## [52] glue_1.4.2             beeswarm_0.2.3       markdown_1.1
## [55] purrr_0.3.3            hms_0.5.2            fastmap_1.1.0
```

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## [58] yaml_2.2.0              colorspace_1.4-1       knitr_1.26
```