



Figure 1 – Single cell sequencing of haemagglutinin specific B cells to study the aged vaccine response

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.utf8      LC_NUMERIC=C
##  [3] LC_TIME=en_GB.utf8      LC_COLLATE=en_GB.utf8
##  [5] LC_MONETARY=en_GB.utf8  LC_MESSAGES=en_GB.utf8
##  [7] LC_PAPER=en_GB.utf8     LC_NAME=C
##  [9] LC_ADDRESS=C            LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.utf8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel stats4 stats graphics grDevices utils datasets
## [8] methods base
##
## other attached packages:
##  [1] forcats_0.4.0          stringr_1.4.0
##  [3] purrr_0.3.3            readr_1.3.1
##  [5] tidyr_1.0.0            tibble_3.0.4
##  [7] tidyverse_1.3.0        org.Hs.eg.db_3.10.0
##  [9] AnnotationDbi_1.48.0   SingleR_1.0.6
## [11] rstatix_0.6.0          ggcyto_1.18.0
## [13] flowWorkspace_3.34.1   ncdfFlow_2.32.0
## [15] BH_1.72.0-2            RcppArmadillo_0.10.1.2.0
## [17] flowCore_1.52.1        scan_1.14.5
## [19] scatter_1.14.5         SingleCellExperiment_1.8.0
## [21] cowplot_1.0.0          pals_1.6
## [23] ggpubr_0.2.4           dplyr_1.0.2
## [25] magrittr_1.5           ggplot2_3.3.2
## [27] MultiAssayExperiment_1.12.1 SummarizedExperiment_1.16.0
## [29] DelayedArray_0.12.0    BiocParallel_1.20.0
## [31] matrixStats_0.55.0     Biobase_2.46.0
## [33] GenomicRanges_1.38.0   GenomeInfoDb_1.22.0
## [35] IRanges_2.20.1         S4Vectors_0.24.1
## [37] BiocGenerics_0.32.0
##
## loaded via a namespace (and not attached):
##  [1] tidyselect_1.1.0        RSQLite_2.1.4
##  [3] grid_3.6.1             munsell_0.5.0
##  [5] statmod_1.4.32         withr_2.1.2
##  [7] colorspace_1.4-1       flowViz_1.48.0
##  [9] knitr_1.26             rstudioapi_0.10
## [11] robustbase_0.93-5      ggsignif_0.6.0
## [13] labeling_0.3           GenomeInfoDbData_1.2.2
## [15] bit64_0.9-7            farver_2.0.1
## [17] vctrs_0.3.6            generics_0.0.2
## [19] xfun_0.31              BiocFileCache_1.10.2
```

## [21]	R6_2.4.1	markdown_1.1
## [23]	ggbeeswarm_0.6.0	rsvd_1.0.2
## [25]	locfit_1.5-9.1	bitops_1.0-6
## [27]	assertthat_0.2.1	promises_1.1.0
## [29]	scales_1.1.0	beeswarm_0.2.3
## [31]	gtable_0.3.0	rlang_0.4.10
## [33]	systemfonts_1.0.4	dichromat_2.0-0
## [35]	hexbin_1.28.0	broom_0.7.3
## [37]	BiocManager_1.30.10	yaml_2.2.0
## [39]	reshape2_1.4.3	abind_1.4-5
## [41]	modelr_0.1.5	backports_1.1.5
## [43]	httpuv_1.5.2	IDPmisc_1.1.20
## [45]	gridtext_0.1.4	tools_3.6.1
## [47]	ellipsis_0.3.0	RColorBrewer_1.1-2
## [49]	Rcpp_1.0.3	plyr_1.8.5
## [51]	zlibbioc_1.32.0	RCurl_1.95-4.12
## [53]	viridis_0.5.1	haven_2.2.0
## [55]	cluster_2.1.0	fs_1.3.1
## [57]	tinytex_0.40	data.table_1.12.8
## [59]	openxlsx_4.1.4	reprex_0.3.0
## [61]	mvtnorm_1.0-11	hms_0.5.2
## [63]	mime_0.7	evaluate_0.14
## [65]	xtable_1.8-4	rio_0.5.16
## [67]	readxl_1.3.1	gridExtra_2.3
## [69]	compiler_3.6.1	maps_3.3.0
## [71]	KernSmooth_2.23-15	crayon_1.3.4
## [73]	htmltools_0.5.2	pcaPP_1.9-73
## [75]	later_1.0.0	ggtext_0.1.1
## [77]	rrcov_1.4-9	RcppParallel_4.4.4
## [79]	lubridate_1.7.4	DBI_1.1.0
## [81]	ExperimentHub_1.12.0	dbplyr_1.4.2
## [83]	MASS_7.3-51.4	rappdirs_0.3.1
## [85]	Matrix_1.2-17	car_3.0-5
## [87]	cli_2.0.0	igraph_1.2.4.2
## [89]	pkgconfig_2.0.3	foreign_0.8-72
## [91]	xml2_1.2.2	svglite_2.1.0
## [93]	vipor_0.4.5	dqrng_0.2.1
## [95]	XVector_0.26.0	rvest_0.3.5
## [97]	digest_0.6.29	graph_1.64.0
## [99]	rmarkdown_2.14	cellranger_1.1.0
## [101]	edgeR_3.28.0	DelayedMatrixStats_1.8.0
## [103]	curl_4.3	shiny_1.4.0
## [105]	lifecycle_0.2.0	jsonlite_1.6
## [107]	carData_3.0-3	BiocNeighbors_1.4.1
## [109]	mapproj_1.2.7	viridisLite_0.3.0
## [111]	limma_3.42.0	fansi_0.4.0
## [113]	pillar_1.4.7	lattice_0.20-38
## [115]	fastmap_1.1.0	httr_1.4.1
## [117]	DEoptimR_1.0-8	interactiveDisplayBase_1.24.0
## [119]	glue_1.4.2	zip_2.0.4
## [121]	BiocVersion_3.10.1	bit_1.1-14
## [123]	Rgraphviz_2.30.0	stringi_1.4.3
## [125]	blob_1.2.0	BiocSingular_1.2.0
## [127]	AnnotationHub_2.18.0	latticeExtra_0.6-28

[129] memoise_1.1.0

irlba_2.3.3