



Supplementary Figure 6 – Differences in heavy chain V segment usage, including broadly neutralizing *IGHV1-69*, in aged individuals after TIV immunization

- (A) V segment family usage in the immunoglobulin heavy chain at day 0 for younger and older individuals. $P=0.048$, by Fisher's test.
- (B) V segment family usage by HA-specific immunoglobulin heavy chains at day 0 for younger and older individuals expressed as the proportion of the cells separated by each UMAP cluster.
- (C) V allele usage in the immunoglobulin heavy chain at day 0 for younger and older individuals. $P=0.017$, by Fisher's 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] pheatmap_1.0.12             readr_1.3.1
## [3] MultiAssayExperiment_1.12.1 stringr_1.4.0
## [5] ggmsa_0.0.4                 ggpubr_0.2.4
## [7] magrittr_1.5                scater_1.14.5
## [9] ggplot2_3.3.2               dplyr_1.0.2
## [11] plyr_1.8.5                  SingleCellExperiment_1.8.0
## [13] SummarizedExperiment_1.16.0 DelayedArray_0.12.0
## [15] BiocParallel_1.20.0         matrixStats_0.55.0
## [17] Biobase_2.46.0              GenomicRanges_1.38.0
## [19] GenomeInfoDb_1.22.0         IRanges_2.20.1
## [21] S4Vectors_0.24.1           BiocGenerics_0.32.0
##
## loaded via a namespace (and not attached):
## [1] viridis_0.5.1               BiocSingular_1.2.0         tidyr_1.0.0
## [4] viridisLite_0.3.0           DelayedMatrixStats_1.8.0   GenomeInfoDbData_1.2.2
## [7] vipor_0.4.5                 yaml_2.2.0                 pillar_1.4.7
## [10] lattice_0.20-38             glue_1.4.2                 digest_0.6.29
## [13] RColorBrewer_1.1-2          ggsignif_0.6.0             XVector_0.26.0
## [16] gridtext_0.1.4              colorspace_1.4-1           cowplot_1.0.0
## [19] htmltools_0.5.2             Matrix_1.2-17              pkgconfig_2.0.3
## [22] zlibbioc_1.32.0             purrr_0.3.3                scales_1.1.0
## [25] tibble_3.0.4                generics_0.0.2             farver_2.0.1
## [28] ellipsis_0.3.0              withr_2.1.2                crayon_1.3.4
## [31] ggtext_0.1.1                evaluate_0.14              xml2_1.2.2
## [34] beeswarm_0.2.3              tools_3.6.1                hms_0.5.2
## [37] lifecycle_0.2.0            munsell_0.5.0             irlba_2.3.3
## [40] Biostings_2.54.0            compiler_3.6.1            rsvd_1.0.2
## [43] rlang_0.4.10                grid_3.6.1                 RCurl_1.95-4.12
## [46] BiocNeighbors_1.4.1         bitops_1.0-6               labeling_0.3
## [49] rmarkdown_2.14              gtable_0.3.0              markdown_1.1
## [52] reshape2_1.4.3             R6_2.4.1                   gridExtra_2.3
```

## [55]	knitr_1.26	fastmap_1.1.0	stringi_1.4.3
## [58]	ggbeeswarm_0.6.0	Rcpp_1.0.3	vctrs_0.3.6
## [61]	tidyselect_1.1.0	xfun_0.31	