



Figure 5 - Germinal center emigrant memory B cells are FCRL5⁺

- (A) UMAP of B cells (n=27265 cells) from fine needle aspirates (FNAs) of draining axillary lymph nodes from a single healthy volunteer on days 0, 5, 12, 28 and 60 after quadrivalent influenza vaccine (QIV), as reported by Turner *et al.*.
- (B) The B cell receptors detected in germinal center (GC) B cells on day 12 after QIV immunization are shared with earlier LN B cells, and are detectable in peripheral blood mononuclear cells (PBMC) that have been enriched for B cell memory (IgD-) at days 28 and 60 post-vaccine. Sharing of a B cell receptor (BCR) requires: i. identical IGHV and IGHJ usage ii. identical heavy chain CDR3 length iii. identical IGLV and IGLJ usage and iv. identical light chain CDR3 length.
- (C) UMAP of circulating B cells (n=21568 cells) from IgD- enriched PBMCs at days 0, 5, 12, 28 and 60 after QIV. Clusters identified by Louvain clustering, and annotated based on (D).
- (D) Dotplot showing the expression of key genes, defined from the HA-specific B cell sequencing (Figure 2B), used to annotate the clusters identified in (C).
- (E) UMAP of circulating QIV-specific B cells from IgD- enriched PBMCs at day 28 which share a germinal center BCR, n=38 cells.
- (F) The percentage of QIV-specific B cells, present in the circulation at day 28, as in (E) is shown for each B cell cluster.

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:
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## [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] grid      parallel  stats4     stats      graphics  grDevices  utils
## [8] datasets  methods    base
##
## other attached packages:
## [1] pheatmap_1.0.12             ggmsa_0.0.4
## [3] plyr_1.8.5                  destiny_3.0.1
## [5] Seurat_3.2.2                edgeR_3.28.0
## [7] limma_3.42.0                gtable_0.3.0
## [9] forcats_0.4.0               stringr_1.4.0
## [11] purrr_0.3.3                 readr_1.3.1
## [13] tidyr_1.0.0                 tibble_3.0.4
## [15] tidyverse_1.3.0             org.Hs.eg.db_3.10.0
## [17] AnnotationDbi_1.48.0        SingleR_1.0.6
## [19] rstatix_0.6.0               ggcyto_1.18.0
## [21] flowWorkspace_3.34.1        ncdfFlow_2.32.0
## [23] BH_1.72.0-2                 RcppArmadillo_0.10.1.2.0
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## [27] scatter_1.14.5              SingleCellExperiment_1.8.0
## [29] cowplot_1.0.0               pals_1.6
## [31] ggpubr_0.2.4                dplyr_1.0.2
## [33] magrittr_1.5                ggplot2_3.3.2
## [35] MultiAssayExperiment_1.12.1 SummarizedExperiment_1.16.0
## [37] DelayedArray_0.12.0         BiocParallel_1.20.0
## [39] matrixStats_0.55.0         Biobase_2.46.0
## [41] GenomicRanges_1.38.0       GenomeInfoDb_1.22.0
## [43] IRanges_2.20.1             S4Vectors_0.24.1
## [45] BiocGenerics_0.32.0
##
## loaded via a namespace (and not attached):
## [1] rsvd_1.0.2                  vcd_1.4-4
## [3] ica_1.0-2                   class_7.3-15
## [5] flowViz_1.48.0              lmtest_0.9-37
## [7] crayon_1.3.4                laeken_0.5.0
## [9] MASS_7.3-51.4               nlme_3.1-141
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