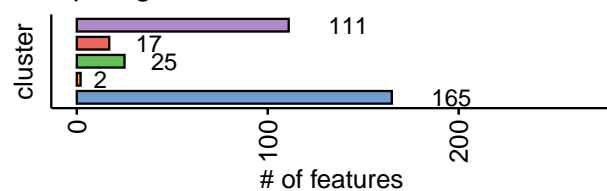
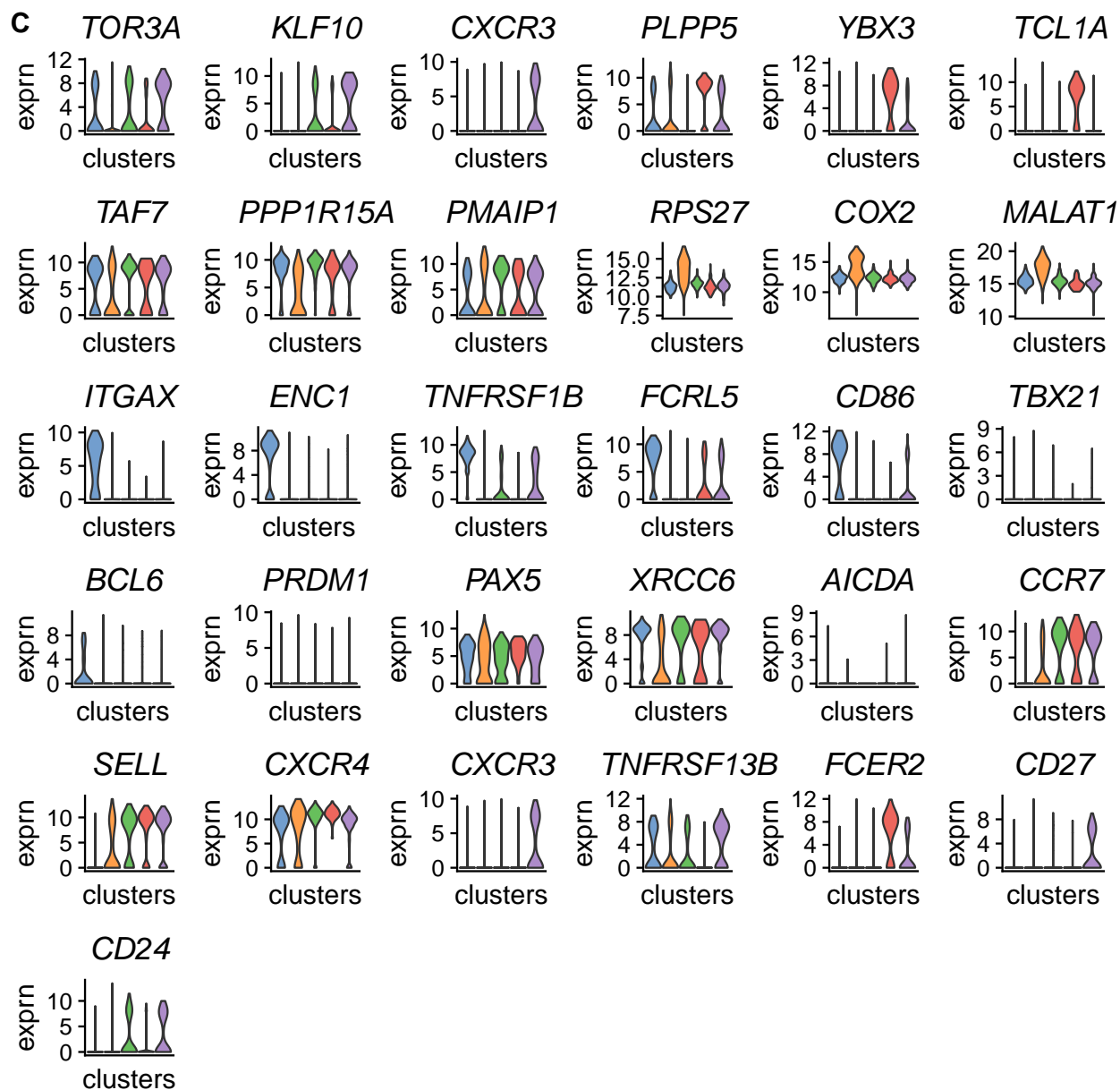
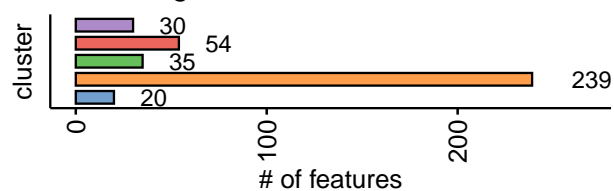


A Up-regulated



B Down-regulated



Supplementary Figure 3: Transcriptional heterogeneity of haemagglutinin specific B cells

- (A) Up-regulated differentially expressed transcripts between a cluster and *any* other cluster, where log2 fold change >2 and Benjamini-Hochberg FDR <0.01 , using pairwise t-tests. For each cluster the numbers of markers is indicated.
- (B) As in (A), for down-regulated markers.
- (C) Violin plots of gene expression of the indicated gene for each of the 5 UMAP clusters. Expression (log-transformed normalized expression) values are plotted. Colors of each UMAP cluster are the same as in (A), (B) and the main figures.

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] 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
## [25] flowCore_1.52.1 scran_1.14.5
## [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
## [11] backports_1.1.5 reprex_0.3.0
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## [17]	irlba_2.3.3	smoother_1.1
## [19]	bit64_0.9-7	glue_1.4.2
## [21]	sctransform_0.3.2.9000	vipor_0.4.5
## [23]	UpSetR_1.4.0	haven_2.2.0
## [25]	tidyselect_1.1.0	rio_0.5.16
## [27]	fitdistrplus_1.1-1	zoo_1.8-8
## [29]	xtable_1.8-4	RcppHNSW_0.2.0
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## [33]	zlibbioc_1.32.0	rstudioapi_0.10
## [35]	miniUI_0.1.1.1	sp_1.3-2
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