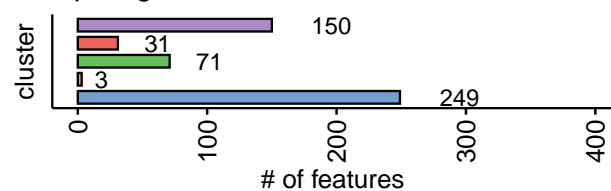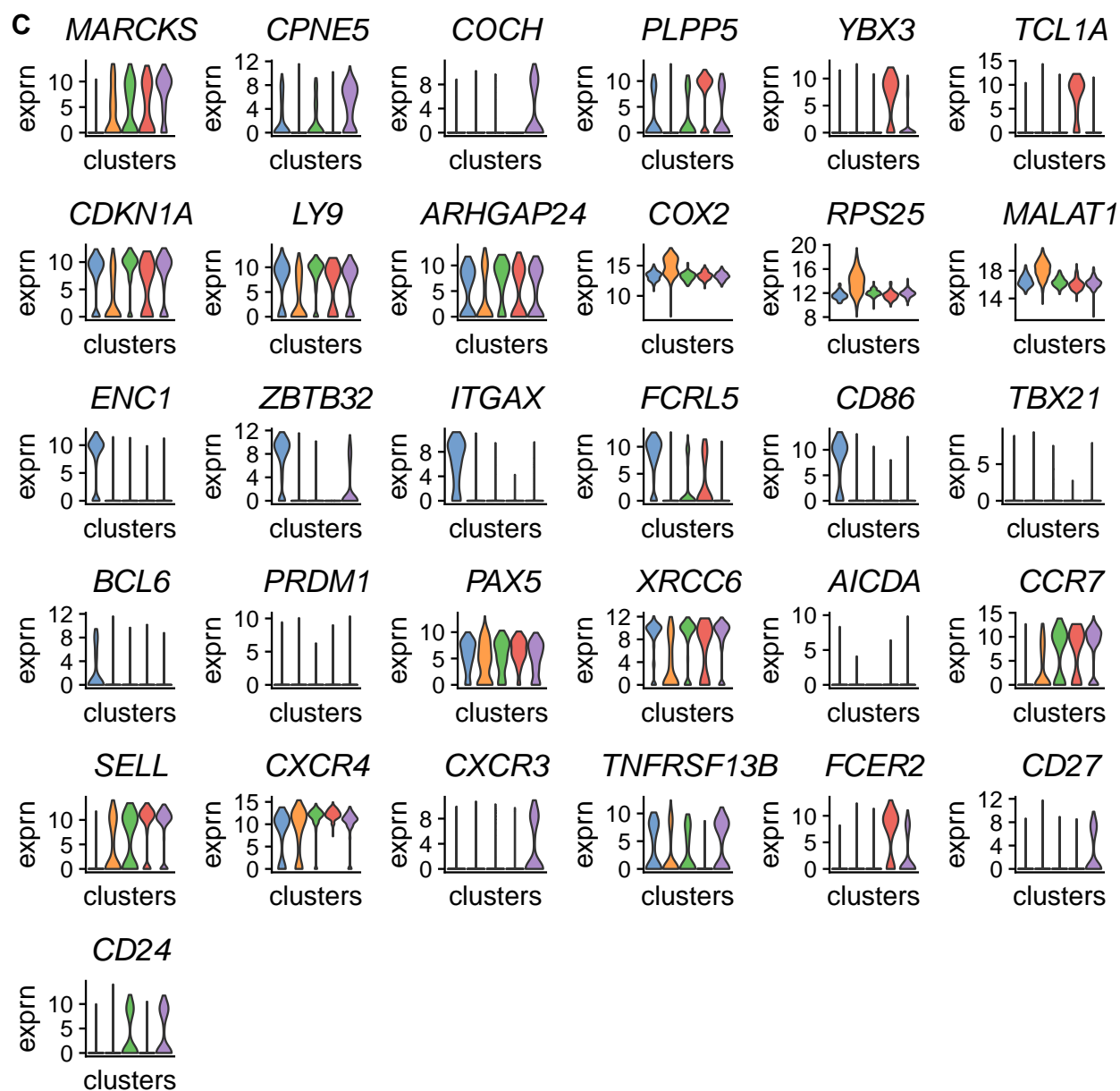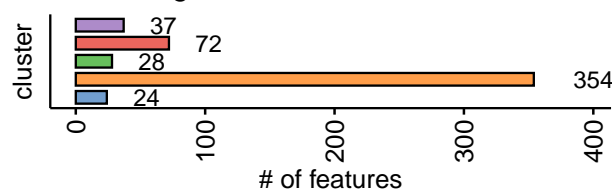**A** Up−regulated

B Down−regulated

C

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 fo 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_US.UTF-8 LC_NUMERIC=C         LC_TIME=C
##  [4] LC_COLLATE=C         LC_MONETARY=C        LC_MESSAGES=C
##  [7] LC_PAPER=C           LC_NAME=C            LC_ADDRESS=C
## [10] LC_TELEPHONE=C       LC_MEASUREMENT=C     LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel  stats4    stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] Seurat_3.2.2              org.Hs.eg.db_3.10.0
##  [3] AnnotationDbi_1.48.0      ggpubr_0.2.4
##  [5] MultiAssayExperiment_1.12.1 magrittr_1.5
##  [7] scran_1.14.5             scater_1.14.5
##  [9] ggplot2_3.3.2            SingleCellExperiment_1.8.0
## [11] SummarizedExperiment_1.16.0 DelayedArray_0.12.0
## [13] BiocParallel_1.20.0      matrixStats_0.55.0
## [15] Biobase_2.46.0           GenomicRanges_1.38.0
## [17] GenomeInfoDb_1.22.0      IRanges_2.20.1
## [19] S4Vectors_0.24.1         BiocGenerics_0.32.0
##
## loaded via a namespace (and not attached):
##   [1] plyr_1.8.5            igraph_1.2.4.2        lazyeval_0.2.2
##   [4] splines_3.6.1         listenv_0.8.0         digest_0.6.23
##   [7] htmltools_0.4.0       viridis_0.5.1         gdata_2.18.0
##  [10] memoise_1.1.0         tensor_1.5            cluster_2.1.0
##  [13] ROCR_1.0-7            limma_3.42.0          globals_0.13.1
##  [16] RcppParallel_4.4.4    colorspace_1.4-1      blob_1.2.0
##  [19] ggrepel_0.8.1         xfun_0.11             dplyr_1.0.2
##  [22] crayon_1.3.4          RCurl_1.95-4.12       jsonlite_1.6
##  [25] spatstat_1.64-1       spatstat.data_1.4-3   survival_2.44-1.1
##  [28] zoo_1.8-8             glue_1.4.2            polyclip_1.10-0
##  [31] gtable_0.3.0          zlibbioc_1.32.0       XVector_0.26.0
##  [34] leiden_0.3.4          BiocSingular_1.2.0    future.apply_1.6.0
##  [37] abind_1.4-5           scales_1.1.0          DBI_1.1.0
##  [40] edgeR_3.28.0          miniUI_0.1.1.1        Rcpp_1.0.3
##  [43] viridisLite_0.3.0     xtable_1.8-4          reticulate_1.14
##  [46] dqrng_0.2.1           bit_1.1-14            rsvd_1.0.2
##  [49] htmlwidgets_1.5.1     httr_1.4.1            gplots_3.0.1.1
##  [52] RColorBrewer_1.1-2    ellipsis_0.3.0        ica_1.0-2
##  [55] farver_2.0.1          pkgconfig_2.0.3       uwot_0.1.5
##  [58] deldir_0.1-23         locfit_1.5-9.1        labeling_0.3
##  [61] tidyselect_1.1.0      rlang_0.4.10          reshape2_1.4.3
```

```
##  [64] later_1.0.0               munsell_0.5.0              tools_3.6.1
##  [67] generics_0.0.2            RSQLite_2.1.4              ggridges_0.5.2
##  [70] evaluate_0.14             stringr_1.4.0             fastmap_1.0.1
##  [73] goftest_1.2-2             yaml_2.2.0                knitr_1.26
##  [76] bit64_0.9-7               fitdistrplus_1.1-1        caTools_1.17.1.3
##  [79] purrr_0.3.3               RANN_2.6.1                nlme_3.1-141
##  [82] pbapply_1.4-2             future_1.20.1            mime_0.7
##  [85] compiler_3.6.1            beeswarm_0.2.3            plotly_4.9.1
##  [88] png_0.1-7                 ggsignif_0.6.0            spatstat.utils_1.17-0
##  [91] tibble_3.0.4              statmod_1.4.32            stringi_1.4.3
##  [94] lattice_0.20-38           Matrix_1.2-17             vctrs_0.3.6
##  [97] pillar_1.4.7              lifecycle_0.2.0           lmtest_0.9-37
## [100] RcppAnnoy_0.0.14          BiocNeighbors_1.4.1       data.table_1.12.8
## [103] cowplot_1.0.0             bitops_1.0-6              irlba_2.3.3
## [106] httpuv_1.5.2              patchwork_1.0.0           R6_2.4.1
## [109] promises_1.1.0            KernSmooth_2.23-15        gridExtra_2.3
## [112] vipor_0.4.5               parallelly_1.21.0         codetools_0.2-16
## [115] MASS_7.3-51.4             gtools_3.8.1              withr_2.1.2
## [118] sctransform_0.3.2.9000    GenomeInfoDbData_1.2.2    mgcv_1.8-28
## [121] rpart_4.1-15              grid_3.6.1                tidyr_1.0.0
## [124] rmarkdown_2.0             DelayedMatrixStats_1.8.0  Rtsne_0.15
## [127] shiny_1.4.0               ggbeeswarm_0.6.0
```