Cluster_DEG

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Contents

1. Read the merged Data

```
##
##                                22q_Astrocyte
##                                        3987
##            22q_Deep layer excitatory neurons
##                                         966
##                      22q_Excitatory neurons
##                                        1121
##  22q_Immature preoptic area (pOA) interneurons
##                                         675
##                             22q_Interneuron
##                                         188
##                        22q_Oligodendrocytes
##                                        1502
##               22q_Outer radial glia cells
##                                         912
##      22q_Proliferating neural progenitor cells
##                                        1639
##                               22q_Unknown
##                                        1973
##           22q_Upper layer excitatory neurons
##                                        4560
##                             CTRL_Astrocyte
##                                        2022
##           CTRL_Deep layer excitatory neurons
##                                        1914
##                     CTRL_Excitatory neurons
##                                        3505
## CTRL_Immature preoptic area (pOA) interneurons
##                                         255
##                            CTRL_Interneuron
##                                        1375
##                       CTRL_Oligodendrocytes
##                                         300
##              CTRL_Outer radial glia cells
##                                        2936
##     CTRL_Proliferating neural progenitor cells
##                                        2284
##                              CTRL_Unknown
##                                        1603
##          CTRL_Upper layer excitatory neurons
##                                        1048

## [1] Astrocyte
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons

## [1] Interneuron
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Proliferating neural progenitor cells
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Outer radial glia cells
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Upper layer excitatory neurons
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
```

```
## [1] Immature preoptic area (pOA) interneurons
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Excitatory neurons
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Unknown
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Oligodendrocytes
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Deep layer excitatory neurons
## 10 Levels: Upper layer excitatory neurons ... Immature preoptic area (pOA) interneurons
```
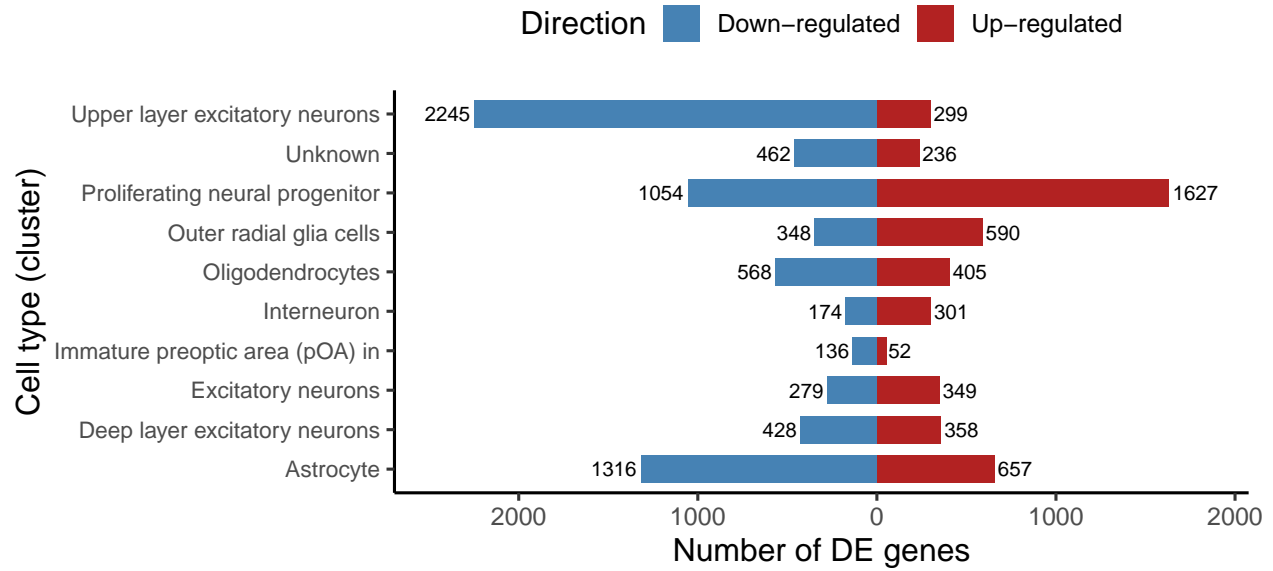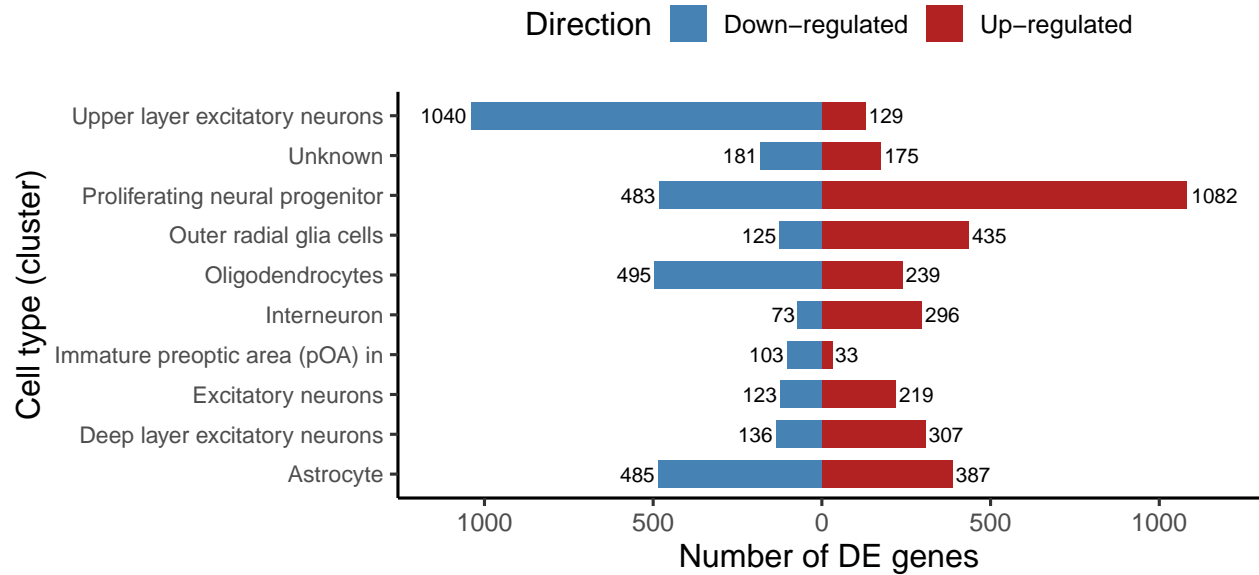

DEG counts (|logFC| > 0.1)

DEG counts (|logFC| > 0.25)

DEG counts (|logFC| > 0.5)
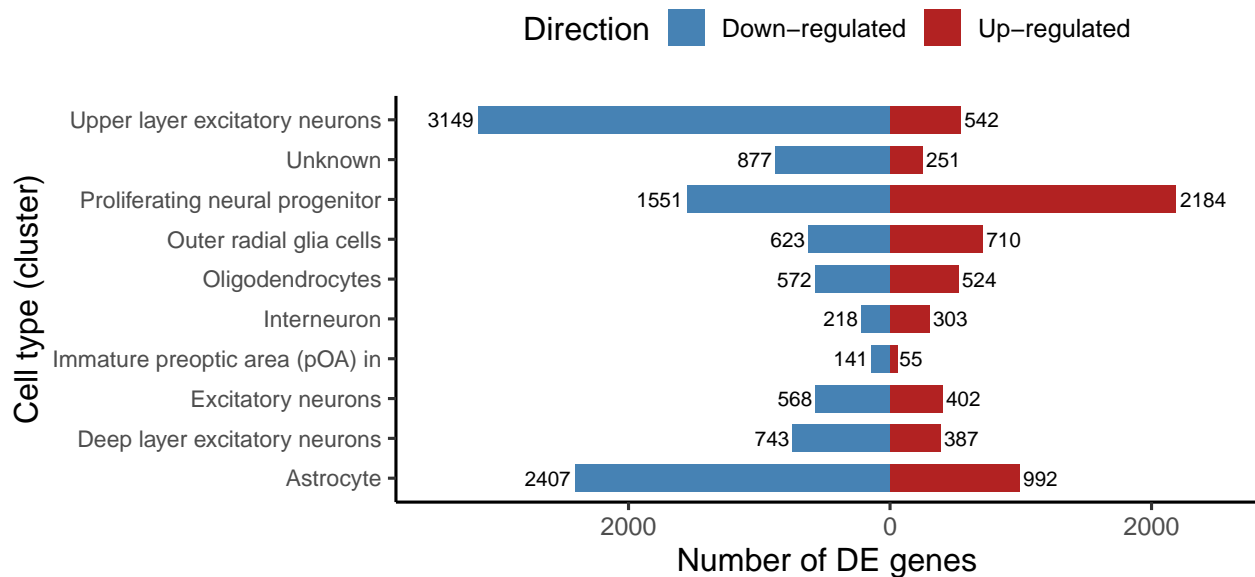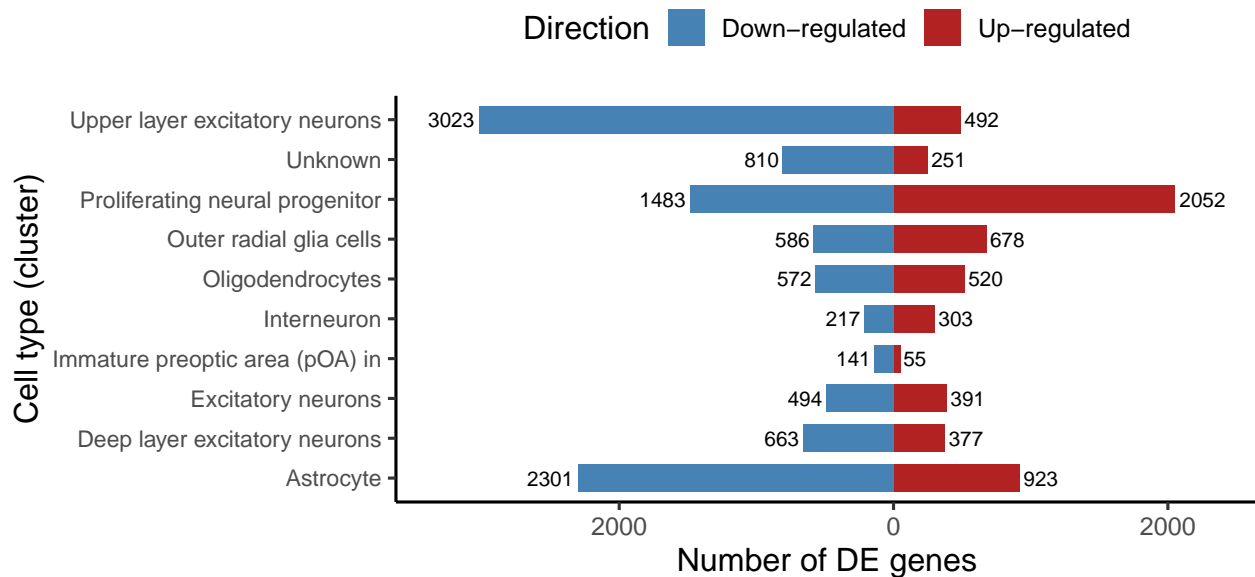
DEG counts (|logFC| > 1)

Session Information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.5
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib;  LAPACK ve
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] kableExtra_1.4.0        patchwork_1.3.0
##  [3] pheatmap_1.0.12         data.table_1.17.2
##  [5] harmony_1.2.3           Rcpp_1.0.14
##  [7] conflicted_1.2.0        openxlsx_4.2.8
##  [9] Seurat_5.3.0            SeuratObject_5.1.0
## [11] sp_2.2-0                AnnotationHub_3.12.0
## [13] BiocFileCache_2.12.0    dbplyr_2.5.0
## [15] simspec_0.0.0.9000      cowplot_1.1.3
## [17] EnsDb.Hsapiens.v86_2.99.0 ensembldb_2.28.1
## [19] AnnotationFilter_1.28.0 GenomicFeatures_1.56.0
## [21] AnnotationDbi_1.66.0    Biobase_2.64.0
## [23] Signac_1.14.0           rtracklayer_1.64.0
## [25] GenomicRanges_1.56.2    GenomeInfoDb_1.40.1
## [27] IRanges_2.38.1          S4Vectors_0.42.1
## [29] BiocGenerics_0.50.0     knitr_1.50
## [31] lubridate_1.9.4         forcats_1.0.0
## [33] stringr_1.5.1           dplyr_1.1.4
## [35] purrr_1.0.4             readr_2.1.5
## [37] tidyr_1.3.1             tibble_3.2.1
## [39] ggplot2_3.5.2           tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##   [1] RcppAnnoy_0.0.22        splines_4.4.0
##   [3] later_1.4.2             BiocIO_1.14.0
##   [5] bitops_1.0-9            filelock_1.0.3
##   [7] polyclip_1.10-7         XML_3.99-0.18
##   [9] fastDummies_1.7.5       lifecycle_1.0.4
##  [11] rprojroot_2.0.4         globals_0.18.0
##  [13] lattice_0.22-7          MASS_7.3-65
##  [15] magrittr_2.0.3          limma_3.60.6
##  [17] plotly_4.10.4           rmarkdown_2.29
##  [19] yaml_2.3.10             httpuv_1.6.16
##  [21] sctransform_0.4.2       zip_2.3.2
```

```
##  [23] spam_2.11-1                  spatstat.sparse_3.1-0
##  [25] reticulate_1.42.0            pbapply_1.7-2
##  [27] DBI_1.2.3                    RColorBrewer_1.1-3
##  [29] abind_1.4-8                  zlibbioc_1.50.0
##  [31] Rtsne_0.17                   presto_1.0.0
##  [33] RCurl_1.98-1.17              rappdirs_0.3.3
##  [35] GenomeInfoDbData_1.2.12      ggrepel_0.9.6
##  [37] irlba_2.3.5.1                spatstat.utils_3.1-3
##  [39] listenv_0.9.1                goftest_1.2-3
##  [41] RSpectra_0.16-2              spatstat.random_3.3-3
##  [43] fitdistrplus_1.2-2           parallelly_1.44.0
##  [45] svglite_2.2.1                codetools_0.2-20
##  [47] DelayedArray_0.30.1          RcppRoll_0.3.1
##  [49] xml2_1.3.8                   tidyselect_1.2.1
##  [51] UCSC.utils_1.0.0             farver_2.1.2
##  [53] spatstat.explore_3.4-2       matrixStats_1.5.0
##  [55] GenomicAlignments_1.40.0     jsonlite_2.0.0
##  [57] progressr_0.15.1             ggridges_0.5.6
##  [59] survival_3.8-3               systemfonts_1.2.3
##  [61] tools_4.4.0                  ragg_1.4.0
##  [63] ica_1.0-3                    glue_1.8.0
##  [65] gridExtra_2.3                SparseArray_1.4.8
##  [67] here_1.0.1                   xfun_0.52
##  [69] MatrixGenerics_1.16.0        withr_3.0.2
##  [71] BiocManager_1.30.25          fastmap_1.2.0
##  [73] digest_0.6.37                timechange_0.3.0
##  [75] R6_2.6.1                     mime_0.13
##  [77] textshaping_1.0.1            colorspace_2.1-1
##  [79] scattermore_1.2              tensor_1.5
##  [81] spatstat.data_3.1-6          dichromat_2.0-0.1
##  [83] RSQLite_2.3.11               generics_0.1.4
##  [85] httr_1.4.7                   htmlwidgets_1.6.4
##  [87] S4Arrays_1.4.1               uwot_0.2.3
##  [89] pkgconfig_2.0.3              gtable_0.3.6
##  [91] blob_1.2.4                   lmtest_0.9-40
##  [93] XVector_0.44.0               htmltools_0.5.8.1
##  [95] dotCall64_1.2                ProtGenerics_1.36.0
##  [97] scales_1.4.0                 png_0.1-8
##  [99] spatstat.univar_3.1-3        rstudioapi_0.17.1
## [101] tzdb_0.5.0                   reshape2_1.4.4
## [103] rjson_0.2.23                 nlme_3.1-168
## [105] curl_6.2.2                   cachem_1.1.0
## [107] zoo_1.8-14                   BiocVersion_3.19.1
## [109] KernSmooth_2.23-26           parallel_4.4.0
## [111] miniUI_0.1.2                 restfulr_0.0.15
## [113] pillar_1.10.2                grid_4.4.0
## [115] vctrs_0.6.5                  RANN_2.6.2
## [117] promises_1.3.2               xtable_1.8-4
## [119] cluster_2.1.8.1              evaluate_1.0.3
## [121] tinytex_0.57                 cli_3.6.5
## [123] compiler_4.4.0               Rsamtools_2.20.0
## [125] rlang_1.1.6                  crayon_1.5.3
## [127] future.apply_1.11.3          labeling_0.4.3
## [129] plyr_1.8.9                   stringi_1.8.7
```

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## [131] deldir_2.0-4               viridisLite_0.4.2
## [133] BiocParallel_1.38.0        Biostrings_2.72.1
## [135] lazyeval_0.2.2             spatstat.geom_3.3-6
## [137] Matrix_1.7-3               RcppHNSW_0.6.0
## [139] hms_1.1.3                  bit64_4.6.0-1
## [141] future_1.49.0              statmod_1.5.0
## [143] KEGGREST_1.44.1            shiny_1.10.0
## [145] SummarizedExperiment_1.34.0 ROCR_1.0-11
## [147] igraph_2.1.4               memoise_2.0.1
## [149] fastmatch_1.1-6            bit_4.6.0
```