

Supplementary file 5: Classification of central nervous system tumors

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Capper et. al., 2018 (<https://www.nature.com/articles/nature26000>) studied subtype classification of central nervous system tumors from DNA methylation data. In their dataset, there are 14 different tumor types (include controls) which are classified into 91 subtypes inferred from 2801 samples.

```
library(spiralize)
library(ComplexHeatmap)
df = readRDS(system.file("extdata", "CNS_tumour_classification.rds", package = "spiralyze"))
n = nrow(df)
spiral_rle = function(x, col, labels = FALSE) {
  x = as.vector(x) # in case it is a factor
  r1 = rle(x)
  for(i in seq_along(r1$lengths)) {
    spiral_rect(sum(r1$lengths[seq_len(i-1)]), 0, sum(r1$lengths[seq_len(i)]), 1, gp = gpar(fill = col[r1$values[i]], col = NA))
  }

  if(labels) {
    for(i in seq_along(r1$lengths)) {
      spiral_text( (sum(r1$lengths[seq_len(i-1)]) + sum(r1$lengths[seq_len(i)]))/2, 0.5, r1$values[i],
        facing = "curved_inside", nice_facing = TRUE)
    }
  }
}

spiral_initialize(xlim = c(0, n), scale_by = "curve_length",
  vp_param = list(x = unit(0, "npc"), just = "left"))
spiral_track(height = 0.4)
meth_col = structure(names = unique(df$meth_class), unique(df$meth_col))
spiral_rle(df$meth_class, col = meth_col)

spiral_track(height = 0.4)
tumor_col = structure(names = unique(as.vector(df$tumor_type)), unique(df$tumor_col))
spiral_rle(df$tumor_type, col = tumor_col, labels = TRUE)

lgd_list = tapply(1:nrow(df), df$tumor_type, function(ind) {
  Legend(title = df$tumor_type[ind][1], at = unique(df$meth_class[ind]),
    legend_gp = gpar(fill = unique(df$meth_col[ind])))
})

# here set max_height to the height of the image so that the legends are automatically arranged
lgd = packLegend(list = lgd_list, max_height = unit(7, "inch"))
draw(lgd, x = unit(1, "npc") + unit(2, "mm"), just = "left")
```

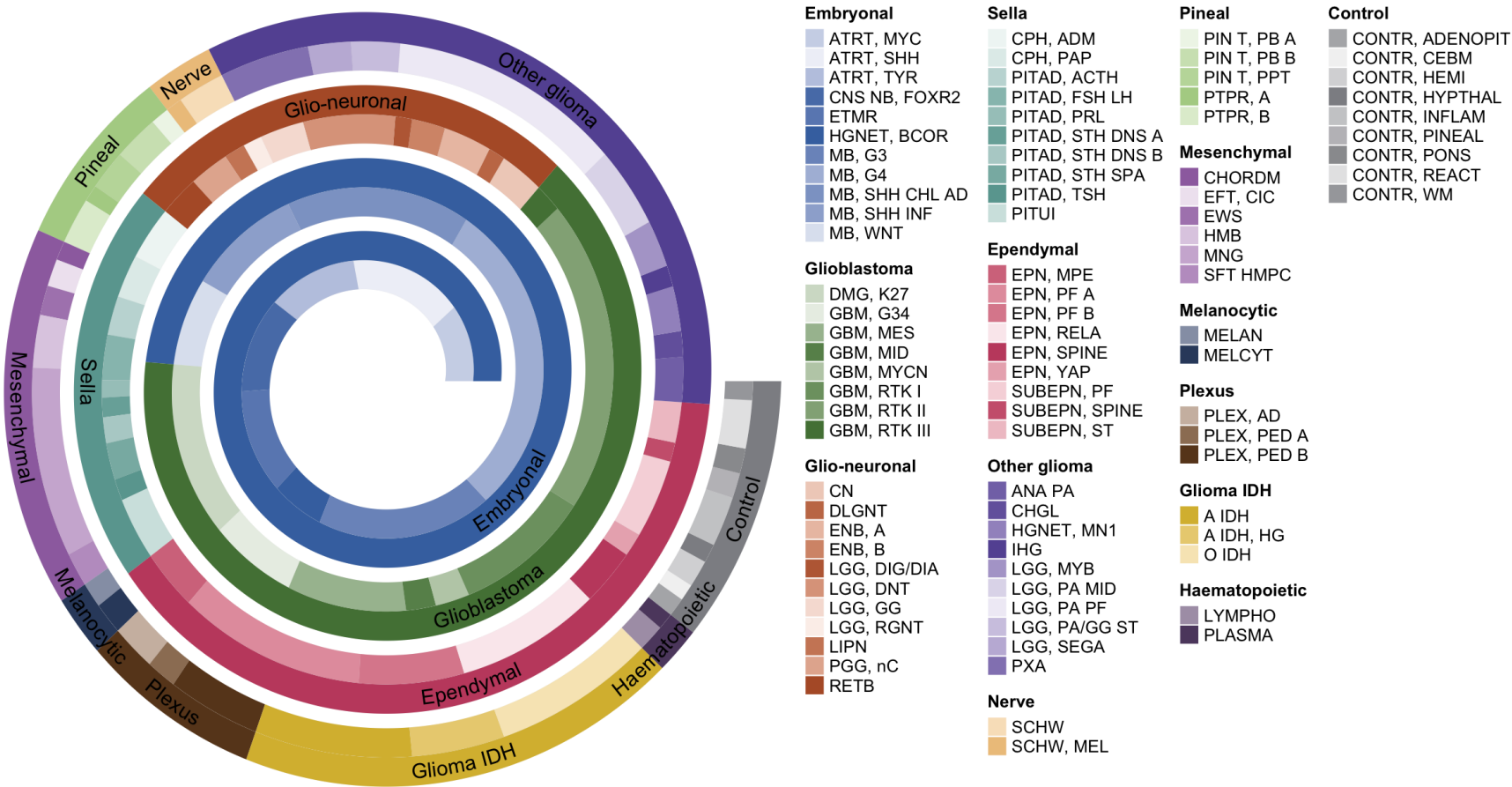


Figure S5.1. Classification of central nervous system tumors.

Session info

sessionInfo()

```
## R version 4.1.0 (2021-05-18)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:      /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.dylib
## LAPACK:    /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] C/UTF-8/C/C/C/C
##
## attached base packages:
## [1] grid      stats      graphics  grDevices utils      datasets  methods
## [8] base
##
## other attached packages:
## [1] ComplexHeatmap_2.9.3  spiralize_1.0.2      knitr_1.33
## [4] rmarkdown_2.9         preprocessCore_1.54.0 RColorBrewer_1.1-2
## [7] cola_1.9.4            BiocManager_1.30.16  colorout_1.2-2
##
## loaded via a namespace (and not attached):
##   [1] colorspace_2.0-2      rjson_0.2.20          ellipsis_0.3.2
##   [4] mclust_5.4.7          circlize_0.4.13       markdown_1.1
##   [7] XVector_0.32.0        GlobalOptions_0.1.2   clue_0.3-59
##  [10] rstudioapi_0.13       bit64_4.0.5           lubridate_1.7.10
##  [13] AnnotationDbi_1.54.1  Polychrome_1.2.6      fansi_0.5.0
##  [16] xml2_1.3.2            codetools_0.2-18      splines_4.1.0
##  [19] doParallel_1.0.16     cachem_1.0.5          impute_1.66.0
##  [22] jsonlite_1.7.2        Cairo_1.5-12.2        annotate_1.70.0
##  [25] cluster_2.1.2         png_0.1-7             data.tree_1.0.0
##  [28] compiler_4.1.0        httr_1.4.2            assertthat_0.2.1
##  [31] Matrix_1.3-4          fastmap_1.1.0         htmltools_0.5.1.1
##  [34] tools_4.1.0           gtable_0.3.0          glue_1.4.2
##  [37] GenomeInfoDbData_1.2.6 dplyr_1.0.7           Rcpp_1.0.7
##  [40] slam_0.1-48           Biobase_2.52.0        eulerr_6.1.0
##  [43] jquerylib_0.1.4       vctrs_0.3.8           Biostrings_2.60.1
##  [46] iterators_1.0.13      xfun_0.24             stringr_1.4.0
##  [49] lifecycle_1.0.0       irlba_2.3.3           XML_3.99-0.6
##  [52] dendextend_1.15.1     zlibbioc_1.38.0       scales_1.1.1
##  [55] microbenchmark_1.4-7  parallel_4.1.0        yaml_2.2.1
##  [58] memoise_2.0.0         gridExtra_2.3         ggplot2_3.3.5
##  [61] sass_0.4.0            stringi_1.6.2         RSQLite_2.2.7
##  [64] highr_0.9             genefilter_1.74.0     S4Vectors_0.30.0
##  [67] foreach_1.5.1         BiocGenerics_0.38.0   shape_1.4.6
##  [70] GenomeInfoDb_1.28.0   rlang_0.4.11          pkgconfig_2.0.3
##  [73] matrixStats_0.59.0    bitops_1.0-7          evaluate_0.14
##  [76] lattice_0.20-44       purrr_0.3.4           bit_4.0.4
##  [79] tidyselect_1.1.1      magrittr_2.0.1        R6_2.5.0
##  [82] IRanges_2.26.0        magick_2.7.2          generics_0.1.0
##  [85] DBI_1.1.1             pillar_1.6.1          survival_3.2-11
##  [88] KEGGREST_1.32.0       scatterplot3d_0.3-41  RCurl_1.98-1.3
##  [91] tibble_3.1.2          crayon_1.4.1          utf8_1.2.1
##  [94] skmeans_0.2-13        viridis_0.6.1         GetoptLong_1.0.3
##  [97] blob_1.2.1            digest_0.6.27         xtable_1.8-4
## [100] brew_1.0-6            stats4_4.1.0          munsell_0.5.0
## [103] viridisLite_0.4.0     bslib_0.2.5.1
```