

Plot for GO term with select on different group

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Load the GO data

```
## [1] "004-128-KD_vs_004_DEG_1.0_down_GO_BP_WN.xlsx"
## [2] "004-128-KD_vs_004_DEG_1.0_up_GO_BP_WN.xlsx"
## [3] "004-185-KD_vs_004_DEG_1.0_down_GO_BP_WN.xlsx"
## [4] "004-185-KD_vs_004_DEG_1.0_up_GO_BP_WN.xlsx"
## [5] "004-214-OE_vs_004_DEG_0.5_down_GO_BP_WN.xlsx"
## [6] "004-214-OE_vs_004_DEG_0.5_up_GO_BP_WN.xlsx"
## [7] "007-128-KD_vs_007_DEG_1.0_down_GO_BP_WN.xlsx"
## [8] "007-128-KD_vs_007_DEG_1.0_up_GO_BP_WN.xlsx"
## [9] "007-185-KD_vs_007_DEG_1.0_down_GO_BP_WN.xlsx"
## [10] "007-185-KD_vs_007_DEG_1.0_up_GO_BP_WN.xlsx"
## [11] "007-214-OE_vs_007_DEG_1.0_down_GO_BP_WN.xlsx"
## [12] "007-214-OE_vs_007_DEG_1.0_up_GO_BP_WN.xlsx"
## [13] "22q001-DGCR8-OE_vs_22q001_DEG_1.5_down_GO_BP_WN.xlsx"
## [14] "22q001-DGCR8-OE_vs_22q001_DEG_1.5_up_GO_BP_WN.xlsx"
## [15] "22q002-128-OE_vs_22q002_DEG_1.0_down_GO_BP_WN.xlsx"
## [16] "22q002-128-OE_vs_22q002_DEG_1.0_up_GO_BP_WN.xlsx"
## [17] "22q002-185-OE_vs_22q002_DEG_1.0_down_GO_BP_WN.xlsx"
## [18] "22q002-185-OE_vs_22q002_DEG_1.0_up_GO_BP_WN.xlsx"
## [19] "22q002-DGCR8-OE_vs_22q002_DEG_1.5_down_GO_BP_WN.xlsx"
## [20] "22q002-DGCR8-OE_vs_22q002_DEG_1.5_up_GO_BP_WN.xlsx"
```

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 v
##
## 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] extrafont_0.19      readxl_1.4.5      fs_1.6.6
## [4] rtracklayer_1.64.0  GenomicRanges_1.56.2  GenomeInfoDb_1.40.1
## [7] IRanges_2.38.1      S4Vectors_0.42.1      BiocGenerics_0.50.0
## [10] knitr_1.50          lubridate_1.9.4      forcats_1.0.0
## [13] stringr_1.5.1       dplyr_1.1.4         purrr_1.0.4
## [16] readr_2.1.5         tidyr_1.3.1         tibble_3.2.1
## [19] ggplot2_3.5.2       tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] SummarizedExperiment_1.34.0 gtable_0.3.6
## [3] rjson_0.2.23              xfun_0.52
## [5] lattice_0.22-7            Biobase_2.64.0
## [7] tzdb_0.5.0                vctrs_0.6.5
## [9] tools_4.4.0               bitops_1.0-9
## [11] generics_0.1.4            curl_6.2.3
## [13] parallel_4.4.0            pkgconfig_2.0.3
## [15] Matrix_1.7-3              RColorBrewer_1.1-3
## [17] lifecycle_1.0.4          GenomeInfoDbData_1.2.12
## [19] compiler_4.4.0           farver_2.1.2
## [21] textshaping_1.0.1        Rsamtools_2.20.0
## [23] Biostrings_2.72.1        codetools_0.2-20
## [25] htmltools_0.5.8.1        RCurl_1.98-1.17
## [27] yaml_2.3.10              Rttf2pt1_1.3.12
## [29] extrafontdb_1.0          pillar_1.10.2
## [31] crayon_1.5.3             BiocParallel_1.38.0
## [33] DelayedArray_0.30.1      abind_1.4-8
## [35] tidyselect_1.2.1         digest_0.6.37
## [37] stringi_1.8.7            restfulr_0.0.15
## [39] labeling_0.4.3           fastmap_1.2.0
## [41] grid_4.4.0              SparseArray_1.4.8
## [43] cli_3.6.5               magrittr_2.0.3
## [45] S4Arrays_1.4.1          dichromat_2.0-0.1
## [47] XML_3.99-0.18           withr_3.0.2
```

## [49] scales_1.4.0	UCSC.utils_1.0.0
## [51] timechange_0.3.0	rmarkdown_2.29
## [53] XVector_0.44.0	httr_1.4.7
## [55] matrixStats_1.5.0	cellranger_1.1.0
## [57] ragg_1.4.0	hms_1.1.3
## [59] evaluate_1.0.3	BiocIO_1.14.0
## [61] rlang_1.1.6	glue_1.8.0
## [63] rstudioapi_0.17.1	jsonlite_2.0.0
## [65] R6_2.6.1	systemfonts_1.2.3
## [67] MatrixGenerics_1.16.0	GenomicAlignments_1.40.0
## [69] zlibbioc_1.50.0	