Create data set compatible with ShinyLib

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Contents

In a first step, the results given by the Nextflow pipeline are loaded.

```
load("../results_controlsgRNAs/fitness/result.Rdata")
load("../input/CRISPR_2022_dataSet_forShinyLib/CRISPRi_library_2022.Rdata")

annotation <- unique(CRISPRi_library_2022[,c(1,26:33)])
DESeq_result_table <- DESeq_result_table %>% left_join(annotation)
DESeq_result_table$FoldChange <- 2^DESeq_result_table$log2FoldChange
CRISPRi_library_2024_CO2data <- DESeq_result_table
```

```
CRISPRi_library_2024_CO2data[grepl("nc_", CRISPRi_library_2024_CO2data$sgRNA),]$sgRNA_type <- "non-codi
CRISPRi_library_2024_CO2data[grepl("nc_", CRISPRi_library_2024_CO2data$sgRNA),]$protein <- "non-coding
CRISPRi_library_2024_CO2data[grepl("nc_", CRISPRi_library_2024_CO2data$sgRNA),]$process <- "non-coding
CRISPRi_library_2024_CO2data[grepl("nc_", CRISPRi_library_2024_CO2data$sgRNA),]$pathway <- "unknown"

df_ncRNAs <- as.data.frame(str_split_fixed(CRISPRi_library_2024_CO2data[grepl("nc_", CRISPRi_library_20
df_ncRNAs$sgRNA_target <- CRISPRi_library_2024_CO2data[grepl("nc_", CRISPRi_library_2024_CO2data$sgRNA)
df_ncRNAs <- unique(df_ncRNAs[,c(2,3)])
names(df_ncRNAs) <- c("locus", "sgRNA_target")
CRISPRi_library_2024_CO2data <- rows_patch(CRISPRi_library_2024_CO2data, df_ncRNAs, by="sgRNA_target")
ncRNA_annotation <- read_tsv("../input/ncRNAs_CRISPRi.csv")
CRISPRi_library_2024_CO2data <- rows_patch(CRISPRi_library_2024_CO2data, ncRNA_annotation, by="locus",
names(df_ncRNAs) <- c("gene_name", "sgRNA_target")
df_ncRNAs <- tibble(df_ncRNAs)
CRISPRi_library_2024_CO2data <- rows_patch(CRISPRi_library_2024_CO2data, df_ncRNAs, by="sgRNA_target")

CRISPRi_library_2024_CO2data[is.na(CRISPRi_library_2024_CO2data$gene_name_short),]$gene_name_short <- C

list_with_locus_tags <- (grepl("sll", CRISPRi_library_2024_CO2data$gene_name) | grepl("slr", CRISPRi_li
CRISPRi_library_2024_CO2data[!list_with_locus_tags, ]$gene_name <- paste(CRISPRi_library_2024_CO2data[!
ncRNAs <- subset(CRISPRi_library_2024_CO2data, CRISPRi_library_2024_CO2data$sgRNA_type=="non-coding")
```

```
save(CRISPRi_library_2024_CO2data, file = "../R_results_controlssgRNAs/CRISPRi_library_2024_CO2data.Rda
```

Session info

```
## R version 4.4.1 (2024-06-14)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 22.04.4 LTS
```

```
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblasp-r0.3.20.so;  LAPACK version 3.10.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=sv_SE.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=sv_SE.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=sv_SE.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=sv_SE.UTF-8 LC_IDENTIFICATION=C
##
## time zone: Europe/Stockholm
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] magrittr_2.0.3  lubridate_1.9.3 forcats_1.0.0   stringr_1.5.1
##  [5] dplyr_1.1.4     purrr_1.0.2     readr_2.1.5     tidyr_1.3.1
##  [9] tibble_3.2.1    ggplot2_3.5.1   tidyverse_2.0.0 knitr_1.48
##
## loaded via a namespace (and not attached):
##  [1] bit_4.5.0         gtable_0.3.5      crayon_1.5.3      compiler_4.4.1
##  [5] tidyselect_1.2.1  parallel_4.4.1    scales_1.3.0      yaml_2.3.10
##  [9] fastmap_1.2.0     R6_2.5.1          generics_0.1.3    munsell_0.5.1
## [13] pillar_1.9.0      tzdb_0.4.0        rlang_1.1.4       utf8_1.2.4
## [17] stringi_1.8.4     xfun_0.48         bit64_4.5.2       timechange_0.3.0
## [21] cli_3.6.3         withr_3.0.1       digest_0.6.37     grid_4.4.1
## [25] vroom_1.6.5       rstudioapi_0.17.0 hms_1.1.3         lifecycle_1.0.4
## [29] vctrs_0.6.5       evaluate_1.0.1    glue_1.8.0        fansi_1.0.6
## [33] colorspace_2.1-1  rmarkdown_2.28    tools_4.4.1       pkgconfig_2.0.3
## [37] htmltools_0.5.8.1
```