

# Prepare empirical-JTK\_CYCLE analysis

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## General directory setting

```
wd <- here::here()
shared <- fs::path(fs::path_dir(wd), "shared")
```

## Loading packages

```
library(magrittr)
library(ggplot2)
```

## Load common R scripts

```
#source(fs::path(wd, "script_r", "MISC.R"))
#source(fs::path(here::here(), "script_r", "MISC_PALETTE.R"))
```

```
parent_out_dir <- fs::path("analysis", "phase_analysis_ejtk")
```

## Input data preparation

### RNA

```
### Setting some parameters
dir_input <- fs::path(parent_out_dir)
dir_output <- fs::path(parent_out_dir, "rna_exon")
path_out <- function(...) fs::path(wd, dir_output, ...)
fs::dir_create(path_out())

### Load read count data
tbl_input <-
  fs::path(wd, "data_preproc", "readcount", "count_rna_exon", "count_by_gene.csv") %>%
  readr::read_csv(show_col_types = FALSE) %>%
  dplyr::select(Geneid, dplyr::matches("^zt\\d+_[12]_rna$")) %>%
  dplyr::select(1:3, 10:13, 4:9)
dplyr::glimpse(tbl_input)
```

```
Rows: 36,917
Columns: 13
$ Geneid      <chr> "AT1G01010", "AT1G01020", "AT1G03987", "AT1G01030", "AT1G01...
$ zt0_1_rna   <dbl> 20, 81, 7, 167, 566, 87, 386, 8, 11062, 62, 0, 371, 1096, 1...
$ zt0_2_rna   <dbl> 30, 82, 7, 205, 633, 111, 427, 5, 12541, 80, 0, 394, 1237, ...
$ zt3_1_rna   <dbl> 31, 72, 9, 114, 489, 89, 271, 3, 901, 53, 0, 426, 1181, 136...
$ zt3_2_rna   <dbl> 27, 80, 5, 121, 532, 100, 284, 2, 956, 72, 0, 446, 1109, 12...
$ zt6_1_rna   <dbl> 32, 66, 3, 93, 454, 73, 254, 2, 53, 31, 0, 441, 969, 1131, ...
$ zt6_2_rna   <dbl> 22, 79, 6, 81, 439, 63, 252, 5, 65, 39, 0, 512, 920, 1072, ...
$ zt12_1_rna  <dbl> 44, 81, 0, 55, 384, 68, 378, 2, 4, 26, 0, 584, 984, 1427, 5...
$ zt12_2_rna  <dbl> 43, 66, 1, 62, 396, 68, 355, 1, 2, 18, 0, 546, 960, 1332, 6...
$ zt18_1_rna  <dbl> 35, 91, 4, 121, 738, 130, 536, 4, 485, 56, 0, 390, 1140, 13...
$ zt18_2_rna  <dbl> 40, 88, 2, 119, 734, 134, 554, 2, 495, 34, 0, 416, 1145, 13...
```

```
$ zt21_1_rna <dbl> 39, 109, 1, 88, 620, 105, 620, 7, 5832, 73, 0, 399, 1086, 1...
$ zt21_2_rna <dbl> 23, 109, 7, 87, 606, 84, 619, 8, 6158, 63, 0, 369, 1072, 16...
```

```
### Load scale factor
sf_default_rna <-
  readRDS(fs::path(wd, "analysis", "deseq2_rna", "sf_default_rna.rds")) %>%
  {.[c(1:2,9:12,3:8)]}
sf_default_rna
```

```
zt0_1_rna  zt0_2_rna  zt3_1_rna  zt3_2_rna  zt6_1_rna  zt6_2_rna  zt12_1_rna
0.8852572  0.9861809  0.9919602  0.9850716  0.9549625  0.9323711  1.1518050
zt12_2_rna zt18_1_rna zt18_2_rna zt21_1_rna zt21_2_rna
1.1281778  1.0642214  1.0457061  0.9602838  0.9825095
```

```
### Check and normalize read count
if(any(colnames(tbl_input[,-1]) != names(sf_default_rna))) stop()
tbl_input[,-1] <- purrr::modify2(tbl_input[,-1], sf_default_rna, ~ .x / .y)
```

```
### Filter AGI
AGI_filtered_rna <-
  readRDS(fs::path(wd, "analysis", "deseq2_rna", "AGI_filtered_rna.rds"))
str(AGI_filtered_rna)
```

```
chr [1:23981] "AT1G01010" "AT1G01020" "AT1G03987" "AT1G01030" "AT1G01040" ...
```

```
tbl_input <- dplyr::filter(tbl_input, Geneid %in% AGI_filtered_rna)
dplyr::glimpse(tbl_input)
```

```
Rows: 23,981
Columns: 13
$ Geneid      <chr> "AT1G01010", "AT1G01020", "AT1G03987", "AT1G01030", "AT1G01...
$ zt0_1_rna   <dbl> 22.592304, 91.498831, 7.907306, 188.645738, 639.362202, 98...
$ zt0_2_rna   <dbl> 30.420381, 83.149041, 7.098089, 207.872603, 641.870039, 112...
$ zt3_1_rna   <dbl> 31.251255, 72.583560, 9.072945, 114.923971, 492.963347, 89...
$ zt3_2_rna   <dbl> 27.409175, 81.212370, 5.075773, 122.833709, 540.062258, 101...
$ zt6_1_rna   <dbl> 33.509168, 69.112660, 3.141485, 97.386020, 475.411326, 76.4...
$ zt6_2_rna   <dbl> 23.595754, 84.730209, 6.435206, 86.875277, 470.842551, 67.5...
$ zt12_1_rna  <dbl> 38.200910, 70.324402, 0.000000, 47.751137, 333.389759, 59.0...
$ zt12_2_rna  <dbl> 38.1145605, 58.5014185, 0.8863851, 54.9558780, 351.0085109,...
$ zt18_1_rna  <dbl> 32.887894, 85.508523, 3.758616, 113.698146, 693.464728, 122...
$ zt18_2_rna  <dbl> 38.251667, 84.153667, 1.912583, 113.798709, 701.918090, 128...
$ zt21_1_rna  <dbl> 40.612994, 113.508111, 1.041359, 91.639576, 645.642465, 109...
$ zt21_2_rna  <dbl> 23.409443, 110.940404, 7.124613, 88.548763, 616.787934, 85...
```

```
### Save eJTK input data
header_line <-
  paste(c("#", paste0("ZT", rep(c(0, 3, 6, 12, 18, 21), each=2))), collapse = "\t")
header_line
```

```
[1] "#\tZT0\tZT0\tZT3\tZT3\tZT6\tZT6\tZT12\tZT12\tZT18\tZT18\tZT21\tZT21"
```

```
dplyr::rowwise(tbl_input) %>%
  dplyr::group_split() %>%
  purrr::map_chr(~ paste(as.character(.x), collapse = "\t")) %>%
```

```
{c(header_line, .)} %>%
  readr::write_lines(path_out("data.txt"))
readr::read_lines(path_out("data.txt"), n_max = 10) %>% cat(sep = "\n")
```

#	ZT0	ZT0	ZT3	ZT3	ZT6	ZT6	ZT12	ZT12	ZT18	ZT18	ZT21	ZT21	
AT1G01010			22.5923039558941				30.4203809915218				31.251255141716		27.4091747292632
33.5091683231262			23.5957542817426				38.2009098308248				38.1145605272843		32.8878936064003
38.2516670289166			40.612993756216			23.409443041413							
AT1G01020			91.498831021371			83.1490413768263					72.5835603291468		81.2123695681872
69.1126596664478			84.7302085571664			70.3244021885638					58.5014184837386		85.5085233766407
84.1536674636164			113.508110754552			110.94040397887							
AT1G03987			7.90730638456292			7.09808889802175					9.07294504114335		5.0757730980117
3.14148453029308			6.43520571320251			0	0.886385128541494				3.75861641216003		1.91258335144583
1.04135881426195			7.12461309956048										
AT1G01030			188.645738031715			207.872603442066					114.923970521149		122.833708971883
97.3860204390855			86.8752771282339			47.751137288531					54.9558779695726		113.698146467841
113.798709411027			91.6395756550515			88.5487628088231							
AT1G01040			639.362201951802			641.87003892111					492.963347235455		540.062257628445
475.411325584353			470.842551349317			333.389758523562					351.008510902432		693.464728043526
701.918089980619			645.642464842409			616.787934047664							
AT1G03993			98.2765222081392			112.555409668631					89.721345406862		101.515461960234
76.4427902371317			67.5696599886264			59.0377697385474					60.2741887408216		122.155033395201
128.14308454687			109.342675497505			85.4953571947258							
AT1G01050			436.031466348755			432.983422779327					273.196456238872		288.303911967065
265.979023564814			270.278639954506			328.180543546631					314.66672063223		503.654599229444
529.785588350494			645.642464842409			630.01935837542							
AT1G03997			9.03692158235763			5.07006349858697					3.02431501371445		2.03030923920468
2.09432302019539			5.36267142766876			1.73640499231022					0.886385128541494		3.75861641216003
1.91258335144583			7.28951169983365			8.14241497092626							
AT1G01060			12495.803318005			12716.7332671558					908.302609118906		970.487816339837
55.4995600351778			69.7147285596939			3.47280998462044					1.77277025708299		455.732239974404
473.364379482842			6073.20460477569			6267.62392387049							

## mORF

```
### Setting some parameters
dir_input <- fs::path(parent_out_dir)
dir_output <- fs::path(parent_out_dir, "ribo_ccds_psite")
path_out <- function(...) fs::path(wd, dir_output, ...)
fs::dir_create(path_out())

### Load read count data
tbl_input <-
  fs::path(wd, "data_preproc", "readcount", "count_ribo_central_cds_psite", "count_by_gene.csv") %>%
  readr::read_csv(show_col_types = FALSE) %>%
  dplyr::select(Geneid, dplyr::matches("^zt\\d+_[12]_ribo$")) %>%
  dplyr::select(1:3, 10:13, 4:9)
dplyr::glimpse(tbl_input)
```

```
Rows: 27,631
Columns: 13
$ Geneid      <chr> "AT1G01010", "AT1G01020", "AT1G01030", "AT1G01040", "AT1G0...
$ zt0_1_ribo  <dbl> 59, 74, 125, 136, 1123, 4257, 389, 1536, 6124, 4419, 134, ...
$ zt0_2_ribo  <dbl> 31, 56, 61, 55, 597, 2356, 258, 1057, 4238, 3196, 73, 1566...
$ zt3_1_ribo  <dbl> 48, 43, 55, 160, 414, 168, 105, 1754, 4415, 3678, 54, 1434...
$ zt3_2_ribo  <dbl> 25, 40, 45, 54, 312, 102, 72, 1084, 3166, 2600, 41, 1108, ...
$ zt6_1_ribo  <dbl> 19, 18, 20, 154, 314, 12, 42, 1443, 2602, 1988, 26, 972, 6...
$ zt6_2_ribo  <dbl> 28, 35, 38, 90, 263, 18, 35, 1387, 2938, 2295, 43, 920, 7,...
$ zt12_1_ribo <dbl> 82, 35, 47, 334, 616, 0, 92, 2489, 3636, 2395, 77, 1658, 1...
$ zt12_2_ribo <dbl> 56, 32, 50, 77, 314, 2, 35, 1205, 2216, 2369, 55, 1065, 11...
```

```
$ zt18_1_ribo <dbl> 65, 55, 63, 175, 1233, 122, 173, 1265, 5103, 2707, 74, 158...
$ zt18_2_ribo <dbl> 45, 50, 57, 177, 1276, 132, 196, 1229, 5235, 2936, 59, 166...
$ zt21_1_ribo <dbl> 31, 46, 43, 123, 887, 1618, 177, 1226, 5083, 2595, 60, 160...
$ zt21_2_ribo <dbl> 41, 56, 74, 139, 1111, 2120, 235, 1431, 5686, 3742, 80, 17...
```

```
### Load scale factor
sf_default_ribo <-
  readRDS(fs::path(wd, "analysis", "deseq2_ribo", "sf_default_ribo.rds")) %>%
  {.[c(1:2,9:12,3:8)]}
sf_default_ribo
```

```
zt0_1_ribo  zt0_2_ribo  zt3_1_ribo  zt3_2_ribo  zt6_1_ribo  zt6_2_ribo
1.3815980   0.8917084   1.0702754   0.7875683   0.7440773   0.8097870
zt12_1_ribo zt12_2_ribo zt18_1_ribo zt18_2_ribo zt21_1_ribo zt21_2_ribo
1.3827508   0.9011186   1.1266239   1.1130669   0.9709120   1.1715257
```

```
### Check and normalize read count
if(any(colnames(tbl_input[,-1]) != names(sf_default_ribo))) stop()
tbl_input[,-1] <- purrr::modify2(tbl_input[,-1], sf_default_ribo, ~ .x / .y)

### Filter AGI
AGI_filtered_ribo <-
  readRDS(fs::path(wd, "analysis", "deseq2_ribo", "AGI_filtered_ribo.rds"))
str(AGI_filtered_ribo)
```

```
chr [1:21274] "AT1G01010" "AT1G01020" "AT1G01030" "AT1G01040" "AT1G01050" ...
```

```
tbl_input <- dplyr::filter(tbl_input, Geneid %in% AGI_filtered_ribo)
dplyr::glimpse(tbl_input)
```

```
Rows: 21,274
Columns: 13
$ Geneid      <chr> "AT1G01010", "AT1G01020", "AT1G01030", "AT1G01040", "AT1G0...
$ zt0_1_ribo  <dbl> 42.704172, 53.561165, 90.474940, 98.436735, 812.826862, 30...
$ zt0_2_ribo  <dbl> 34.764726, 62.800796, 68.408009, 61.679353, 669.501339, 26...
$ zt3_1_ribo  <dbl> 44.848271, 40.176576, 51.388644, 149.494237, 386.816338, 1...
$ zt3_2_ribo  <dbl> 31.743279, 50.789247, 57.137903, 68.565483, 396.156126, 12...
$ zt6_1_ribo  <dbl> 25.534980, 24.191034, 26.878926, 206.967733, 421.999143, 1...
$ zt6_2_ribo  <dbl> 34.576992, 43.221240, 46.925918, 111.140332, 324.776749, 2...
$ zt12_1_ribo <dbl> 59.302081, 25.311864, 33.990217, 241.547502, 445.488805, 0...
$ zt12_2_ribo <dbl> 62.144984, 35.511420, 55.486593, 85.449353, 348.455804, 2...
$ zt18_1_ribo <dbl> 57.694496, 48.818420, 55.919281, 155.331336, 1094.420210, ...
$ zt18_2_ribo <dbl> 40.42884, 44.92093, 51.20986, 159.02009, 1146.38214, 118.5...
$ zt21_1_ribo <dbl> 31.928743, 47.378135, 44.288257, 126.685014, 913.574041, 1...
$ zt21_2_ribo <dbl> 34.997097, 47.800913, 63.165493, 118.648696, 948.335979, 1...
```

```
### Save eJTK input data
header_line <-
  paste0("#", paste0("ZT", rep(c(0, 3, 6, 12, 18, 21), each=2))), collapse = "\t")
header_line
```

```
[1] "#\tZT0\tZT0\tZT3\tZT3\tZT6\tZT6\tZT12\tZT12\tZT18\tZT18\tZT21\tZT21"
```

```
dplyr::rowwise(tbl_input) %>%
  dplyr::group_split() %>%
  purrr::map_chr(~ paste(as.character(.x), collapse = "\t")) %>%
  {c(header_line, .)} %>%
  readr::write_lines(path_out("data.txt"))
readr::read_lines(path_out("data.txt"), n_max = 10) %>% cat(sep = "\n")
```

#	ZT0	ZT3	ZT6	ZT12	ZT18	ZT21	
AT1G01010	42.7041717476715	34.7647261362627	44.8482710326735	31.7432793623567			
25.5349799892894	34.5769923102144	59.3020812425734	62.1449841296481	57.6944960786652			
40.4288371482759	31.9287432760018	34.997097341495					
AT1G01020	53.5611645648761	62.8007956009906	40.1765761334367	50.7892469797708			
24.1910336740636	43.221240387768	25.3118639450008	35.5114195026561	48.8184197588705			
44.920930164751	47.3781351837446	47.800913442042					
AT1G01030	90.4749401433718	68.4080094939362	51.388643891605	57.1379028522421			
26.8789263045151	46.9259181352909	33.9902172975725	55.4865929729001	55.9192808147063			
51.2098603878161	44.288256802196	63.1654927626984					
AT1G01040	98.4367348759886	61.6793528224015	149.494236775578	68.5654834226906			
206.967732544766	111.140332425689	241.547501646579	85.4493531782661	155.331335596406			
159.020092783219	126.685013643491	118.648695865069					
AT1G01050	812.826862248053	669.501338817704	386.816337656809	396.156126442212			
421.999142980887	324.776749199514	445.488805432014	348.455803869813	1094.42021023068			
1146.38213780445	913.574041477858	948.335979180512					
AT1G01060	3081.21456152267	2642.11918635596	156.968948614357	129.512579798415			
16.1273557827091	22.2280664851378	0	2.219463718916	108.288131101495	118.591255634943		
1666.47440711519	1809.6060088773						
AT1G01070	281.558013726173	289.332236875993	98.1055928839732	91.4206445635874			
56.4457452394817	43.221240387768	66.5340423697164	38.8406150810301	153.556120332447			
176.090046245824	182.302824511365	200.593118908569					
AT1G01080	1111.75606448175	1185.3650169687	1638.83057065228	1376.38859315179			
1939.31453287077	1712.79601193812	1800.03512454592	1337.22689064689	1122.82365445402			
1104.15646344958	1262.73029859285	1221.48405599218					
AT1G01090	4432.54826750407	4752.67449566068	4125.10659602611	4019.96889844886			
3496.94831221742	3628.11440740749	2629.54106582923	2459.16580055893	4529.46174599121			
4703.22138824943	5235.28393780378	4853.49988984734					

## uORF

```
### Setting some parameters
dir_input <- fs::path(parent_out_dir)
dir_output <- fs::path(parent_out_dir, "ribo_uorf_psite")
path_out <- function(...) fs::path(wd, dir_output, ...)
fs::dir_create(path_out())

### Load read count data
tbl_input <-
  fs::path(wd, "data_preproc", "readcount", "count_ribo_uorf_psite", "count_by_gene.csv") %>%
  readr::read_csv(show_col_types = FALSE) %>%
  dplyr::select(Geneid, dplyr::matches("^zt\\d+_[12]_ribo$")) %>%
  dplyr::select(1:3, 10:13, 4:9)
dplyr::glimpse(tbl_input)
```

```
Rows: 4,778
Columns: 13
$ Geneid      <chr> "AT1G01060", "AT1G01210", "AT1G01230", "AT1G01240", "AT1G01250", ...
$ zt0_1_ribo  <dbl> 1158, 15, 12, 27, 12, 1, 29, 47, 0, 39, 15, 1, 2, 25, 28, ...
$ zt0_2_ribo  <dbl> 909, 7, 3, 21, 11, 1, 14, 27, 1, 25, 17, 2, 4, 26, 30, 11, ...
$ zt3_1_ribo  <dbl> 101, 7, 21, 32, 11, 5, 9, 30, 2, 16, 27, 1, 0, 47, 34, 10, ...
$ zt3_2_ribo  <dbl> 63, 4, 17, 22, 8, 2, 11, 21, 3, 10, 28, 0, 0, 31, 19, 9, 9, ...
$ zt6_1_ribo  <dbl> 7, 5, 18, 24, 14, 2, 7, 16, 1, 9, 12, 5, 0, 27, 42, 12, 10, ...
```

```
$ zt6_2_ribo <dbl> 11, 5, 15, 16, 13, 3, 7, 28, 1, 10, 17, 0, 0, 28, 32, 15, ...
$ zt12_1_ribo <dbl> 0, 3, 25, 9, 16, 2, 11, 35, 4, 12, 32, 2, 1, 51, 48, 8, 21...
$ zt12_2_ribo <dbl> 3, 5, 14, 10, 10, 4, 4, 30, 2, 15, 12, 1, 0, 31, 36, 9, 8,...
$ zt18_1_ribo <dbl> 31, 21, 10, 9, 13, 1, 22, 25, 2, 37, 12, 3, 1, 31, 43, 19,...
$ zt18_2_ribo <dbl> 29, 15, 6, 11, 7, 0, 20, 22, 6, 39, 20, 0, 0, 21, 42, 7, 1...
$ zt21_1_ribo <dbl> 432, 8, 5, 19, 11, 2, 14, 25, 2, 37, 13, 2, 1, 23, 33, 12,...
$ zt21_2_ribo <dbl> 580, 9, 7, 20, 7, 0, 13, 24, 1, 46, 25, 1, 1, 27, 24, 12, ...
```

```
### Load scale factor
sf_default_ribo <-
  readRDS(fs::path(wd, "analysis", "deseq2_ribo", "sf_default_ribo.rds")) %>%
  {.[c(1:2,9:12,3:8)]}
sf_default_ribo
```

```
zt0_1_ribo zt0_2_ribo zt3_1_ribo zt3_2_ribo zt6_1_ribo zt6_2_ribo
1.3815980 0.8917084 1.0702754 0.7875683 0.7440773 0.8097870
zt12_1_ribo zt12_2_ribo zt18_1_ribo zt18_2_ribo zt21_1_ribo zt21_2_ribo
1.3827508 0.9011186 1.1266239 1.1130669 0.9709120 1.1715257
```

```
### Check and normalize read count
if(any(colnames(tbl_input[,-1]) != names(sf_default_ribo))) stop()
tbl_input[,-1] <- purrr::modify2(tbl_input[,-1], sf_default_ribo, ~ .x / .y)
```

```
### Filter AGI
AGI_filtered_ribo <-
  readRDS(fs::path(wd, "analysis", "deseq2_ribo", "AGI_filtered_ribo.rds"))
str(AGI_filtered_ribo)
```

```
chr [1:21274] "AT1G01010" "AT1G01020" "AT1G01030" "AT1G01040" "AT1G01050" ...
```

```
tbl_input <- dplyr::filter(tbl_input, Geneid %in% AGI_filtered_ribo)
dplyr::glimpse(tbl_input)
```

```
Rows: 4,753
Columns: 13
$ Geneid <chr> "AT1G01060", "AT1G01210", "AT1G01230", "AT1G01240", "AT1G0...
$ zt0_1_ribo <dbl> 838.1598455, 10.8569928, 8.6855943, 19.5425871, 8.6855943,...
$ zt0_2_ribo <dbl> 1019.391486, 7.850099, 3.364328, 23.550298, 12.335871, 1.1...
$ zt3_1_ribo <dbl> 94.368237, 6.540373, 19.621119, 29.898847, 10.277729, 4.67...
$ zt3_2_ribo <dbl> 79.993064, 5.078925, 21.585430, 27.934086, 10.157849, 2.53...
$ zt6_1_ribo <dbl> 9.407624, 6.719732, 24.191034, 32.254712, 18.815248, 2.687...
$ zt6_2_ribo <dbl> 13.583818, 6.174463, 18.523389, 19.758281, 16.053604, 3.70...
$ zt12_1_ribo <dbl> 0.0000000, 2.1695883, 18.0799028, 6.5087650, 11.5711378, 1...
$ zt12_2_ribo <dbl> 3.329196, 5.548659, 15.536246, 11.097319, 11.097319, 4.438...
$ zt18_1_ribo <dbl> 27.5158366, 18.6397603, 8.8760763, 7.9884687, 11.5388992, ...
$ zt18_2_ribo <dbl> 26.0541395, 13.4762790, 5.3905116, 9.8826046, 6.2889302, 0...
$ zt21_1_ribo <dbl> 444.942487, 8.239676, 5.149797, 19.569230, 11.329554, 2.05...
$ zt21_2_ribo <dbl> 495.0808892, 7.6822897, 5.9751142, 17.0717548, 5.9751142, ...
```

```
### Save eJTK input data
header_line <-
  paste(c("#", paste0("ZT", rep(c(0, 3, 6, 12, 18, 21), each=2))), collapse = "\t")
header_line
```

```
[1] "#\tZT0\tZT0\tZT3\tZT3\tZT6\tZT6\tZT12\tZT12\tZT18\tZT18\tZT21\tZT21"
```

```
dplyr::rowwise(tbl_input) %>%
  dplyr::group_split() %>%
  purrr::map_chr(~ paste(as.character(.x), collapse = "\t")) %>%
  {c(header_line, .)} %>%
  readr::write_lines(path_out("data.txt"))
readr::read_lines(path_out("data.txt"), n_max = 10) %>% cat(sep = "\n")
```

#	ZT0	ZT0	ZT3	ZT3	ZT6	ZT6	ZT12	ZT12	ZT18	ZT18	ZT21	ZT21
AT1G01060			838.159845488197				1019.39148573751				94.3682369645838	79.993063993139
9.40762420658029				13.5838184075842			0	3.329195578374	27.5158365913634			26.0541394955556
444.942486942993			495.080889221149									
AT1G01210			10.8569928172046				7.85009945012383				6.54037285893155	5.07892469797708
6.71973157612878			6.17446291253828				2.16958833814293				5.54865929729001	18.6397602715688
13.4762790494253			8.2396756841295				7.68228966032818					
AT1G01230			8.6855942537637				3.36432833576736				19.6211185767947	21.5854299664026
24.1910336740636			18.5233887376148					18.0799028178577			15.536246032412	8.87607631979464
5.39051161977012			5.14979730258094				5.97511418025525					
AT1G01240			19.5425870709683				23.5502983503715				29.8988473551157	27.9340858388739
32.2547115654181			19.7582813201225				6.50876501442878				11.09731859458	7.98846868781518
9.88260463624522			19.5692297498076				17.0717548007293					
AT1G01260			8.6855942537637				12.3358705644803				10.1578493959542	18.8152484131606
16.0536035725995			11.5711378034289					11.09731859458			11.538899215733	6.28893022306514
11.3295540656781			5.97511418025525									
AT1G01370			0.723799521146975				1.12144277858912				4.67169489923682	2.53946234898854
2.68789263045151			3.70467774752297				1.44639222542862				4.43892743783201	0.887607631979464
0			2.05991892103237				0					
AT1G01430			20.9901861132623				15.7001989002477				8.40905081862628	13.967042919437
9.40762420658029			8.6442480775536				7.9551572398574				4.43892743783201	19.5273679035482
17.9683720659004			14.4194324472266				11.096640620474					
AT1G01440			34.0185774939078				30.2789550219062				28.0301693954209	26.6643546643797
21.5031410436121			34.5769923102144				25.3118639450008				33.29195578374	22.1901907994866
19.7652092724904			25.7489865129047				20.4861057608751					
AT1G01490			0				1.12144277858912				3.80919352348281	1.34394631522576
1.23489258250766			2.89278445085724					2.219463718916			1.77521526395893	5.39051161977012
2.05991892103237			0.853587740036464									

## Sessioninfo

```
sessionInfo()
```

```
R version 4.2.1 (2022-06-23)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.1

Matrix products: default
BLAS: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats graphics grDevices datasets utils methods base

other attached packages:
[1] ggplot2_3.4.2 magrittr_2.0.3

loaded via a namespace (and not attached):
[1] compiler_4.2.1 pillar_1.9.0 BiocManager_1.30.18
```

[4] tools_4.2.1	bit_4.0.5	digest_0.6.31
[7] jsonlite_1.8.4	evaluate_0.20	lifecycle_1.0.3
[10] tibble_3.2.1	gtable_0.3.1	pkgconfig_2.0.3
[13] rlang_1.1.0	cli_3.6.0	rstudioapi_0.14
[16] parallel_4.2.1	yaml_2.3.6	xfun_0.40
[19] fastmap_1.1.0	withr_2.5.0	dplyr_1.1.1
[22] knitr_1.42	generics_0.1.3	fs_1.5.2
[25] vctrs_0.6.1	hms_1.1.3	bit64_4.0.5
[28] rprojroot_2.0.3	grid_4.2.1	tidyselect_1.2.0
[31] glue_1.6.2	here_1.0.1	R6_2.5.1
[34] fansi_1.0.3	vroom_1.6.0	rmarkdown_2.24
[37] purrr_1.0.1	tzdb_0.3.0	readr_2.1.4
[40] scales_1.2.1	htmltools_0.5.3	colorspace_2.0-3
[43] renv_1.0.3	utf8_1.2.2	munSELL_0.5.0
[46] crayon_1.5.2		