

DEG analysis using DESeq2 (TE, uORF)

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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"))
```

Directory setting

```
dir_output <- fs::path("analysis", "deseq2_te_morf_uorf")
path_out <- function(...) fs::path(wd, dir_output, ...)
fs::dir_create(path_out())
```

Loading input files

```
dir_readcount <- fs::path("data_preproc", "readcount")

# data.frame of RNA-seq read count
rcdf_rna <-
  fs::path(wd, dir_readcount, "count_rna_exon", "count_by_gene.csv") %>%
  readr::read_csv(show_col_types = FALSE) %>%
  dplyr::select(Geneid,
    dplyr::starts_with("zt0"), dplyr::starts_with("zt3"),
    dplyr::starts_with("zt6"), dplyr::starts_with("zt12"),
    dplyr::starts_with("zt18"), dplyr::starts_with("zt21")) %>%
  ngsmisc::ds2_tbl_to_rcdf()
head(rcdf_rna)
```

	zt0_1_rna	zt0_2_rna	zt3_1_rna	zt3_2_rna	zt6_1_rna	zt6_2_rna
AT1G01010	20	30	31	27	32	22
AT1G01020	81	82	72	80	66	79
AT1G03987	7	7	9	5	3	6
AT1G01030	167	205	114	121	93	81
AT1G01040	566	633	489	532	454	439
AT1G03993	87	111	89	100	73	63

	zt12_1_rna	zt12_2_rna	zt18_1_rna	zt18_2_rna	zt21_1_rna	zt21_2_rna
AT1G01010	44	43	35	40	39	23
AT1G01020	81	66	91	88	109	109
AT1G03987	0	1	4	2	1	7
AT1G01030	55	62	121	119	88	87

AT1G01040	384	396	738	734	620	606
AT1G03993	68	68	130	134	105	84

```
dim(rcdf_rna)
```

```
[1] 36917    12
```

```
# data.frame of Ribo-seq (mORF) read count
rcdf_ribo <-
  fs::path(wd, dir_readcount, "count_ribo_central_cds_psite", "count_by_gene.csv") %>%
  readr::read_csv(show_col_types = FALSE) %>%
  dplyr::select(Geneid,
    dplyr::starts_with("zt0"), dplyr::starts_with("zt3"),
    dplyr::starts_with("zt6"), dplyr::starts_with("zt12"),
    dplyr::starts_with("zt18"), dplyr::starts_with("zt21")) %>%
  ngsmisc::ds2_tbl_to_rcdf()
head(rcdf_ribo)
```

	zt0_1_ribo	zt0_2_ribo	zt3_1_ribo	zt3_2_ribo	zt6_1_ribo	zt6_2_ribo
AT1G01010	59	31	48	25	19	28
AT1G01020	74	56	43	40	18	35
AT1G01030	125	61	55	45	20	38
AT1G01040	136	55	160	54	154	90
AT1G01050	1123	597	414	312	314	263
AT1G01060	4257	2356	168	102	12	18

	zt12_1_ribo	zt12_2_ribo	zt18_1_ribo	zt18_2_ribo	zt21_1_ribo
AT1G01010	82	56	65	45	31
AT1G01020	35	32	55	50	46
AT1G01030	47	50	63	57	43
AT1G01040	334	77	175	177	123
AT1G01050	616	314	1233	1276	887
AT1G01060	0	2	122	132	1618

	zt21_2_ribo
AT1G01010	41
AT1G01020	56
AT1G01030	74
AT1G01040	139
AT1G01050	1111
AT1G01060	2120

```
dim(rcdf_ribo)
```

```
[1] 27631    12
```

```
# data.frame of Ribo-seq (uORF) read count
rcdf_ribo_uorf <-
  fs::path(wd, dir_readcount, "count_ribo_uorf_psite", "count_by_gene.csv") %>%
  readr::read_csv(show_col_types = FALSE) %>%
  dplyr::select(Geneid,
    dplyr::starts_with("zt0"), dplyr::starts_with("zt3"),
    dplyr::starts_with("zt6"), dplyr::starts_with("zt12"),
    dplyr::starts_with("zt18"), dplyr::starts_with("zt21")) %>%
  ngsmisc::ds2_tbl_to_rcdf()
head(rcdf_ribo_uorf)
```

	zt0_1_ribo	zt0_2_ribo	zt3_1_ribo	zt3_2_ribo	zt6_1_ribo	zt6_2_ribo
AT1G01060	1158	909	101	63	7	11
AT1G01210	15	7	7	4	5	5
AT1G01230	12	3	21	17	18	15
AT1G01240	27	21	32	22	24	16
AT1G01260	12	11	11	8	14	13
AT1G01370	1	1	5	2	2	3

	zt12_1_ribo	zt12_2_ribo	zt18_1_ribo	zt18_2_ribo	zt21_1_ribo
AT1G01060	0	3	31	29	432
AT1G01210	3	5	21	15	8
AT1G01230	25	14	10	6	5
AT1G01240	9	10	9	11	19
AT1G01260	16	10	13	7	11
AT1G01370	2	4	1	0	2

	zt21_2_ribo
AT1G01060	580
AT1G01210	9
AT1G01230	7
AT1G01240	20
AT1G01260	7
AT1G01370	0

```
dim(rcdf_ribo_uorf)
```

```
[1] 4778 12
```

```
## Filter genes
common_rownames <-
  list(rcdf_rna, rcdf_ribo, rcdf_ribo_uorf) %>%
  purrr::map(row.names) %>%
  purrr::reduce(intersect)
length(common_rownames)
```

```
[1] 4778
```

```
rcdf_ribo_uorf <- rcdf_ribo_uorf[row.names(rcdf_ribo_uorf) %in% common_rownames,]
rcdf_ribo_uorf <- rcdf_ribo_uorf[order(row.names(rcdf_ribo_uorf)),]
head(rcdf_ribo_uorf)
```

	zt0_1_ribo	zt0_2_ribo	zt3_1_ribo	zt3_2_ribo	zt6_1_ribo	zt6_2_ribo
AT1G01060	1158	909	101	63	7	11
AT1G01210	15	7	7	4	5	5
AT1G01230	12	3	21	17	18	15
AT1G01240	27	21	32	22	24	16
AT1G01260	12	11	11	8	14	13
AT1G01370	1	1	5	2	2	3

	zt12_1_ribo	zt12_2_ribo	zt18_1_ribo	zt18_2_ribo	zt21_1_ribo
AT1G01060	0	3	31	29	432
AT1G01210	3	5	21	15	8
AT1G01230	25	14	10	6	5
AT1G01240	9	10	9	11	19
AT1G01260	16	10	13	7	11
AT1G01370	2	4	1	0	2

	zt21_2_ribo
AT1G01060	580
AT1G01210	9
AT1G01230	7

```
AT1G01240      20
AT1G01260       7
AT1G01370       0
```

```
nrow(rcdf_ribo_uorf)
```

```
[1] 4778
```

```
rcdf_ribo <- rcdf_ribo[row.names(rcdf_ribo) %in% common_rownames,]
rcdf_ribo <- rcdf_ribo[order(row.names(rcdf_ribo)),]
head(rcdf_ribo)
```

	zt0_1_ribo	zt0_2_ribo	zt3_1_ribo	zt3_2_ribo	zt6_1_ribo	zt6_2_ribo
AT1G01060	4257	2356	168	102	12	18
AT1G01210	104	68	26	19	24	20
AT1G01230	306	218	349	284	275	300
AT1G01240	151	105	115	72	90	77
AT1G01260	211	155	149	104	104	110
AT1G01370	31	16	31	25	16	21

	zt12_1_ribo	zt12_2_ribo	zt18_1_ribo	zt18_2_ribo	zt21_1_ribo
AT1G01060	0	2	122	132	1618
AT1G01210	44	32	105	91	86
AT1G01230	427	331	231	232	213
AT1G01240	71	53	62	63	87
AT1G01260	207	142	160	180	138
AT1G01370	19	20	14	14	15

	zt21_2_ribo
AT1G01060	2120
AT1G01210	111
AT1G01230	285
AT1G01240	121
AT1G01260	161
AT1G01370	21

```
nrow(rcdf_ribo)
```

```
[1] 4778
```

```
rcdf_rna <- rcdf_rna[row.names(rcdf_rna) %in% common_rownames,]
rcdf_rna <- rcdf_rna[order(row.names(rcdf_rna)),]
head(rcdf_rna)
```

	zt0_1_rna	zt0_2_rna	zt3_1_rna	zt3_2_rna	zt6_1_rna	zt6_2_rna
AT1G01060	11062	12541	901	956	53	65
AT1G01210	152	125	63	68	66	69
AT1G01230	75	90	131	119	139	143
AT1G01240	75	81	343	345	404	337
AT1G01260	179	207	234	253	227	210
AT1G01370	31	32	46	45	51	37

	zt12_1_rna	zt12_2_rna	zt18_1_rna	zt18_2_rna	zt21_1_rna	zt21_2_rna
AT1G01060	4	2	485	495	5832	6158
AT1G01210	62	80	121	122	123	137
AT1G01230	138	162	114	103	124	150
AT1G01240	130	126	130	125	152	132

AT1G01260	219	217	205	203	182	197
AT1G01370	42	43	29	30	15	29

```
nrow(rcdf_rna)
```

```
[1] 4778
```

```
identical(row.names(rcdf_rna), row.names(rcdf_ribo))
```

```
[1] TRUE
```

```
identical(row.names(rcdf_ribo), row.names(rcdf_ribo_uorf))
```

```
[1] TRUE
```

```
# setting sample information
zt_lev <- paste0("zt", c(0, 3, 6, 12, 18, 21))
rna_condition <-
  rep(paste0("zt", c(0, 3, 6, 12, 18, 21)), each = 2) %>%
  forcats::fct_relevel(zt_lev)
ribo_condition <- rna_condition
```

DESeq2 testing

Prepare Design matrix

```
coldata <- data.frame(
  zt =
    c(
      colnames(rcdf_rna),
      colnames(rcdf_ribo),
      colnames(rcdf_ribo)
    ) %>%
    stringr::str_extract("zt\\d+") %>%
    forcats::fct_relevel(zt_lev),
  type = forcats::fct_inorder(c("rna", "ribo", "ribo")) %>% rep(each = 12),
  region = forcats::fct_inorder(c("main", "main", "uorf")) %>% rep(each = 12)
)

full_mat <- model.matrix(~ zt + type + region + zt:type + zt:region, data = coldata)
colnames(full_mat)
```

```
[1] "(Intercept)" "ztzt3" "ztzt6"
[4] "ztzt12" "ztzt18" "ztzt21"
[7] "typeribo" "regionuorf" "ztzt3:typeribo"
[10] "ztzt6:typeribo" "ztzt12:typeribo" "ztzt18:typeribo"
[13] "ztzt21:typeribo" "ztzt3:regionuorf" "ztzt6:regionuorf" [16] "ztzt12:regionuorf" "ztzt18:regionuorf" "ztzt21:region-
uorf"
```

```
reduced_mat <- full_mat[,1:13]
```

negative-bionomial LRT

```

dds <-
  ngsmisc::ds2_rcdf_to_dds(
    rcdf =
      cbind(
        rcdf_rna,
        rcdf_ribo %>% purrr::set_names(~ stringr::str_replace(., "_ribo", "_morf")),
        rcdf_ribo_uorf %>% purrr::set_names(~ stringr::str_replace(., "_ribo", "_uorf"))
      ),
    coldata = coldata,
    design = full_mat
  )

sf_default_rna <-
  readRDS(fs::path(wd, "analysis", "deseq2_rna", "sf_default_rna.rds"))
sf_default_ribo <-
  readRDS(fs::path(wd, "analysis", "deseq2_ribo", "sf_default_ribo.rds"))

dds <-
  dds %>%
    ngsmisc::ds2_dds_set_sizefactor(c(sf_default_rna, sf_default_ribo, sf_default_ribo)) %>%
    ngsmisc::ds2_dds_estimate_disp() %>%
    ngsmisc::ds2_dds_test_nbinomLRT(reduced = reduced_mat)

```

gene-wise dispersion estimates

mean-dispersion relationship

final dispersion estimates

```

ddr <- DESeq2::results(dds, alpha = .01, independentFiltering = FALSE)
ddr %>% DESeq2::summary()

```

```

out of 4778 with nonzero total read count
adjusted p-value < 0.1
LFC > 0 (up)      : 316, 6.6%
LFC < 0 (down)    : 358, 7.5%
outliers [1]     : 0, 0%
low counts [2]   : 0, 0%
(mean count < 0)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results

```

save results

```

tbl_result <-
  dds %>%
    ngsmisc::ds2_dds_to_tbl() %>%
    dplyr::rename(AGI = Geneid) %>%
    return()
dplyr::glimpse(tbl_result)

```

```

Rows: 4,778
Columns: 55
$ AGI      <chr> "AT1G01060", "AT1G01210", "AT1G01230", "AT1G01240..."
$ baseMean <dbl> 1530.71875, 57.87887, 140.13952, 99.25572, 124.61...

```

```

$ baseVar          <dbl> 9913845.9478, 2606.5319, 14334.7879, 8877.0808, 7...
$ allZero          <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, ...
$ dispGeneEst      <dbl> 0.00000001, 0.00000001, 0.00000001, 0.00000001, 0...
$ dispGeneIter     <dbl> 43, 35, 9, 1, 7, 12, 11, 5, 11, 9, 10, 1, 8, 8, 7...
$ dispFit          <dbl> 0.03914498, 0.04449340, 0.04123055, 0.04217618, 0...
$ dispersion       <dbl> 0.02112039, 0.02484232, 0.02821887, 0.02166030, 0...
$ dispIter        <int> 8, 10, 9, 10, 8, 9, 10, 10, 10, 10, 11, 9, 9, 10,...
$ dispOutlier      <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, ...
$ dispMAP          <dbl> 0.02112039, 0.02484232, 0.02821887, 0.02166030, 0...
$ Intercept        <dbl> 13.621855, 7.218726, 6.460157, 6.382012, 7.687091...
$ ztzt3           <dbl> -3.951551448, -1.373876337, 0.316165377, 1.855404...
$ ztzt6           <dbl> -7.815629488, -1.218857771, 0.602432740, 2.073204...
$ ztzt12          <dbl> -11.99468160, -1.02832598, 0.80961319, 0.66018340...
$ ztzt18          <dbl> -4.66849062, -0.27722065, 0.31787880, 0.62894539,...
$ ztzt21          <dbl> -0.987989896, -0.111839663, 0.722990950, 0.850623...
$ typeribo        <dbl> -2.1388569, -0.9758990, 1.4020044, 0.4416547, -0.1...
$ regionuorf      <dbl> -1.625176, -2.978151, -5.161011, -2.413706, -3.99...
$ ztzt3.typeribo  <dbl> -0.65393788, -0.56244019, -0.03316685, -2.3276603...
$ ztzt6.typeribo  <dbl> 0.07665504, -0.72809877, -0.46009098, -2.67687048...
$ ztzt12.typeribo <dbl> 0.40990091, -0.04925267, -0.17775419, -1.61034031...
$ ztzt18.typeribo <dbl> 0.31155181, 0.76822557, -0.18904240, -1.35998144,...
$ ztzt21.typeribo <dbl> 0.7316876, 0.8515328, -0.2664910, -0.6148410, 0.2...
$ ztzt3.regionuorf <dbl> 0.9096049, 0.9373190, 1.0837044, 0.6286365, 0.256...
$ ztzt6.regionuorf <dbl> 0.88809613, 0.84091440, 1.03736591, 0.35182138, 1...
$ ztzt12.regionuorf <dbl> 2.20890952, -0.28826057, 0.87124230, -0.31018296,...
$ ztzt18.regionuorf <dbl> -0.47740286, 0.51962430, 0.27241413, -0.24070624,...
$ ztzt21.regionuorf <dbl> -0.260205492, -0.552942982, -0.209648126, 0.00409...
$ SE_Intercept    <dbl> 0.1485535, 0.1825827, 0.2049992, 0.1894756, 0.183...
$ SE_ztzt3        <dbl> 0.2125283, 0.2739961, 0.2823478, 0.2479268, 0.256...
$ SE_ztzt6        <dbl> 0.2483501, 0.2731393, 0.2806628, 0.2474942, 0.257...
$ SE_ztzt12       <dbl> 0.6251896, 0.2717729, 0.2798832, 0.2580152, 0.257...
$ SE_ztzt18       <dbl> 0.2148757, 0.2602972, 0.2845776, 0.2580798, 0.258...
$ SE_ztzt21       <dbl> 0.2102887, 0.2592118, 0.2810355, 0.2564683, 0.259...
$ SE_typeribo     <dbl> 0.2106727, 0.2677201, 0.2747627, 0.2584790, 0.259...
$ SE_regionuorf   <dbl> 0.2129016, 0.4005090, 0.4525055, 0.3117991, 0.390...
$ SE_ztzt3.typeribo <dbl> 0.3122130, 0.4313572, 0.3819825, 0.3555601, 0.369...
$ SE_ztzt6.typeribo <dbl> 0.4187254, 0.4314032, 0.3810870, 0.3566123, 0.371...
$ SE_ztzt12.typeribo <dbl> 1.2156682, 0.4064987, 0.3793255, 0.3697005, 0.366...
$ SE_ztzt18.typeribo <dbl> 0.3140455, 0.3776866, 0.3851173, 0.3697246, 0.367...
$ SE_ztzt21.typeribo <dbl> 0.2984556, 0.3768117, 0.3821253, 0.3595588, 0.369...
$ SE_ztzt3.regionuorf <dbl> 0.3322606, 0.6704092, 0.5674956, 0.4392189, 0.572...
$ SE_ztzt6.regionuorf <dbl> 0.5236905, 0.6837858, 0.5746274, 0.4547769, 0.543...
$ SE_ztzt12.regionuorf <dbl> 1.3519478, 0.7071246, 0.5648718, 0.5182609, 0.542...
$ SE_ztzt18.regionuorf <dbl> 0.3635974, 0.5301768, 0.6316568, 0.5125685, 0.565...
$ SE_ztzt21.regionuorf <dbl> 0.3031744, 0.5875419, 0.6643201, 0.4535879, 0.575...
$ LRTStatistic    <dbl> 22.033045, 8.118942, 9.559685, 5.335670, 5.658612...
$ LRTPvalue       <dbl> 0.0005160788, 0.1498011548, 0.0887171430, 0.37630...
$ fullBetaConv    <lgl> TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, T...
$ reducedBetaConv <lgl> TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, T...
$ betaIter        <dbl> 5, 3, 3, 2, 3, 4, 3, 3, 4, 2, 3, 6, 4, 3, 3, 4...
$ deviance        <dbl> 324.5975, 225.7619, 282.2621, 259.5636, 276.8161,...
$ maxCooks        <lgl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N...
$ padj            <dbl> 0.01033260, 0.40627189, 0.30957780, 0.64748059, 0...

```

```

tbl_out <-
  dplyr::select(tbl_result, AGI:baseVar, Intercept:LRTPvalue, padj)
dplyr::glimpse(tbl_out)

```

Rows: 4,778
 Columns: 42

```

$ AGI <chr> "AT1G01060", "AT1G01210", "AT1G01230", "AT1G01240...
$ baseMean <dbl> 1530.71875, 57.87887, 140.13952, 99.25572, 124.61...
$ baseVar <dbl> 9913845.9478, 2606.5319, 14334.7879, 8877.0808, 7...
$ Intercept <dbl> 13.621855, 7.218726, 6.460157, 6.382012, 7.687091...
$ ztzt3 <dbl> -3.951551448, -1.373876337, 0.316165377, 1.855404...
$ ztzt6 <dbl> -7.815629488, -1.218857771, 0.602432740, 2.073204...
$ ztzt12 <dbl> -11.99468160, -1.02832598, 0.80961319, 0.66018340...
$ ztzt18 <dbl> -4.66849062, -0.27722065, 0.31787880, 0.62894539,...
$ ztzt21 <dbl> -0.987989896, -0.111839663, 0.722990950, 0.850623...
$ typeribo <dbl> -2.1388569, -0.9758990, 1.4020044, 0.4416547, -0...
$ regionuorf <dbl> -1.625176, -2.978151, -5.161011, -2.413706, -3.99...
$ ztzt3.typeribo <dbl> -0.65393788, -0.56244019, -0.03316685, -2.3276603...
$ ztzt6.typeribo <dbl> 0.07665504, -0.72809877, -0.46009098, -2.67687048...
$ ztzt12.typeribo <dbl> 0.40990091, -0.04925267, -0.17775419, -1.61034031...
$ ztzt18.typeribo <dbl> 0.31155181, 0.76822557, -0.18904240, -1.35998144,...
$ ztzt21.typeribo <dbl> 0.7316876, 0.8515328, -0.2664910, -0.6148410, 0.2...
$ ztzt3.regionuorf <dbl> 0.9096049, 0.9373190, 1.0837044, 0.6286365, 0.256...
$ ztzt6.regionuorf <dbl> 0.88809613, 0.84091440, 1.03736591, 0.35182138, 1...
$ ztzt12.regionuorf <dbl> 2.20890952, -0.28826057, 0.87124230, -0.31018296,...
$ ztzt18.regionuorf <dbl> -0.47740286, 0.51962430, 0.27241413, -0.24070624,...
$ ztzt21.regionuorf <dbl> -0.260205492, -0.552942982, -0.209648126, 0.00409...
$ SE_Intercept <dbl> 0.1485535, 0.1825827, 0.2049992, 0.1894756, 0.183...
$ SE_ztzt3 <dbl> 0.2125283, 0.2739961, 0.2823478, 0.2479268, 0.256...
$ SE_ztzt6 <dbl> 0.2483501, 0.2731393, 0.2806628, 0.2474942, 0.257...
$ SE_ztzt12 <dbl> 0.6251896, 0.2717729, 0.2798832, 0.2580152, 0.257...
$ SE_ztzt18 <dbl> 0.2148757, 0.2602972, 0.2845776, 0.2580798, 0.258...
$ SE_ztzt21 <dbl> 0.2102887, 0.2592118, 0.2810355, 0.2564683, 0.259...
$ SE_typeribo <dbl> 0.2106727, 0.2677201, 0.2747627, 0.2584790, 0.259...
$ SE_regionuorf <dbl> 0.2129016, 0.4005090, 0.4525055, 0.3117991, 0.390...
$ SE_ztzt3.typeribo <dbl> 0.3122130, 0.4313572, 0.3819825, 0.3555601, 0.369...
$ SE_ztzt6.typeribo <dbl> 0.4187254, 0.4314032, 0.3810870, 0.3566123, 0.371...
$ SE_ztzt12.typeribo <dbl> 1.2156682, 0.4064987, 0.3793255, 0.3697005, 0.366...
$ SE_ztzt18.typeribo <dbl> 0.3140455, 0.3776866, 0.3851173, 0.3697246, 0.367...
$ SE_ztzt21.typeribo <dbl> 0.2984556, 0.3768117, 0.3821253, 0.3595588, 0.369...
$ SE_ztzt3.regionuorf <dbl> 0.3322606, 0.6704092, 0.5674956, 0.4392189, 0.572...
$ SE_ztzt6.regionuorf <dbl> 0.5236905, 0.6837858, 0.5746274, 0.4547769, 0.543...
$ SE_ztzt12.regionuorf <dbl> 1.3519478, 0.7071246, 0.5648718, 0.5182609, 0.542...
$ SE_ztzt18.regionuorf <dbl> 0.3635974, 0.5301768, 0.6316568, 0.5125685, 0.565...
$ SE_ztzt21.regionuorf <dbl> 0.3031744, 0.5875419, 0.6643201, 0.4535879, 0.575...
$ LRTStatistic <dbl> 22.033045, 8.118942, 9.559685, 5.335670, 5.658612...
$ LRTPvalue <dbl> 0.0005160788, 0.1498011548, 0.0887171430, 0.37630...
$ padj <dbl> 0.01033260, 0.40627189, 0.30957780, 0.64748059, 0...

```

```

coefs <-
  c("intercept", "zt3", "zt6", "zt12", "zt18", "zt21",
    "ribo", "uorf",
    paste0("te_", c("zt3", "zt6", "zt12", "zt18", "zt21")),
    paste0("uorf_", c("zt3", "zt6", "zt12", "zt18", "zt21")))
  ) %>%
  paste0("coef_", .)
ses <- coefs %>% stringr::str_replace("^coef_", "se_")
colnames(tbl_out) <-
  c("AGI", "baseMean", "baseVar", coefs, ses, "stat_LRT", "pvalue", "padj")

readr::write_csv(tbl_out, path_out("deg_all.csv"))
readr::write_csv(ngsmisc::ds2dds_get_normalized_count_tbl(dds, "AGI"), path_out("nc.csv"))

```

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] MatrixGenerics_1.8.1      Biobase_2.56.0
 [3] httr_1.4.5                splines_4.2.1
 [5] bit64_4.0.5              vroom_1.6.0
 [7] jsonlite_1.8.4           here_1.0.1
 [9] BiocManager_1.30.18      stats4_4.2.1
[11] blob_1.2.3               renv_1.0.3
[13] GenomeInfoDbData_1.2.8   yaml_2.3.6
[15] pillar_1.9.0             RSQLite_2.2.18
[17] lattice_0.20-45          glue_1.6.2
[19] digest_0.6.31            RColorBrewer_1.1-3
[21] GenomicRanges_1.48.0     XVector_0.36.0
[23] colorspace_2.0-3         htmltools_0.5.3
[25] Matrix_1.6-4             DESeq2_1.36.0
[27] XML_3.99-0.11            pkgconfig_2.0.3
[29] genefilter_1.78.0        zlibbioc_1.42.0
[31] purrr_1.0.1              xtable_1.8-4
[33] scales_1.2.1             tzdb_0.3.0
[35] BiocParallel_1.30.4      tibble_3.2.1
[37] annotate_1.74.0          KEGGREST_1.36.3
[39] generics_0.1.3           IRanges_2.30.1
[41] cachem_1.0.6            withr_2.5.0
[43] SummarizedExperiment_1.26.1 BiocGenerics_0.42.0
[45] cli_3.6.0               survival_3.3-1
[47] crayon_1.5.2            memoise_2.0.1
[49] evaluate_0.20           fs_1.5.2
[51] fansi_1.0.3             forcats_1.0.0
[53] tools_4.2.1             hms_1.1.3
[55] lifecycle_1.0.3         matrixStats_0.62.0
[57] stringr_1.5.0           S4Vectors_0.34.0
[59] locfit_1.5-9.6          munsell_0.5.0
[61] DelayedArray_0.22.0     Biostrings_2.64.1
[63] AnnotationDbi_1.58.0    compiler_4.2.1
[65] GenomeInfoDb_1.32.4     rlang_1.1.0
[67] grid_4.2.1              RCurl_1.98-1.9
[69] rstudioapi_0.14         ngsmisc_0.4.0
[71] bitops_1.0-7            rmarkdown_2.24
[73] gtable_0.3.1           codetools_0.2-18
[75] DBI_1.1.3              R6_2.5.1
[77] knitr_1.42             dplyr_1.1.1
[79] fastmap_1.1.0          bit_4.0.5
[81] utf8_1.2.2             rprojroot_2.0.3
[83] readr_2.1.4            stringi_1.7.12
[85] parallel_4.2.1         Rcpp_1.0.11
[87] geneplotter_1.74.0      png_0.1-7

```

```
[89] vctrs_0.6.1      tidyselect_1.2.0  
[91] xfun_0.40
```