Proteomics Heart Ventricle Cox7a KO- Garcia-Poyotas, 2024

AUTHOR
Prateek Arora

PUBLISHED
January 24, 2024

1 Clear Memory, set working directory, load packages

▶ Code

A matrix: 2 × 6 of type dbl

	used	(Mb)	gc trigger	(Mb)	max used	(Mb)
Ncells	636862	34.1	1411237	75.4	1085459	58.0
Vcells	1181812	9.1	8388608	64.0	1815676	13.9

'/mnt/Data_8TB/Carolina_data/Cell_paper'

▶ Code

```
── Attaching core tidyverse packages ──────────────────── tidyverse 2.0.0 ──
✔ dplyr     1.1.2     ✔ readr     2.1.4
✔ forcats   1.0.0     ✔ stringr   1.5.0
✔ ggplot2   3.4.2     ✔ tibble    3.2.1
✔ lubridate 1.9.2     ✔ tidyr     1.3.0
✔ purrr     1.0.1
── Conflicts ──────────────────────────────────── tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to
become errors
```

```
clusterProfiler v4.8.1  For help: https://yulab-smu.top/biomedical-knowledge-mining-
book/

If you use clusterProfiler in published research, please cite:
T Wu, E Hu, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X
Bo, and G Yu. clusterProfiler 4.0: A universal enrichment tool for interpreting omics
data. The Innovation. 2021, 2(3):100141


Attaching package: 'clusterProfiler'


The following object is masked from 'package:purrr':

    simplify
```

The following object is masked from 'package:stats':

    filter

Loading required package: AnnotationDbi

Loading required package: stats4

Loading required package: BiocGenerics

Attaching package: 'BiocGenerics'

The following objects are masked from 'package:lubridate':

    intersect, setdiff, union

The following objects are masked from 'package:dplyr':

    combine, intersect, setdiff, union

The following objects are masked from 'package:stats':

    IQR, mad, sd, var, xtabs

The following objects are masked from 'package:base':

    anyDuplicated, aperm, append, as.data.frame, basename, cbind,
    colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
    get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
    match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
    Position, rank, rbind, Reduce, rownames, sapply, setdiff, sort,
    table, tapply, union, unique, unsplit, which.max, which.min

Loading required package: Biobase

Welcome to Bioconductor

    Vignettes contain introductory material; view with
    'browseVignettes()'. To cite Bioconductor, see
    'citation("Biobase")', and for packages 'citation("pkgname")'.

Loading required package: IRanges

Loading required package: S4Vectors

Attaching package: 'S4Vectors'

The following object is masked from 'package:clusterProfiler':

    rename

The following objects are masked from 'package:lubridate':

    second, second<-

The following objects are masked from 'package:dplyr':

    first, rename

The following object is masked from 'package:tidyr':

    expand

The following object is masked from 'package:utils':

    findMatches

The following objects are masked from 'package:base':

    expand.grid, I, unname

Attaching package: 'IRanges'

The following object is masked from 'package:clusterProfiler':

    slice

The following object is masked from 'package:lubridate':

    %within%

The following objects are masked from 'package:dplyr':

    collapse, desc, slice

The following object is masked from 'package:purrr':

```
    reduce


Attaching package: 'AnnotationDbi'


The following object is masked from 'package:clusterProfiler':

    select


The following object is masked from 'package:dplyr':

    select




Loading required package: grid

========================================
ComplexHeatmap version 2.16.0
Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/
Github page: https://github.com/jokergoo/ComplexHeatmap
Documentation: http://jokergoo.github.io/ComplexHeatmap-reference

If you use it in published research, please cite either one:
- Gu, Z. Complex Heatmap Visualization. iMeta 2022.
- Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional
    genomic data. Bioinformatics 2016.


The new InteractiveComplexHeatmap package can directly export static
complex heatmaps into an interactive Shiny app with zero effort. Have a try!

This message can be suppressed by:
  suppressPackageStartupMessages(library(ComplexHeatmap))
========================================



Attaching package: 'limma'


The following object is masked from 'package:BiocGenerics':

    plotMA
```

2 Load data and perform Limma analysis

A data.frame: 6 × 10

	protein	KO1	KO2	KO3	WT1	WT2	WT3
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
ece2b	A0A024B5K5	-1.1941835	-0.2506414	-1.70543961	-2.03512879	0.2338551	-0.143739
plxna3	A0A0A0MPG5	-0.6901571	-0.3534482	-1.22659009	1.29660601	-1.0030470	-1.167046
fscn1b	A0A0A0MPL5	2.0097387	-0.5939624	0.04846747	-1.15162119	-1.7366124	-0.158380
si:ch211-22k7.9	A0A0A0MPR3	0.6794696	-0.7174569	-0.17531474	-1.50924571	0.8886631	-0.494296
aasdh	A0A0A0MPS9	-3.1809933	1.2959482	-2.96366964	-0.05643476	-0.8573626	5.390621!
ewsr1a	A0A0B4J1A5	-0.8354951	0.5101992	-0.18884247	-1.62514144	-2.4937632	-0.287050(

A matrix: 6 × 6 of type dbl

	KO1	KO2	KO3	WT1	WT2	WT3
ece2b	-1.1941835	-0.2506414	-1.70543961	-2.03512879	0.2338551	-0.1437395
plxna3	-0.6901571	-0.3534482	-1.22659009	1.29660601	-1.0030470	-1.1670465
fscn1b	2.0097387	-0.5939624	0.04846747	-1.15162119	-1.7366124	-0.1583802
si:ch211-22k7.9	0.6794696	-0.7174569	-0.17531474	-1.50924571	0.8886631	-0.4942965
aasdh	-3.1809933	1.2959482	-2.96366964	-0.05643476	-0.8573626	5.3906215
ewsr1a	-0.8354951	0.5101992	-0.18884247	-1.62514144	-2.4937632	-0.2870502

A data.frame: 6 × 2

samples	group
<chr>	<chr>
KO1	KO
KO2	KO
KO3	KO
WT1	WT
WT2	WT
WT3	WT

A matrix: 6 × 2 of type dbl

	KO	WT
1	1	0
2	1	0
3	1	0
4	0	1
5	0	1
6	0	1

```
An object of class "MArrayLM"
$coefficients
                        KO          WT
ece2b           -1.05008817 -0.6483377
plxna3          -0.75673181 -0.2911625
fscn1b           0.48808127 -1.0155379
si:ch211-22k7.9 -0.07110069 -0.3716264
aasdh           -1.61623825  1.4922747
ewsr1a          -0.17137945 -1.4686516

$rank
[1] 2

$assign
[1] 1 1

$qr
$qr
          KO          WT
1 -1.7320508  0.0000000
2  0.5773503 -1.7320508
3  0.5773503  0.0000000
4  0.0000000  0.5773503
5  0.0000000  0.5773503
6  0.0000000  0.5773503
attr(,"assign")
[1] 1 1
attr(,"contrasts")
attr(,"contrasts")$`metadata$group`
[1] "contr.treatment"


$qraux
[1] 1.57735 1.00000

$pivot
[1] 1 2
```

```
$tol
[1] 1e-07

$rank
[1] 2

$df.residual
[1] 4 4 4 4 4 4

$sigma
          ece2b          plxna3          fscn1b si:ch211-22k7.9          aasdh
      1.0056636       1.0225945       1.1127339       0.9860968       2.9942137
         ewsr1a
      0.9188891

$cov.coefficients
          KO          WT
KO 0.3333333 0.0000000
WT 0.0000000 0.3333333

$stdev.unscaled
                          KO          WT
ece2b            0.5773503 0.5773503
plxna3           0.5773503 0.5773503
fscn1b           0.5773503 0.5773503
si:ch211-22k7.9 0.5773503 0.5773503
aasdh            0.5773503 0.5773503
ewsr1a           0.5773503 0.5773503

$pivot
[1] 1 2

$Amean
          ece2b          plxna3          fscn1b si:ch211-22k7.9          aasdh
     -0.84921294     -0.52394715     -0.26372834     -0.22136353     -0.06198176
         ewsr1a
     -0.82001552

$method
[1] "ls"

$design
  KO WT
1  1  0
2  1  0
3  1  0
4  0  1
5  0  1
6  0  1
attr(,"assign")
[1] 1 1
attr(,"contrasts")
attr(,"contrasts")$`metadata$group`
```

```
[1] "contr.treatment"
```

▶ Code

A matrix: 2 × 1 of type dbl

	ko_vs_wt
KO	1
WT	-1

▶ Code

A data.frame: 6 × 4

	gene	ko_vs_wt_logFC	ko_vs_wt_P.Value	ko_vs_wt_adj.P.Val
	<chr>	<dbl>	<dbl>	<dbl>
1	ndufa4a	-7.513439	1.147101e-05	0.0483962
2	cox5ab	-3.924994	2.120659e-04	0.3256911
3	twf2	3.580944	3.250880e-04	0.3256911
4	bloc1s6	-4.260404	4.055141e-04	0.3256911
5	ank2b_1	3.590296	5.255563e-04	0.3256911
6	prdx6	-3.553210	6.231779e-04	0.3256911

▶ Code

4219 · 12

4219 · 4

A data.frame: 6 × 12

	gene	protein	KO1	KO2	KO3	WT1	WT2	WT3
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	44986	A0A2R8PWS6	0.1545013	0.94989998	0.1845100	0.2563195	0.2193404	1.24941529
2	45171	F1QW60	-0.6527151	0.19627087	-0.2632826	-0.3947994	0.7537580	0.09811806
3	45175	F1R3Q3	-0.4547053	-0.11640637	-0.1106835	0.3867737	-0.4108361	-0.1190836
4	45179	Q568B3	0.3430870	0.62495576	0.5810429	-0.8501196	-0.1761369	0.05073808
5	45184	A0JMF4	2.3908417	0.04751272	0.9208836	1.5454670	1.6800118	-0.0140980
6	a2ml	F6NTZ9	0.1247026	-0.62873965	-2.2726963	4.7372387	-2.6636864	-2.7735242

▶ Code

3 Pathway Analysis

3.1 Overrepresentation Analysis

▶ Code

▶ Code

▶ Code

```
Loading required package: biomaRt
```

```
  EnsmblID_Zebrafish ZFIN.symbol MGI.symbol     EnsmblID_Mouse
1 ENSDARG00000052674      csnk1a1    Csnk1a1 ENSMUSG00000024576
2 ENSDARG00000076393       tmem65     Tmem65 ENSMUSG00000062373
3 ENSDARG00000093945        vma21      Vma21 ENSMUSG00000073131
4 ENSDARG00000016319           c9         C9 ENSMUSG00000022149
5 ENSDARG00000019332       ndufb4     Ndufb4 ENSMUSG00000022820
6 ENSDARG00000040712         adprh      Adprh ENSMUSG00000002844
                                                        Gene.description
1                      casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]
2                       transmembrane protein 65 [Source:MGI Symbol;Acc:MGI:1922118]
3 VMA21 vacuolar H+-ATPase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914298]
4                         complement component 9 [Source:MGI Symbol;Acc:MGI:1098282]
5         NADH:ubiquinone oxidoreductase subunit B4 [Source:MGI Symbol;Acc:MGI:1915444]
6                     ADP-ribosylarginine hydrolase [Source:MGI Symbol;Acc:MGI:1098234]
```

A data.frame: 6 × 5

	EnsmblID_Zebrafish	ZFIN.symbol	MGI.symbol	EnsmblID_Mouse	Gene.description
	<chr>	<chr>	<chr>	<chr>	<chr>
1	ENSDARG00000052674	csnk1a1	Csnk1a1	ENSMUSG00000024576	casein kinase 1, alpha [Source:MGI Symbol;Acc:MGI:1934
2	ENSDARG00000076393	tmem65	Tmem65	ENSMUSG00000062373	transmembrane prote [Source:MGI Symbol;Acc:MGI:192:
3	ENSDARG00000093945	vma21	Vma21	ENSMUSG00000073131	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae) [Source:M(Symbol;Acc:MGI:1914
4	ENSDARG00000016319	c9	C9	ENSMUSG00000022149	complement compone [Source:MGI Symbol;Acc:MGI:109%
5	ENSDARG00000019332	ndufb4	Ndufb4	ENSMUSG00000022820	NADH:ubiquinone oxidoreductase subun [Source:MGI Symbol;Acc:MGI:191!
6	ENSDARG00000040712	adprh	Adprh	ENSMUSG00000002844	ADP-ribosylarginine hydrolase [Source:M(

EnsmblID_Zebrafish	ZFIN.symbol	MGI.symbol	EnsmblID_Mouse	Gene.description
<chr>	<chr>	<chr>	<chr>	<chr>
				Symbol;Acc:MGI:109

▶ Code

▶ Code

'/mnt/Data_8TB/Carolina_data/Cell_paper'

▶ Code

```
Warning message in
dir.create("./proteomics_n_3_ventricle_technical_avg/GO_analysis/Moleuclar_Function",
:
"'./proteomics_n_3_ventricle_technical_avg/GO_analysis/Moleuclar_Function' already
exists"
Warning message in
dir.create("./proteomics_n_3_ventricle_technical_avg/GO_analysis/Cellular_Components",
:
"'./proteomics_n_3_ventricle_technical_avg/GO_analysis/Cellular_Components' already
exists"
Warning message in
dir.create("./proteomics_n_3_ventricle_technical_avg/GO_analysis/Biological_Process",
:
"'./proteomics_n_3_ventricle_technical_avg/GO_analysis/Biological_Process' already
exists"
Warning message in
dir.create("./proteomics_n_3_ventricle_technical_avg/GO_analysis/Reactome", :
"'./proteomics_n_3_ventricle_technical_avg/GO_analysis/Reactome' already exists"
ReactomePA v1.44.0  For help: https://yulab-smu.top/biomedical-knowledge-mining-book/

If you use ReactomePA in published research, please cite:
Guangchuang Yu, Qing-Yu He. ReactomePA: an R/Bioconductor package for reactome pathway
analysis and visualization. Molecular BioSystems 2016, 12(2):477-479

Pathway analysis GO:MF for Cell Type :  done

****************************************************************************************
**




Pathway analysis GO:CC for Cell Type :  done

****************************************************************************************
**
```
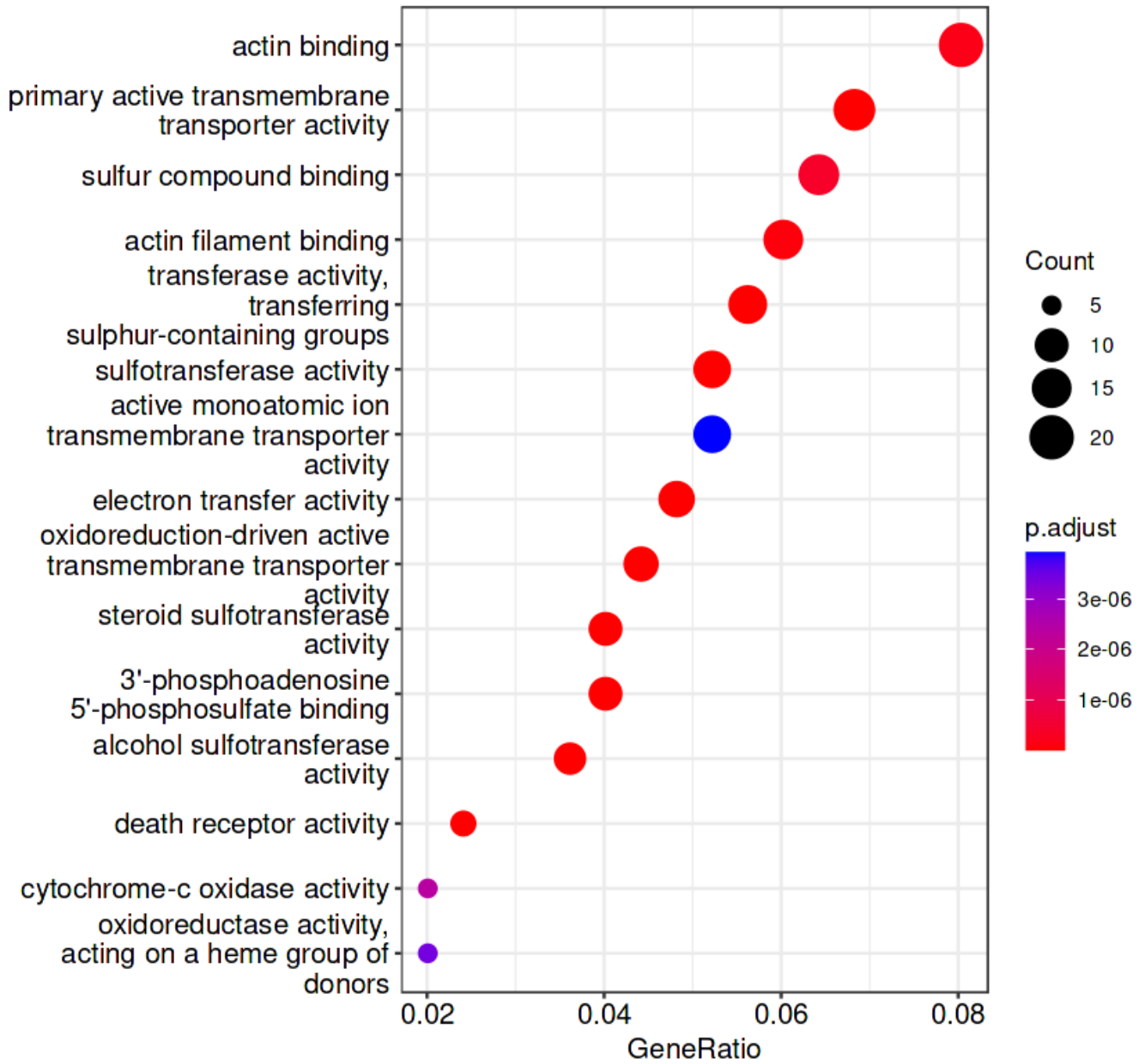
GO Pathway Enrichment Analysis
Moleuclar Function

Pathway analysis GO:BP for Cell Type : done

****
**

GO Pathway Enrichment Analysis
Cellular Components
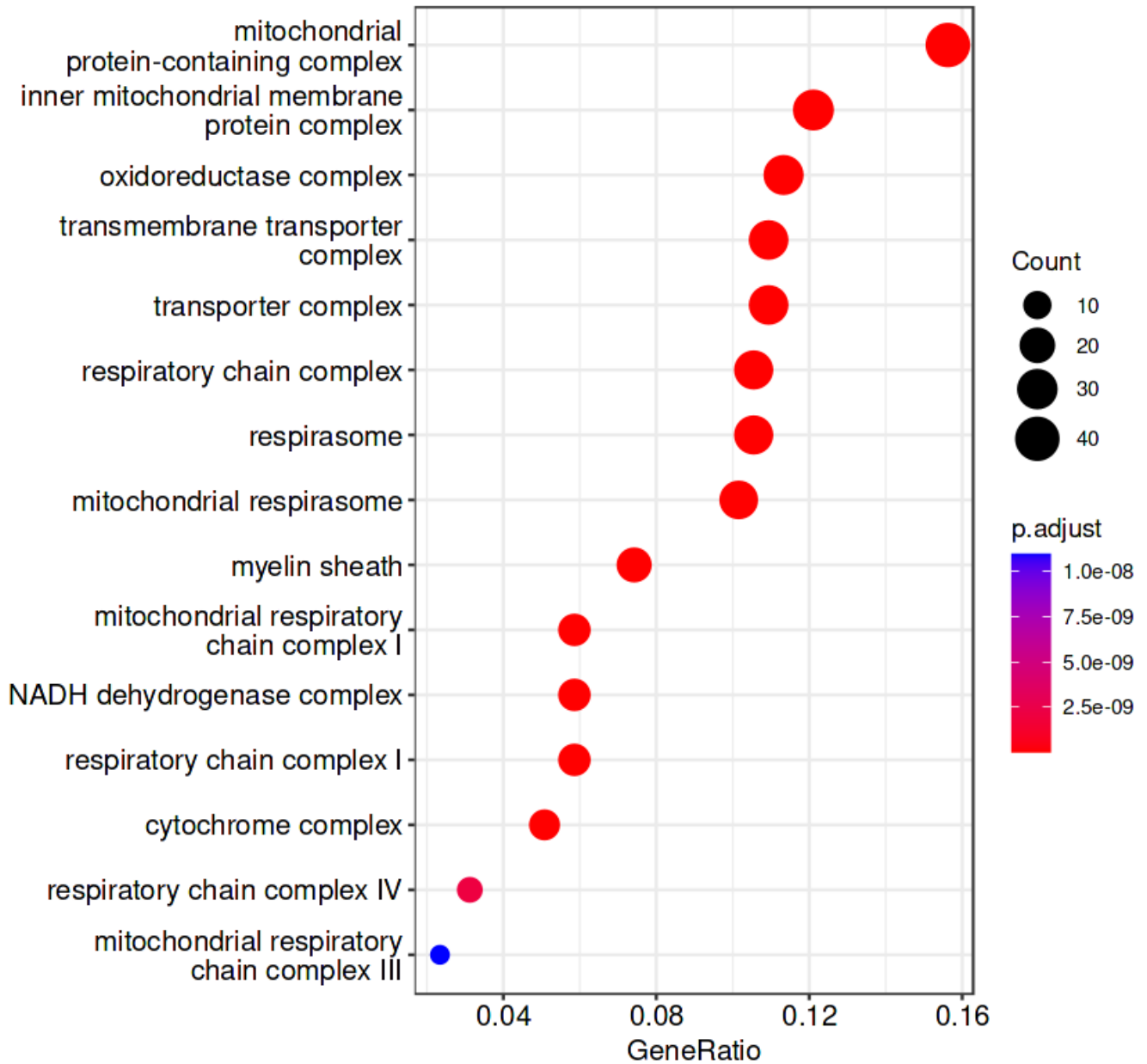
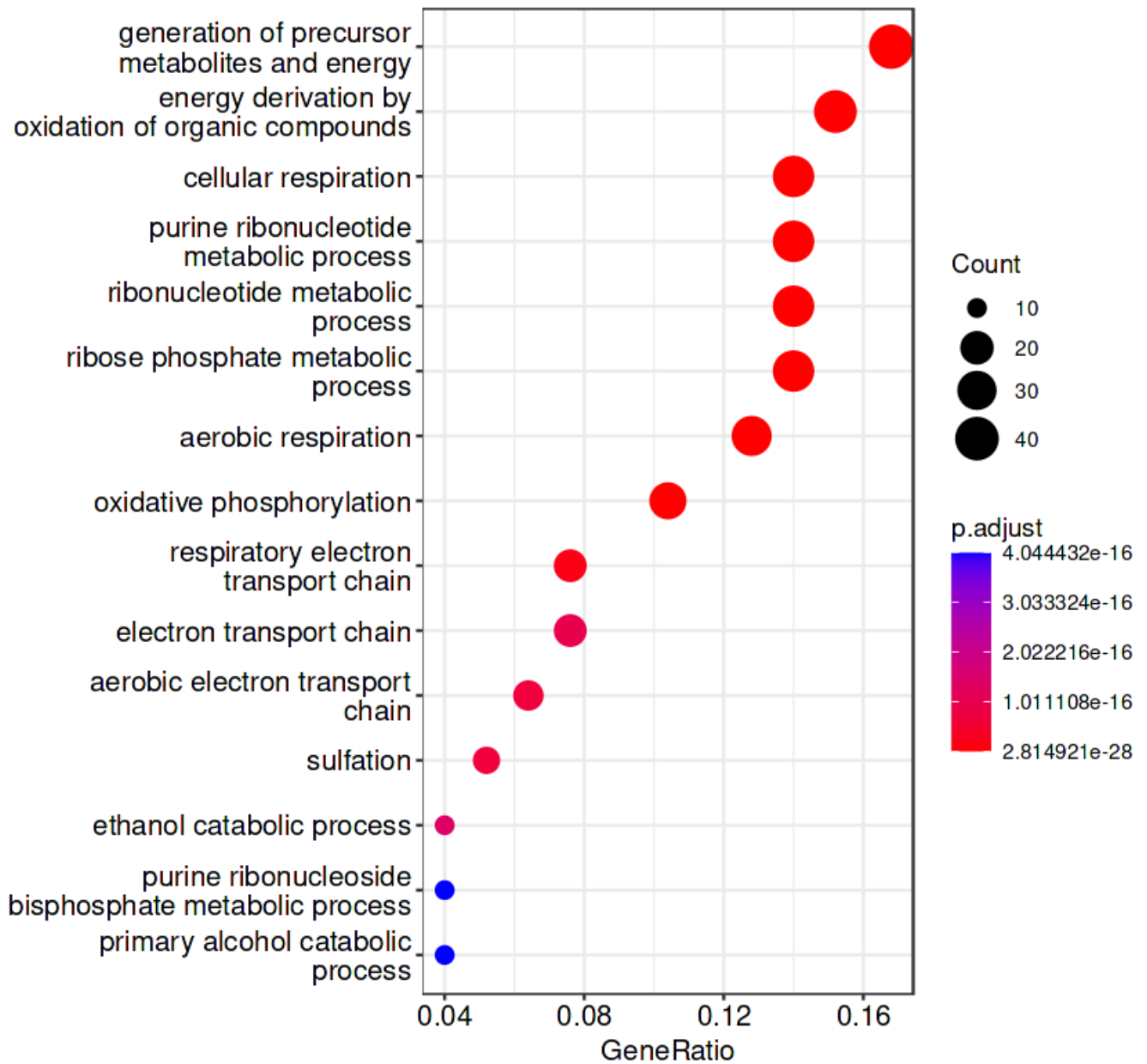'select()' returned 1:1 mapping between keys and columns

Warning message in bitr(gene_list, fromType = "SYMBOL", toType = "ENTREZID", OrgDb = orgdb):
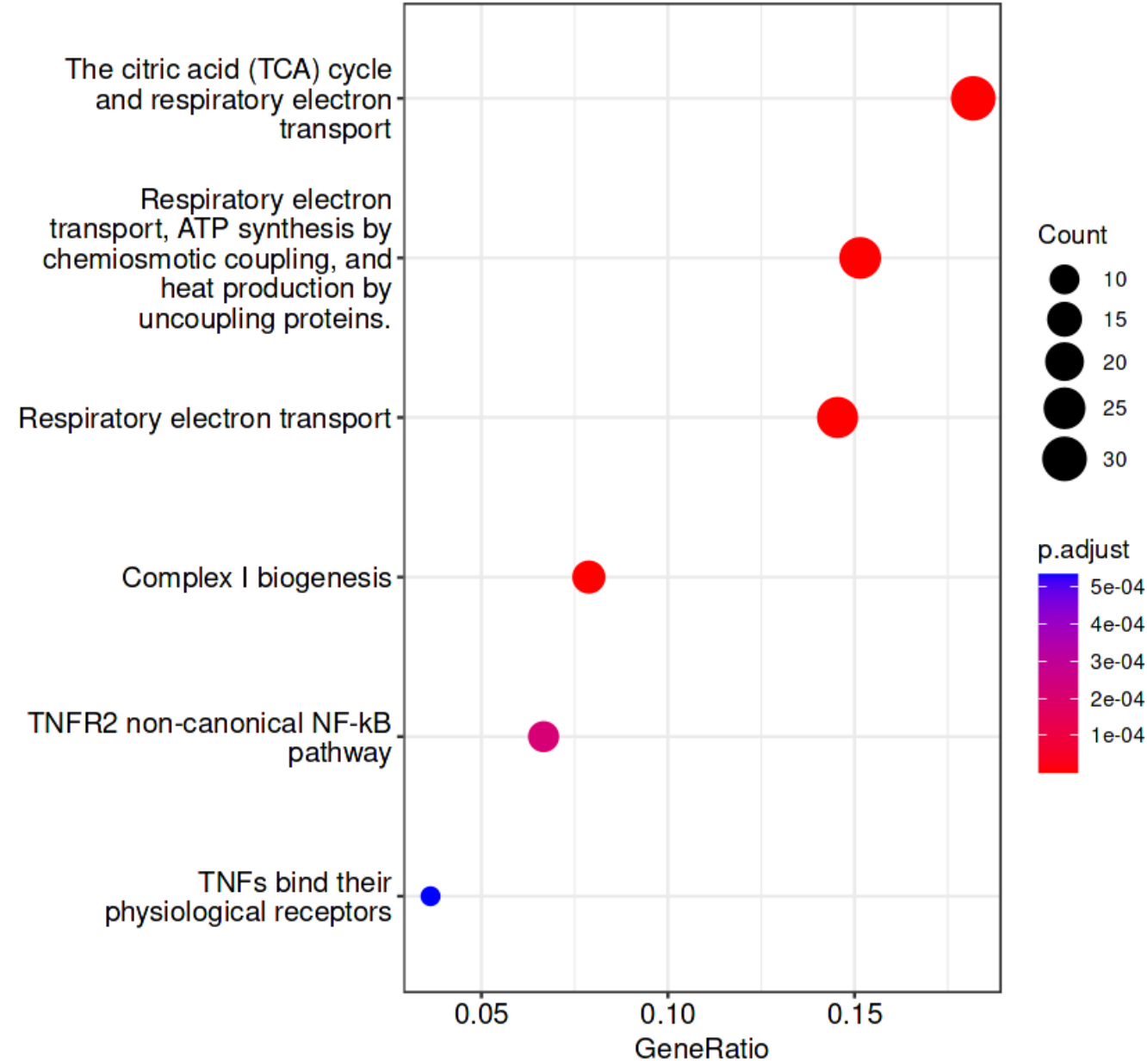"1.14% of input gene IDs are fail to map..."
Pathway analysis GO:reactome for Cell Type : done

****
**

GO Pathway Enrichment Analysis
Biological Pathways

GO Pathway Enrichment Analysis
Reactome Pathways

▶ Code

A data.frame: 6 × 12

	gene	protein	KO1	KO2	KO3	WT1	WT2	WT3	NOP
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
18	abcb4	E7F1E3	1.7525085	1.7090815	1.978427	1.1078013	0.5348448	-0.81522116	10
53	ace	E7FFA5	1.6871115	1.0844029	2.288098	0.3588941	-0.2542683	-0.21695543	2
57	aco2	F8W4M7	2.5830499	7.0838927	6.014105	1.0510744	-1.5396532	2.11937458	3
81	actbb	Q7ZVF9	0.2352243	0.6041838	1.538134	-2.3004842	-0.5111959	-0.02033702	16
83	actc1a	Q6IQR3	0.8865733	1.3519529	2.040819	-0.1322955	0.8073278	-1.34496843	39
87	actn4	H9GX78	1.3914703	0.6613983	1.547322	-1.3435473	-0.1823949	-0.98224993	2

180 · 12

▶ Code

A data.frame: 6 × 12

	gene	protein	KO1	KO2	KO3	WT1	WT2	WT3
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
167	alad	A0A0R4IPV1	-1.8937150	-0.5833043	-1.4975788	0.672693	0.6583896	0.23791
183	aldh9a1b	Q802W2	-1.0758477	-4.2714832	-5.1340732	-2.182588	1.8254340	0.74382
328	ass1	Q66I24	-5.1539131	-13.8782872	-10.1274136	3.102007	1.6143561	-2.8702
349	atp2a1l	A0JMP4	-0.6378300	-1.0112399	-1.0630356	1.619401	1.4437790	-0.3482
352	atp2a3	A2BIP1	-0.2727453	-1.6609984	-0.9738952	1.283634	-0.3407920	0.83831
356	atp5f1d	Q1LVG7	-0.8699470	-4.3085576	-2.1564179	1.304702	1.9223411	-1.5032

132 · 12

▶ Code

A data.frame: 6 × 12

	gene	protein	KO1	KO2	KO3	WT1	WT2	WT3	NOP
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
18	abcb4	E7F1E3	1.7525085	1.7090815	1.978427	1.1078013	0.5348448	-0.81522116	10
53	ace	E7FFA5	1.6871115	1.0844029	2.288098	0.3588941	-0.2542683	-0.21695543	2
57	aco2	F8W4M7	2.5830499	7.0838927	6.014105	1.0510744	-1.5396532	2.11937458	3
81	actbb	Q7ZVF9	0.2352243	0.6041838	1.538134	-2.3004842	-0.5111959	-0.02033702	16
83	actc1a	Q6IQR3	0.8865733	1.3519529	2.040819	-0.1322955	0.8073278	-1.34496843	39
87	actn4	H9GX78	1.3914703	0.6613983	1.547322	-1.3435473	-0.1823949	-0.98224993	2

▶ Code
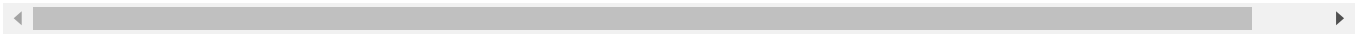
▶ Code

```
  EnsmblID_Zebrafish ZFIN.symbol MGI.symbol     EnsmblID_Mouse
1 ENSDARG00000041314     ndufb9     Ndufb9 ENSMUSG00000022354
2 ENSDARG00000093945     vma21      Vma21 ENSMUSG00000073131
3 ENSDARG00000019332     ndufb4     Ndufb4 ENSMUSG00000022820
4 ENSDARG00000052674    csnk1a1    Csnk1a1 ENSMUSG00000024576
5 ENSDARG00000040712      adprh      Adprh ENSMUSG00000002844
6 ENSDARG00000038978     dnajb4     Dnajb4 ENSMUSG00000028035
                                                    Gene.description
1         NADH:ubiquinone oxidoreductase subunit B9 [Source:MGI Symbol;Acc:MGI:1913468]
2 VMA21 vacuolar H+-ATPase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914298]
3         NADH:ubiquinone oxidoreductase subunit B4 [Source:MGI Symbol;Acc:MGI:1915444]
```

```
4                        casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]
5                        ADP-ribosylarginine hydrolase [Source:MGI Symbol;Acc:MGI:1098234]
6 DnaJ heat shock protein family (Hsp40) member B4 [Source:MGI Symbol;Acc:MGI:1914285]
```

A data.frame: 6 × 5

	EnsmblID_Zebrafish	ZFIN.symbol	MGI.symbol	EnsmblID_Mouse	Gene.description
	<chr>	<chr>	<chr>	<chr>	<chr>
1	ENSDARG00000041314	ndufb9	Ndufb9	ENSMUSG00000022354	NADH:ubiquinone oxidoreductase subun [Source:MGI Symbol;Acc:MGI:1913
2	ENSDARG00000093945	vma21	Vma21	ENSMUSG00000073131	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914
3	ENSDARG00000019332	ndufb4	Ndufb4	ENSMUSG00000022820	NADH:ubiquinone oxidoreductase subun [Source:MGI Symbol;Acc:MGI:1915
4	ENSDARG00000052674	csnk1a1	Csnk1a1	ENSMUSG00000024576	casein kinase 1, alpha [Source:MGI Symbol;Acc:MGI:1934
5	ENSDARG00000040712	adprh	Adprh	ENSMUSG00000002844	ADP-ribosylarginine hydrolase [Source:MGI Symbol;Acc:MGI:1098
6	ENSDARG00000038978	dnajb4	Dnajb4	ENSMUSG00000028035	DnaJ heat shock prote family (Hsp40) membe [Source:MGI Symbol;Acc:MGI:1914

▶ Code

```
  EnsmblID_Zebrafish ZFIN.symbol MGI.symbol     EnsmblID_Mouse
1 ENSDARG00000016319          c9         C9 ENSMUSG00000022149
2 ENSDARG00000042172         c7a         C7 ENSMUSG00000079105
3 ENSDARG00000076393      tmem65     Tmem65 ENSMUSG00000062373
4 ENSDARG00000009341        nrap       Nrap ENSMUSG00000049134
5 ENSDARG00000101318     pcdh2ab9    Pcdhac2 ENSMUSG00000102697
6 ENSDARG00000044132        ogna        Ogn ENSMUSG00000021390
                                             Gene.description
1          complement component 9 [Source:MGI Symbol;Acc:MGI:1098282]
2          complement component 7 [Source:MGI Symbol;Acc:MGI:88235]
3          transmembrane protein 65 [Source:MGI Symbol;Acc:MGI:1922118]
4  nebulin-related anchoring protein [Source:MGI Symbol;Acc:MGI:1098765]
5 protocadherin alpha subfamily C, 2 [Source:MGI Symbol;Acc:MGI:1891443]
6                 osteoglycin [Source:MGI Symbol;Acc:MGI:109278]
```

A data.frame: 6 × 5

	EnsmblID_Zebrafish	ZFIN.symbol	MGI.symbol	EnsmblID_Mouse	Gene.description
	<chr>	<chr>	<chr>	<chr>	<chr>
1	ENSDARG00000016319	c9	C9	ENSMUSG00000022149	complement compone [Source:MGI Symbol;Acc:MGI:1098
2	ENSDARG00000042172	c7a	C7	ENSMUSG00000079105	complement compone [Source:MGI Symbol;Acc:MGI:882:
3	ENSDARG00000076393	tmem65	Tmem65	ENSMUSG00000062373	transmembrane prote [Source:MGI Symbol;Acc:MGI:192:
4	ENSDARG00000009341	nrap	Nrap	ENSMUSG00000049134	nebulin-related ancho protein [Source:MGI Symbol;Acc:MGI:1098
5	ENSDARG00000101318	pcdh2ab9	Pcdhac2	ENSMUSG00000102697	protocadherin alpha subfamily C, 2 [Source Symbol;Acc:MGI:189:
6	ENSDARG00000044132	ogna	Ogn	ENSMUSG00000021390	osteoglycin [Source:M Symbol;Acc:MGI:1092

▶ Code

3.2 GSEA

▶ Code

▶ Code

'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' · 'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' · 'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' · 'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' · 'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' · 'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'

▶ Code

```
   Usp38    Ywhab   Pcdhac2    Rnf123     Ift74     Decr1
8.898706 8.111737 7.996985 7.558226 7.435486 7.346143


preparing geneSet collections...

GSEA analysis...
```

no term enriched under specific pvalueCutoff...

No GSEA:MF

****
**

```
   Usp38    Ywhab  Pcdhac2   Rnf123    Ift74    Decr1
8.898706 8.111737 7.996985 7.558226 7.435486 7.346143
```

preparing geneSet collections...

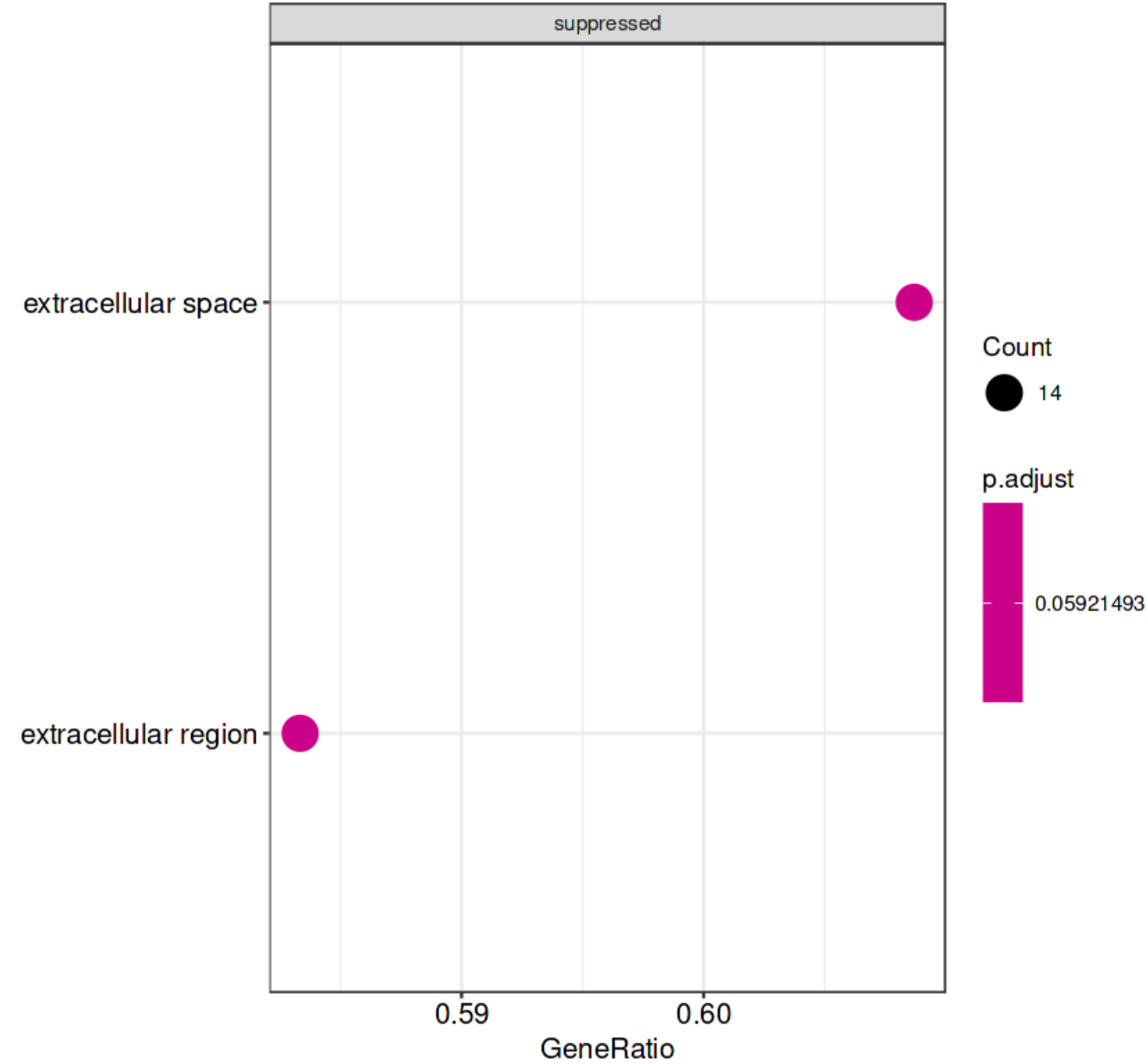GSEA analysis...

leading edge analysis...

done...

[1] "Cellular Components CC"

DEG Pathway analysis GO:CC done

****
**

```
   Usp38    Ywhab  Pcdhac2   Rnf123    Ift74    Decr1
8.898706 8.111737 7.996985 7.558226 7.435486 7.346143
```

preparing geneSet collections...

GSEA analysis...

no term enriched under specific pvalueCutoff...

No GSEA:BP

****
**

DEG GO Pathway Enrichment Analysis
Cellular Components

▶ Code

A tibble: 6 × 2

term	gene
<chr>	<chr>
ABC transporters	Abca9
ABC transporters	Abcb10
ABC transporters	Abcb6
ABC transporters	Abcb7
ABC transporters	Abcb8
ABC transporters	Abcd1

```
   Usp38    Ywhab Pcdhac2   Rnf123    Ift74    Decr1
8.898706 8.111737 7.996985 7.558226 7.435486 7.346143
```

▶ Code

'Decr1' · 'Mthfs' · 'Aco2' · 'Idh3b' · 'Cyc1' · 'Uqcrq' · 'Ndufs8' · 'Bcat2' · 'Uqcr10' · 'Phb' · 'Ndufb7' · 'Etfb' ·
'Adhfe1' · 'Ndufb10' · 'Ndufa10' · 'Ndufb8' · 'Uqcrh' · 'Ndufs5' · 'Cyb5r3' · 'Ndufb4' · 'Mlycd' ·
'Nipsnap2' · 'Ndufb9' · 'Atp23' · 'Uqcrc2' · 'Phb2' · 'Uqcrc1' · 'Ndufa2' · 'Tomm70a' · 'Ndufa3' ·
'Ndufab1' · 'Pdha2' · 'Snap29' · 'Prdx4' · 'Agk' · 'Ndufs6' · 'Mrps36' · 'Chchd6' · 'Sod2' · 'Maip1' · 'Nadk2' ·
'Mrpl22' · 'Bckdhb' · 'Mrpl2' · 'Cox6a2' · 'Tfam' · 'Atp5d' · 'Cox4i1' · 'Aldh1b1' · 'Cox7c' · 'Cox5a' ·
'Ndufa4' · 'Tmem177' · 'Cox6b2'
'Cox7c'
'Cox7a1' · 'Cox7a2' · 'Cox7a2l' · 'Cox7b' · 'Cox7c' · 'Cox7a1' · 'Cox7a2' · 'Cox7a2l' · 'Cox7b' · 'Cox7c' ·
'Cox7a1' · 'Cox7a2' · 'Cox7a2l' · 'Cox7b' · 'Cox7c' · 'Cox7a2l' · 'Cox7a1' · 'Cox7a2' · 'Cox7a2l' · 'Cox7b' ·
'Cox7c' · 'Cox7a2l'

▶ Code

```
preparing geneSet collections...

GSEA analysis...

no term enriched under specific pvalueCutoff...

ERROR: Error in `$<-.data.frame`(`*tmp*`, ".sign", value = "activated"): replacement
has 1 row, data has 0
```

4 Annotations

4.1 Pull annotations from biomart

▶ Code

A data.frame: 6 × 7

	ensembl_gene_id	zfin_id_symbol	description	definition_1006	name_1006	na
	<chr>	<chr>	<chr>	<chr>	<chr>	<c
1	ENSDARG00000056314	a2ml	alpha-2-macroglobulin-like [Source:ZFIN;Acc:ZDB-GENE-090212-1]	Binds to and stops, prevents or reduces the activity of an endopeptidase, any enzyme that hydrolyzes nonterminal	endopeptidase inhibitor activity	m

	ensembl_gene_id	zfin_id_symbol	description	definition_1006	name_1006	na
	<chr>	<chr>	<chr>	<chr>	<chr>	<c
				peptide bonds in polypeptides.		
2	ENSDARG00000056314	a2ml	alpha-2-macroglobulin-like [Source:ZFIN;Acc:ZDB-GENE-090212-1]	That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.	extracellular space	ce
3	ENSDARG00000056314	a2ml	alpha-2-macroglobulin-like [Source:ZFIN;Acc:ZDB-GENE-090212-1]	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.	extracellular region	ce
4	ENSDARG00000103957	aamdc	adipogenesis associated, Mth938 domain containing [Source:ZFIN;Acc:ZDB-GENE-050522-64]			
5	ENSDARG00000069142	aars1	alanyl-tRNA synthetase 1 [Source:ZFIN;Acc:ZDB-GENE-030131-3663]	Binding to a metal ion.	metal ion binding	m

	ensembl_gene_id	zfin_id_symbol	description	definition_1006	name_1006	na
	<chr>	<chr>	<chr>	<chr>	<chr>	<c
6	ENSDARG00000069142	aars1	alanyl-tRNA synthetase 1 [Source:ZFIN;Acc:ZDB-GENE-030131-3663]	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.	ATP binding	m

▶ Code

A tibble: 2 × 6

gene	gene_full_name_zf	GO_description_zf	associated_phenotype_zf	GO_name_zf	GO_family
<chr>	<chr>	<chr>	<chr>	<chr>	<chr>
a2ml	alpha-2-macroglobulin-like [Source:ZFIN;Acc:ZDB-GENE-090212-1]	Binds to and stops, prevents or reduces the activity of an endopeptidase, any enzyme that hydrolyzes nonterminal peptide bonds in polypeptides.; That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.; The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space		endopeptidase inhibitor activity; extracellular space; extracellular region	molecular cellular_co

gene	gene_full_name_zf	GO_description_zf	associated_phenotype_zf	GO_name_zf	GO_family
<chr>	<chr>	<chr>	<chr>	<chr>	<chr>
		outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.			
aamdc	adipogenesis associated, Mth938 domain containing [Source:ZFIN;Acc:ZDB-GENE-050522-64]				

▶ Code

	gene	protein	KO1	KO2	KO3	WT1	WT2	WT3
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	44986	A0A2R8PWS6	0.1545013	0.94989998	0.1845100	0.2563195	0.2193404	1.24941529
2	45171	F1QW60	-0.6527151	0.19627087	-0.2632826	-0.3947994	0.7537580	0.09811806
3	45175	F1R3Q3	-0.4547053	-0.11640637	-0.1106835	0.3867737	-0.4108361	-0.1190836
4	45179	Q568B3	0.3430870	0.62495576	0.5810429	-0.8501196	-0.1761369	0.05073808
5	45184	A0JMF4	2.3908417	0.04751272	0.9208836	1.5454670	1.6800118	-0.0140980
6	a2ml	F6NTZ9	0.1247026	-0.62873965	-2.2726963	4.7372387	-2.6636864	-2.7735242

gene	protein	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>

▶ Code

▶ Code

```
  EnsmblID_Zebrafish ZFIN.symbol MGI.symbol     EnsmblID_Mouse
1 ENSDARG00000063911     mt-atp6    mt-Atp6 ENSMUSG00000064357
2 ENSDARG00000063921     mt-nd5     mt-Nd5 ENSMUSG00000064367
3 ENSDARG00000063908     mt-co2     mt-Co2 ENSMUSG00000064354
4 ENSDARG00000038780       ubtfl           ENSMUSG00000094915
5 ENSDARG00000038780       ubtfl           ENSMUSG00000094514
6 ENSDARG00000063895     mt-nd1     mt-Nd1 ENSMUSG00000064341
                                                      Gene.description
1         mitochondrially encoded ATP synthase 6 [Source:MGI Symbol;Acc:MGI:99927]
2     mitochondrially encoded NADH dehydrogenase 5 [Source:MGI Symbol;Acc:MGI:102496]
3 mitochondrially encoded cytochrome c oxidase II [Source:MGI Symbol;Acc:MGI:102503]
4
5
6     mitochondrially encoded NADH dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:101787]
```

'EnsmblID_Zebrafish' · 'ZFIN.symbol' · 'MGI.symbol' · 'EnsmblID_Mouse' · 'Gene.description'

▶ Code

A data.frame: 6 × 6

	mgi_symbol	description	definition_1006	name_1006	namespace_1003	phen
	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>
1	Acsf2	acyl-CoA synthetase family member 2 [Source:MGI Symbol;Acc:MGI:2388287]	A semiautonomous, self replicating organelle that occurs in varying numbers, shapes, and sizes in the cytoplasm of virtually all eukaryotic cells. It is notably the site of tissue respiration.	mitochondrion	cellular_component	abno beha
2	Acsf2	acyl-CoA synthetase family member 2 [Source:MGI Symbol;Acc:MGI:2388287]	The chemical reactions and pathways involving lipids, compounds soluble in an organic solvent but not, or sparingly, in an aqueous solvent. Includes fatty acids; neutral fats, other fatty-acid esters, and soaps; long-chain (fatty) alcohols and waxes; sphingoids and other long-chain bases; glycolipids, phospholipids and sphingolipids; and carotenes, polyprenols, sterols, terpenes and other isoprenoids.	lipid metabolic process	biological_process	abno beha
3	Acsf2	acyl-CoA synthetase family member 2 [Source:MGI	Binding to a nucleotide, any	nucleotide binding	molecular_function	abno beha

	mgi_symbol	description	definition_1006	name_1006	namespace_1003	phen
	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>
		Symbol;Acc:MGI:2388287]	compound consisting of a nucleoside that is esterified with (ortho)phosphate or an oligophosphate at any hydroxyl group on the ribose or deoxyribose.			
4	Acsf2	acyl-CoA synthetase family member 2 [Source:MGI Symbol;Acc:MGI:2388287]	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.	ATP binding	molecular_function	abnor beha
5	Acsf2	acyl-CoA synthetase family member 2 [Source:MGI Symbol;Acc:MGI:2388287]	Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzymes possess specific binding sites for substrates, and are usually composed wholly or largely of	catalytic activity	molecular_function	abnor beha

	mgi_symbol	description	definition_1006	name_1006	namespace_1003	phenc
	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>
			protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic.			
6	Acsf2	acyl-CoA synthetase family member 2 [Source:MGI Symbol;Acc:MGI:2388287]	Catalysis of the joining of two molecules, or two groups within a single molecule, using the energy from the hydrolysis of ATP, a similar triphosphate, or a pH gradient.	ligase activity	molecular_function	abnor behav

▶ Code

'MGI.symbol' · 'EnsmblID_Zebrafish' · 'ZFIN.symbol' · 'EnsmblID_Mouse' · 'Gene.description' · 'description' · 'definition_1006' · 'name_1006' · 'namespace_1003' · 'phenotype_description'
`summarise()` has grouped output by 'ZFIN.symbol'. You can override using the `.groups` argument.

'ZFIN.symbol' · 'MGI.symbol' · 'description' · 'definition_1006' · 'phenotype_description' · 'name_1006' · 'namespace_1003'

A grouped_df: 2 × 7

| gene_zf	gene_mouse	gene_full_name_mouse	GO_description_mouse	associated_phenotype_mous
<chr>	<chr>	<chr>	<chr>	<chr>
a2ml	A2ml1	alpha-2-macroglobulin like 1 [Source:MGI Symbol;Acc:MGI:3039594]	A location, relative to cellular compartments and structures, occupied by a macromolecular machine when it carries out a molecular function. There are two ways in which the gene ontology describes locations of gene	abnormal sternum morphology; preweaning lethality incomplete penetrance; abnormal spleen morphology

gene_zf	gene_mouse	gene_full_name_mouse	GO_description_mouse	associated_phenotype_mous
<chr>	<chr>	<chr>	<chr>	<chr>
			products: (1) relative to cellular structures (e.g., cytoplasmic side of plasma membrane) or compartments (e.g., mitochondrion), and (2) the stable macromolecular complexes of which they are parts (e.g., the ribosome).; Binds to and stops, prevents or reduces the activity of an endopeptidase, any enzyme that hydrolyzes nonterminal peptide bonds in polypeptides.; That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.; The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.; Binds to and stops, prevents or reduces the activity of a peptidase, any enzyme that catalyzes the hydrolysis peptide bonds.; Any process that stops or reduces	

gene_zf	gene_mouse	gene_full_name_mouse	GO_description_mouse	associated_phenotype_mous
<chr>	<chr>	<chr>	<chr>	<chr>
			the rate of peptidase activity, the hydrolysis of peptide bonds within proteins.; Binds to and stops, prevents or reduces the activity of serine-type endopeptidases, enzymes that catalyze the hydrolysis of nonterminal peptide bonds in a polypeptide chain; a serine residue (and a histidine residue) are at the active center of the enzyme.;	
a2ml	Gm7298	predicted gene 7298 [Source:MGI Symbol;Acc:MGI:3648717]	Any process that stops or reduces the rate of peptidase activity, the hydrolysis of peptide bonds within proteins.; Binds to and stops, prevents or reduces the activity of an endopeptidase, any enzyme that hydrolyzes nonterminal peptide bonds in polypeptides.; Binds to and stops, prevents or reduces the activity of a peptidase, any enzyme that catalyzes the hydrolysis peptide bonds.; The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host	

gene_zf	gene_mouse	gene_full_name_mouse	GO_description_mouse	associated_phenotype_mous
<chr>	<chr>	<chr>	<chr>	<chr>
			cell environment outside an intracellular parasite.; That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.; Binding to a protease or a peptidase.; Binds to and stops, prevents or reduces the activity of serine-type endopeptidases, enzymes that catalyze the hydrolysis of nonterminal peptide bonds in a polypeptide chain; a serine residue (and a histidine residue) are at the active center of the enzyme.	

▶ Code

	gene	protein	KO1	KO2	KO3	WT1	WT2	WT3	NOP	ko_vs_
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	44986	A0A2R8PWS6	0.1545013	0.9499	0.18451	0.2563195	0.2193404	1.249415	3	-0.145

◀ ▬▬▬▬▬▬ ▶
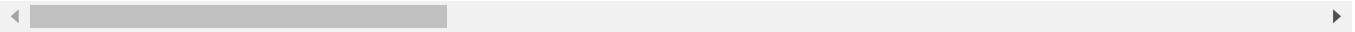
4.2 Mitocarta

▶ Code

'Symbol' · 'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways'
1140 · 4

A tibble: 6 × 4

Symbol	Description	MitoCarta3.0_SubMitoLocalization	MitoCarta3.0_MitoPathways
<chr>	<chr>	<chr>	<chr>
Cyc1	cytochrome c-1	MIM	OXPHOS > Complex III > CIII subunits | Metabolism > Metals and cofactors > Heme-containing proteins | Metabolism > Electron carriers > Cytochromes | OXPHOS > OXPHOS subunits
Pdha1	pyruvate dehydrogenase E1 alpha 1	Matrix	Metabolism > Carbohydrate metabolism > Pyruvate metabolism
Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	MIM	OXPHOS > Complex V > CV subunits | OXPHOS > OXPHOS subunits
Isca2	iron-sulfur cluster assembly 2	Matrix	Metabolism > Metals and cofactors > Fe-S cluster biosynthesis | Metabolism > Metals and cofactors > Fe-S-containing proteins
Pdhb	pyruvate dehydrogenase (lipoamide) beta	Matrix	Metabolism > Carbohydrate metabolism > Pyruvate metabolism
Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	MIM	Protein import, sorting and homeostasis > Protein import and sorting > Preprotein cleavage | OXPHOS > Complex III > CIII subunits | OXPHOS > OXPHOS subunits

▶ Code

4850 · 26
'gene_mouse' · 'gene' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' ·
'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' ·
'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' ·
'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' ·
'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways'

5 manual curation

▶ Code

```
New names:
```
• `` -> `...22`

'gene' · 'protein' · 'AKO1' · 'AKO2' · 'AKO3' · 'AWT1' · 'AWT2' · 'AWT3' · 'JWT1' · 'JWT2' · 'JWT3' ·
'NOP' · 'adult_ko_vs_adult_wt_logFC' · 'adult_ko_vs_adult_wt_P.Value' · 'adult_ko_vs_adult_wt_adj.P.Val' ·
'adult_ko_vs_juvenile_wt_logFC' · 'adult_ko_vs_juvenile_wt_P.Value' · 'adult_ko_vs_juvenile_wt_adj.P.Val' ·
'adult_wt_vs_juvenile_wt_logFC' · 'adult_wt_vs_juvenile_wt_P.Value' · 'adult_wt_vs_juvenile_wt_adj.P.Val' ·
'confirmation_status_muscle' · 'info_genecards_uniprot_nadia'
'gene' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' · 'ko_vs_wt_logFC' ·
'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'

A data.frame: 6 × 4

	gene	confirmation_status_muscle	confirmation_status_ventricle	info_genecards_uniprot_nadia
	<chr>	<chr>	<chr>	<chr>
1	aamdc			
2	aars1			
3	aass			
4	abcb10			
5	abcb11a			ATP Binding Cassette Subfamily B Member 11,transporter activity and ATPase-coupled transmembrane transporter activity.liver
6	abcb11b			

▶ Code

5418 · 29

'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' ·
'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' ·
'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' ·
'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' ·
'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' ·
'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'

▶ Code

29

▶ Code

▶ Code

```
'data.frame':	5418 obs. of  29 variables:
 $ gene                        : chr  "44986" "45171" "45175" "45179" ...
 $ gene_mouse                  : chr  NA NA NA NA ...
 $ protein                     : chr  "A0A2R8PWS6" "F1QW60" "F1R3Q3" "Q568B3" ...
 $ KO1                         : num  0.155 -0.653 -0.455 0.343 2.391 ...
 $ KO2                         : num  0.9499 0.1963 -0.1164 0.625 0.0475 ...
 $ KO3                         : num  0.185 -0.263 -0.111 0.581 0.921 ...
 $ WT1                         : num  0.256 -0.395 0.387 -0.85 1.545 ...
```

```
 $ WT2                          : num  0.219 0.754 -0.411 -0.176 1.68 ...
 $ WT3                          : num  1.2494 0.0981 -0.1191 0.0507 -0.0141 ...
 $ NOP                          : num  3 10 9 4 2 6 6 6 6 6 ...
 $ ko_vs_wt_logFC               : num  -0.1454 -0.3923 -0.1795 0.8415 0.0493 ...
 $ ko_vs_wt_P.Value             : num  0.798 0.493 0.724 0.132 0.952 ...
 $ ko_vs_wt_adj.P.Val           : num  0.965 0.873 0.948 0.721 0.992 ...
 $ gene_full_name_zf            : chr  NA NA NA NA ...
 $ GO_description_zf            : chr  NA NA NA NA ...
 $ associated_phenotype_zf      : chr  NA NA NA NA ...
 $ GO_name_zf                   : chr  NA NA NA NA ...
 $ GO_family_zf                 : chr  NA NA NA NA ...
 $ gene_full_name_mouse         : chr  NA NA NA NA ...
 $ GO_description_mouse         : chr  NA NA NA NA ...
 $ associated_phenotype_mouse   : chr  NA NA NA NA ...
 $ GO_name_mouse                : chr  NA NA NA NA ...
 $ GO_family_mouse              : chr  NA NA NA NA ...
 $ Description                  : chr  NA NA NA NA ...
 $ MitoCarta3.0_SubMitoLocalization: chr  NA NA NA NA ...
 $ MitoCarta3.0_MitoPathways    : chr  NA NA NA NA ...
 $ confirmation_status_muscle   : chr  NA NA NA NA ...
 $ confirmation_status_ventricle: chr  NA NA NA NA ...
 $ info_genecards_uniprot_nadia : chr  NA NA NA NA ...
```

▶ Code

▶ Code

'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' ·
'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' ·
'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' ·
'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' ·
'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' ·
'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'
'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' ·
'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' ·
'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' ·
'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' ·
'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' ·
'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'
'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' ·
'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' ·
'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' ·
'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' ·
'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' ·
'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'
61 · 29
'mrpl2' · 'mrpl22' · 'mrps36'
'mrpl1' · 'mrpl11' · 'mrpl12' · 'mrpl14' · 'mrpl15' · 'mrpl18' · 'mrpl19' · 'mrpl2' · 'mrpl21' · 'mrpl22' ·
'mrpl24' · 'mrpl28' · 'mrpl3' · 'mrpl30' · 'mrpl32' · 'mrpl37' · 'mrpl4' · 'mrpl41' · 'mrpl42' · 'mrpl43' ·
'mrpl44' · 'mrpl45' · 'mrpl46' · 'mrpl47' · 'mrpl48' · 'mrpl9' · 'mrps14' · 'mrps15' · 'mrps17' · 'mrps21' ·
'mrps22' · 'mrps23' · 'mrps25' · 'mrps26' · 'mrps27' · 'mrps28' · 'mrps30' · 'mrps31' · 'mrps34' ·

'mrps36' · 'mrps5' · 'mrps7' · 'mrps9' · 'aars2' · 'cluha' · 'dars2' · 'fis1' · 'gfm1' · 'iars2' · 'lars2' · 'mrrf' · 'mtif2' · 'mtres1' · 'mtus1a' · 'rars2' · 'shmt2' · 'taco1' · 'tsfm' · 'tufm' · 'vars2' · 'yars2' 'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' · 'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' · 'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' · 'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' · 'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' · 'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'

▶ Code

'aldh9a1b' · 'ank2b' · 'atp6v0d1' · 'bckdhb' · 'bfb' · 'camsap3' · 'cfb' · 'ciao2b' · 'clu' · 'crkl' · 'csnk1a1' · 'ctdspla' · 'cttn' · 'dlg5a' · 'dpt' · 'dynlrb1' · 'eml2' · 'epdl1' · 'epg5' · 'ezrb' · 'fam83d' · 'fermt2' · 'fn1b' · 'fn1b' · 'fn1b' · 'fn1b' · 'gdf6b' · 'h1m' · 'hexa' · 'hif1al' · 'hnrnpua' · 'hspa8b' · 'ift74' · 'insra' · 'klhl7' · 'mcm4' · 'mdh1aa' · 'nae1' · 'ndrg4' · 'ntrk2b' · 'nup153' · 'ogna' · 'pcyox1' · 'pdha1a' · 'pdha1a' · 'phb' · 'phb2a' · 'plaub' · 'plcd1a' · 'ppp2cb' · 'prdx4' · 'psme2' · 'psme2' · 'rab14' · 'rida' · 'rmdn1' · 'rpl13' · 'rpl19' · 'rtel1' · 'rtn4a' · 'rtn4a' · 'rtn4a' · 'sept8a' · 'serpine1' · 'sh3bp4' · 'slit2' · 'snap29' · 'sod2' · 'srsf5b' · 'syne1b' · 'tacc1' · 'tenm4' · 'tnfrsfa' · 'tnfrsfa' · 'tnfrsfa' · 'tprb' · 'tsg101a' · 'tuba8l3' · 'tubb6' · 'vma21' · 'vps4b' · 'wdfy3'

▶ Code

'clu' · 'dpt' · 'fn1b' · 'fn1b' · 'fn1b' · 'fn1b' · 'glg1b' · 'lamb1a' · 'ogna' · 'pkmb' · 'prdx4' · 'serpine1' · 'slit2' · 'spock3'

▶ Code

34
'actc1a' · 'actn4' · 'aldh9a1b' · 'bloc1s6' · 'camsap3' · 'coro6' · 'cttn' · 'cyb5r3' · 'ehd2b' · 'ezrb' · 'fermt2' · 'flnca' · 'fmn1' · 'gpd1b' · 'gsna' · 'hexa' · 'hnrnpua' · 'idh3b' · 'mdh1aa' · 'ndufs8a' · 'nrap' · 'pcyox1' · 'pdha1a' · 'pdlim5b' · 'pfn2a' · 'ptgr1.1' · 'rtel1' · 'sipa1l1' · 'slit2' · 'smyhc2' · 'syne1b' · 'synpo2lb' · 'tln2b' · 'tmod4'

▶ Code

29
'actc1a' · 'ank2b' · 'atp1a1b' · 'crkl' · 'cttn' · 'eomesb' · 'flnca' · 'gsna' · 'hnrnpua' · 'hspa8b' · 'lamb1a' · 'mybpc1' · 'ndrg4' · 'ndufs6' · 'nrap' · 'ogna' · 'pdlim5b' · 'phb' · 'pkmb' · 'plaub' · 'serpine1' · 'slit2' · 'smyhc2' · 'sod2' · 'sorbs2a' · 'syne1b' · 'tenm4' · 'tmod4' · 'tomm70a'

▶ Code

11
▶ Code

1
'pkmb'
▶ Code

4
'gpd1b' · 'mdh1aa' · 'pgam1a' · 'pgam1b'
▶ Code

11
'alad' · 'c3a.1' · 'decr1' · 'etfb' · 'fitm2' · 'ilvbl' · 'mlycd' · 'ndufab1a' · 'ndufs6' · 'rbp7b' · 'rida'

▶ Code

14
'ace' · 'ank2b' · 'atp23' · 'bfb' · 'c3a.1' · 'capn1b' · 'capns1b' · 'cfb' · 'hspa8b' · 'metap2b' · 'plaub' · 'rnf123' · 'uqcrc2b' · 'usp38'
▶ Code

0
▶ Code

23
'csnk1a1' · 'ddx1' · 'eomesb' · 'h1m' · 'hdac10' · 'hmga1a' · 'hnrnpua' · 'macroh2a2' · 'mcm4' · 'pfdn1' · 'phb' · 'pkmb' · 'ppp2cb' · 'prpf8' · 'psme4a' · 'scai' · 'si:ch73-281n10.2' · 'si:dkey-108k21.14' · 'tacc1' · 'tprb' · 'trmt61b' · 'tsg101a' · 'ywhabb'
▶ Code

2
'alad' · 'mthfs'
▶ Code

6
'igf2bp1' · 'insra' · 'pkmb' · 'srsf3b' · 'srsf5b' · 'tnfrsfa'
▶ Code

19
'camsap3' · 'csnk1a1' · 'dynlrb1' · 'ehd2b' · 'eml2' · 'ezrb' · 'fam83d' · 'fmn1' · 'hnrnpua' · 'hspa8b' · 'ppp2cb' · 'ppp5c' · 'rmdn1' · 'sept8a' · 'syne1b' · 'tacc1' · 'tsg101a' · 'tuba8l3' · 'tubb6'
▶ Code

10
'c3a.1' · 'hspa8b' · 'insra' · 'oxtrb' · 'pde10a' · 'phb' · 'plcd1a' · 'pld2' · 'tas1r2.2' · 'ywhabb'
▶ Code

37
'abcb4' · 'actc1a' · 'agk' · 'atp1a1b' · 'atp2a1l' · 'atp2a3' · 'cnga3a' · 'csnk1a1' · 'cyb5r3' · 'ddx1' · 'ehd2b' · 'eif2b1' · 'epg5' · 'etfb' · 'farsb' · 'fmo5' · 'hnrnpua' · 'hspa12a' · 'hspa8b' · 'iars1' · 'ilvbl' · 'insra' · 'mcm4' · 'mthfs' · 'nadk2' · 'nt5c1bb' · 'ntrk2b' · 'pde10a' · 'pkmb' · 'rab14' · 'rtel1' · 'sept8a' · 'slc35a4' · 'smyhc2' · 'tubb6' · 'ugp2a' · 'vps4b'
▶ Code

29
'agk' · 'alad' · 'aldh9a1b' · 'atp1a1b' · 'atp5f1d' · 'bcat2' · 'bpnt1' · 'c3a.1' · 'clu' · 'cyb5r3' · 'fitm2' · 'fn1b' · 'gnpda2' · 'hexa' · 'ilvbl' · 'insra' · 'mdh1aa' · 'mlycd' · 'mthfs' · 'nadk2' · 'ndufab1a' · 'pdha1a' · 'phb' · 'pkmb' · 'plcd1a' · 'pld2' · 'sccpdhb' · 'sod2' · 'ugp2a'
▶ Code

3
'adprh' · 'srsf3b' · 'srsf5b'
▶ Code

17

'cyb5r3' · 'gpd1b' · 'idh3b' · 'mdh1aa' · 'ndufa10' · 'ndufa2' · 'ndufa3' · 'ndufab1a' · 'ndufb10' · 'ndufb11' · 'ndufb4' · 'ndufb7' · 'ndufb8' · 'ndufb9' · 'ndufs5' · 'ndufs6' · 'ndufs8a'

▶ Code

9

'bfb' · 'c3a.1' · 'c4b' · 'c7a' · 'c8a' · 'c9' · 'cfb' · 'cfh' · 'phb'

▶ Code

2

'hnrnpua' · 'rtel1'

▶ Code

6

'fermt2' · 'ift74' · 'insra' · 'snap29' · 'tprb' · 'tsg101a'

▶ Code

18

'abcb4' · 'atp1a1b' · 'camsap3' · 'csnk1a1' · 'cttn' · 'fn1b' · 'glg1b' · 'heatr5b' · 'lrpap1' · 'pld2' · 'rab14' · 'sgce' · 'slc35a4' · 'snap29' · 'syne1b' · 'tnfrsfa' · 'trip11' · 'vma21'

▶ Code

26

NA ·

'SA node cell to atrial cardiac muscle cell communication; plasma membrane; perinuclear region of cytoplasm; atrial cardiac muscle cell to AV node cell communication; membrane; positive regulation of potassium ion transmembrane transporter activity; cytoplasm; positive regulation of calcium ion transmembrane transporter activity; A band; costamere; regulation of calcium ion transmembrane transporter activity; positive regulation of gene expression; regulation of cardiac muscle cell contraction; postsynaptic density; regulation of apoptotic process; positive regulation of potassium ion transport; regulation of heart rate by cardiac conduction; protein-macromolecule adaptor activity; phosphorylation-dependent protein binding; positive regulation of cation channel activity; regulation of ventricular cardiac muscle cell membrane repolarization; T-tubule organization; regulation of release of sequestered calcium ion into cytosol; protein binding; signal transduction; regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion; regulation of cardiac muscle contraction by calcium ion signaling; regulation of SA node cell action potential; regulation of atrial cardiac muscle cell action potential; protein stabilization; intercalated disc; protein localization to endoplasmic reticulum; ventricular cardiac muscle cell action potential; ATPase binding; positive regulation of calcium ion transport; regulation of protein stability; potassium channel regulator activity; protein localization to cell surface; atrial septum development; regulation of cardiac muscle cell membrane potential; extrinsic component of cytoplasmic side of plasma membrane; protein localization to plasma membrane; membrane raft; paranodal junction; structural constituent of cytoskeleton; spectrin binding; enzyme binding; M band; regulation of cardiac muscle contraction; sarcolemma; cardiac muscle contraction; regulation of calcium ion transport; protein transport; cytoskeleton organization; synapse; postsynaptic membrane; cytoskeleton; lysosome; T-tubule; cellular calcium ion homeostasis; mitochondrion; endosome; early endosome; recycling endosome; protein localization; localization; endocytosis; basolateral plasma membrane; protein kinase binding; transmembrane transporter binding; regulation of heart rate; Z disc; protein localization to organelle; neuron projection; atrial cardiac muscle cell action potential; regulation of AV node cell action potential; SA node cell action potential; regulation of cation channel activity; protein localization to M-band; protein localization to T-tubule; ; nervous system development; paranodal junction assembly; response to methylmercury; cellular anatomical entity' ·

'ATPase-coupled cation transmembrane transporter activity; establishment of localization in cell; sodium ion transport; P-type sodium:potassium-exchanging transporter activity; flagellated sperm motility; sperm midpiece; sodium ion export across plasma membrane; sodium:potassium-exchanging ATPase complex; establishment or maintenance of transmembrane electrochemical gradient; fertilization; cell projection; sodium ion transmembrane transport; potassium ion transmembrane transport; regulation of membrane potential; regulation of cellular pH; potassium ion import across plasma membrane; plasma membrane; ion transport; cellular sodium ion homeostasis; cellular potassium ion homeostasis; metal ion binding; proton transmembrane transport; photoreceptor cell cilium; membrane; ATP binding; potassium ion transport; rod photoreceptor outer segment; nucleotide binding; ATP hydrolysis activity; transporter activity; P-type potassium transmembrane transporter activity; spermatogenesis' ·

'endoplasmic reticulum calcium ion homeostasis; activation of cysteine-type endopeptidase activity involved in apoptotic process; endoplasmic reticulum membrane; calcium ion transmembrane transport; sarcoplasmic reticulum; sarcoplasmic reticulum membrane; ; protein binding; metal ion binding; endoplasmic reticulum; transmembrane transporter binding; intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress; cellular calcium ion homeostasis; negative regulation of receptor binding; calcium ion transmembrane transporter activity; organelle membrane; calcium ion transport from cytosol to endoplasmic reticulum; cysteine-type endopeptidase activator activity involved in apoptotic process; calcium-dependent ATPase activity; transporter activity; P-type calcium transporter activity; ion transport; calcium ion transport; nucleotide binding; ATP hydrolysis activity; ATP binding; membrane' ·

'voltage-gated calcium channel activity; neurotransmitter receptor transport, postsynaptic endosome to lysosome; protein targeting; channel regulator activity; transmission of nerve impulse; positive regulation of synaptic transmission, glutamatergic; postsynaptic neurotransmitter receptor diffusion trapping; neurotransmitter receptor internalization; neurotransmitter receptor localization to postsynaptic specialization membrane; positive regulation of AMPA receptor activity; somatodendritic compartment; membrane; calcium ion transport; ion transport; glutamatergic synapse; voltage-gated ion channel activity; calcium channel activity; regulation of ion transmembrane transport; calcium ion transmembrane transport; protein binding; protein localization; dendrite; PDZ domain binding; Schaffer collateral - CA1 synapse; excitatory synapse; postsynaptic density membrane; ionotropic glutamate receptor binding; regulation of AMPA receptor activity; AMPA glutamate receptor complex' ·

'metal ion binding; hydrolase activity; peptidase activity; cytoplasmic vesicle; cytoplasm; cysteine-type peptidase activity; acrosomal vesicle; calcium-dependent cysteine-type endopeptidase activity; proteolysis; calcium ion binding' ·

'calcium ion binding; protein binding; protein-containing complex binding; cytosol; cytoplasm; membrane; proteolysis; calpain complex; metal ion binding; plasma membrane; protein catabolic process; calcium-dependent cysteine-type endopeptidase activity' ·

'membrane; metal ion binding; microtubule cytoskeleton; nucleotide binding; ATP binding; plasma membrane; hydrolase activity; intercellular bridge; protein binding; perinuclear region of cytoplasm; endosome; cytoplasm; caveola; protein domain specific binding; GTP binding; calcium ion binding; cilium assembly; endosome membrane; endocytic vesicle; recycling endosome membrane; identical protein binding; protein localization to plasma membrane; endocytic recycling; early endosome; cytosol; cortical actin cytoskeleton organization; endocytosis; positive regulation of myoblast fusion; plasma membrane tubulation; positive regulation of endocytic recycling' ·

'metal ion binding; lipid transport; endoplasmic reticulum-plasma membrane tethering; membrane; calcium ion binding; protein binding; phosphatidylinositol binding; phosphatidylcholine binding; calcium-dependent phospholipid binding; phosphatidylethanolamine binding; plasma membrane; endoplasmic reticulum; endoplasmic reticulum membrane; intermembrane lipid transfer; phospholipid transfer activity; identical protein binding; phospholipid transport; lipid binding' ·

'neural crest cell migration involved in autonomic nervous system development; cellular response to mercury ion; negative regulation of transforming growth factor beta production; negative regulation of monocyte activation; identical protein binding; substrate adhesion-dependent cell spreading; angiogenesis; protease binding; extracellular matrix organization; cell-matrix adhesion; endoplasmic reticulum-Golgi intermediate compartment; integrin binding; regulation of ERK1 and ERK2 cascade; cell-substrate junction assembly; positive regulation of chemotaxis; nervous system development; wound healing; integrin activation; cellular response to interleukin-1; peptidase activator activity; negative regulation of collagen biosynthetic process; proteoglycan binding; cell activation; calcium-independent cell-matrix adhesion; mercury ion binding; endodermal cell differentiation; biological process involved in interaction with symbiont; positive regulation of cell population proliferation; regulation of gene expression; extracellular space; apical plasma membrane; positive regulation of substrate-dependent cell migration, cell attachment to substrate; negative regulation of apoptotic process; positive regulation of gene expression; positive regulation of fibroblast proliferation; extracellular exosome; regulation of protein phosphorylation; extracellular matrix; signaling receptor binding; collagen-containing extracellular matrix; extracellular matrix structural constituent; positive regulation of phosphatidylinositol 3-kinase signaling; glial cell migration; peptide cross-linking; positive regulation of axon extension; positive regulation of cell migration; heart development; integrin-mediated signaling pathway; fibrinogen complex; basement membrane; ; extracellular region; protein binding; heparin binding; acute-phase response; cell adhesion; regulation of cell shape' ·

'sequestering of actin monomers; positive regulation of protein processing in phagocytic vesicle; actin filament binding; nucleus; protein binding; positive regulation of gene expression; apoptotic process; cytosol; cellular response to interferon-gamma; phosphatidylinositol-4,5-bisphosphate binding; central nervous system development; cortical actin cytoskeleton; regulation of plasma membrane raft polarization; regulation of receptor clustering; podosome; negative regulation of viral entry into host cell; actin cap; actin filament polymerization; regulation of cell adhesion; myelin sheath; hepatocyte apoptotic process; relaxation of cardiac muscle; amyloid fibril formation; cellular response to cadmium ion; phagocytosis, engulfment; actin polymerization or depolymerization; regulation of podosome assembly; phosphatidylinositol 3-kinase catalytic subunit binding; myosin II binding; striated muscle atrophy; cell projection assembly; actin cytoskeleton organization; actin filament depolymerization; response to muscle stretch; positive regulation of actin nucleation; cardiac muscle cell contraction; renal protein absorption; positive regulation of keratinocyte apoptotic process; regulation of establishment of T cell polarity; cytoplasm; metal ion binding; extracellular space; sarcoplasm; phosphatidylinositol-mediated signaling; plasma membrane; cell projection organization; extracellular region; cytoskeleton; actin filament organization; lamellipodium; focal adhesion; actin binding; actin filament capping; barbed-end actin filament capping; actin filament severing; cilium assembly; calcium ion binding; protein destabilization; actin cytoskeleton; ruffle; positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway; phagocytic vesicle; vesicle-mediated transport; ; protein-containing complex; perinuclear region of cytoplasm' ·

'receptor complex; protein binding; endocytosis; membrane; calcium ion binding' ·

'; inner mitochondrial membrane organization; protein insertion into mitochondrial membrane; ribosome binding; protein insertion into mitochondrial inner membrane from matrix; mitochondrion; mitochondrial calcium ion homeostasis; mitochondrial inner membrane; mitochondrial matrix; calcium import into the mitochondrion' ·

'neuronal action potential propagation; regulation of GTPase activity; positive regulation of phosphatidylinositol 3-kinase signaling; glutamate secretion; positive regulation of axonogenesis; oligodendrocyte differentiation; cerebral cortex development; regulation of protein kinase B signaling; brain-derived neurotrophic factor binding; regulation of neurotransmitter secretion; presynaptic active zone; long-term memory; positive regulation of kinase activity; positive regulation of glucocorticoid receptor signaling pathway; positive regulation of synaptic transmission, glutamatergic; trans-synaptic signaling by BDNF, modulating synaptic transmission; negative regulation of amyloid-beta formation; rough endoplasmic reticulum; learning; peptidyl-serine phosphorylation; peripheral nervous system neuron development; long-term synaptic potentiation; trans-synaptic signaling by neuropeptide, modulating synaptic transmission; cellular response to brain-derived neurotrophic factor stimulus; negative regulation of anoikis; membrane; ATP binding; plasma membrane; protein binding; neurotrophin binding; brain-derived neurotrophic factor receptor activity; feeding behavior; regulation of MAPK cascade; positive regulation of neuron projection development; positive regulation of synapse assembly; regulation of metabolic process; mechanoreceptor differentiation; protein phosphorylation; protein kinase activity; transmembrane receptor protein tyrosine kinase signaling pathway; transmembrane receptor protein tyrosine kinase activity; protein tyrosine kinase activity; neurotrophin receptor activity; cellular response to amino acid stimulus; positive regulation of cell population proliferation; negative regulation of neuron apoptotic process; retina development in camera-type eye; regulation of dendrite development; postsynaptic density; cytosol; cytoplasm; axon; retinal rod cell development; cell projection; transferase activity; nucleotide binding; perinuclear region of cytoplasm; cell surface; cell differentiation; synapse; kinase activity; phosphorylation; neuron migration; dendrite; neuron differentiation; nervous system development; growth cone; protease binding; neuronal cell body; cell communication; regulation of cell death; neurotrophin signaling pathway; cellular response to stimulus; endosome; early endosome; endosome membrane; positive regulation of MAPK cascade; protein homodimerization activity; glutamatergic synapse; protein autophosphorylation; early endosome membrane; circadian rhythm; vasculogenesis; positive regulation of peptidyl-serine phosphorylation; perikaryon; terminal bouton; central nervous system neuron development; receptor tyrosine kinase binding; dendritic spine; brain-derived neurotrophic factor receptor signaling pathway; axon terminus; postsynapse; myelination in peripheral nervous system; receptor complex; postsynaptic membrane; excitatory synapse; positive regulation of gene expression; ; calcium-mediated signaling using intracellular calcium source' ·
'plasma membrane; membrane; calcium ion binding; homophilic cell adhesion via plasma membrane adhesion molecules; cell adhesion; molecular_function; metal ion binding; serotonergic neuron axon guidance' ·
'intracellular signal transduction; lipid catabolic process; phosphatidylinositol-4,5-bisphosphate binding; phosphatidylinositol metabolic process; cytoplasm; calcium ion binding; signal transduction; GTPase activating protein binding; phosphatidylinositol phospholipase C activity; phosphoric diester hydrolase activity; lipid metabolic process; metal ion binding; hydrolase activity; regulation of phospholipase C activity; nucleus; protein binding; cytosol; angiogenesis; regulation of cell population proliferation; membrane; G protein-coupled receptor signaling pathway; regulation of cytosolic calcium ion concentration; mitochondrial membrane; membrane raft; labyrinthine layer blood vessel development; phosphatidylinositol-mediated signaling; release of sequestered calcium ion into cytosol; response to calcium ion; phospholipid binding; response to peptide hormone; positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway; positive regulation of norepinephrine secretion; calcium-dependent phospholipid binding; inositol 1,4,5 trisphosphate binding; positive regulation of inositol trisphosphate biosynthetic process' ·

'phospholipase C activity; cytoplasm; membrane; phosphoric diester hydrolase activity; plasma membrane; hydrolase activity; phosphatidylinositol-mediated signaling; metal ion binding; phosphatidylinositol metabolic process; release of sequestered calcium ion into cytosol; ; lipid catabolic process; intracellular signal transduction; lipid metabolic process; phosphatidylinositol phospholipase C activity; signal transduction; calcium ion binding' ·

'dystrophin-associated glycoprotein complex; protein binding; cytoskeleton; dendrite; sarcolemma; dendrite membrane; membrane; sarcoglycan complex; cell projection; cytoplasm; Golgi apparatus; plasma membrane' ·

'plasma membrane; negative regulation of cell growth; negative regulation of chemokine-mediated signaling pathway; extracellular region; negative regulation of actin filament polymerization; chemotaxis; cell differentiation; negative regulation of cell migration; collagen-containing extracellular matrix; calcium ion binding; in utero embryonic development; negative regulation of gene expression; Roundabout signaling pathway; negative regulation of inflammatory response; negative regulation of cell population proliferation; cytoplasm; negative regulation of protein phosphorylation; extracellular space; heparin binding; cell surface; protein homodimerization activity; neuron development; cellular component organization; kidney development; positive regulation of apoptotic process; neuron projection morphogenesis; Roundabout binding; negative chemotaxis; axonogenesis; cell migration involved in sprouting angiogenesis; negative regulation of axon extension; heparan sulfate proteoglycan binding; GTPase inhibitor activity; motor neuron axon guidance; axon guidance; negative regulation of vascular permeability; chemorepellent activity; retinal ganglion cell axon guidance; branching morphogenesis of an epithelial tube; negative regulation of neutrophil chemotaxis; mammary gland duct morphogenesis; pulmonary valve morphogenesis; ventricular septum morphogenesis; ureteric bud development; negative regulation of endothelial cell migration; negative regulation of smooth muscle cell migration; negative regulation of smooth muscle cell chemotaxis; negative regulation of leukocyte chemotaxis; negative regulation of monocyte chemotaxis; proteoglycan binding; negative regulation of cellular response to growth factor stimulus; aortic valve morphogenesis; axon extension involved in axon guidance; mammary duct terminal end bud growth; cellular response to heparin; laminin-1 binding; cell-cell adhesion; signaling receptor binding; nervous system development; identical protein binding; extracellular matrix structural constituent; olfactory bulb development; metanephros development; corticospinal neuron axon guidance through spinal cord; induction of negative chemotaxis; negative regulation of mononuclear cell migration; negative regulation of retinal ganglion cell axon guidance; protein binding; telencephalon cell migration; negative regulation of small GTPase mediated signal transduction; chemorepulsion involved in postnatal olfactory bulb interneuron migration; negative regulation of lamellipodium assembly; dorsal/ventral axon guidance; ; cellular response to hormone stimulus; response to cortisol; apoptotic process involved in luteolysis' ·

'ATP binding; visceral muscle development; myosin complex; protein binding; actin filament binding; cytoskeletal motor activity; regulation of ATP-dependent activity; actin filament-based movement; myofibril assembly; cardiac muscle contraction; microfilament motor activity; myosin filament; myosin II complex; calcium-dependent ATPase activity; ATP metabolic process; regulation of the force of heart contraction; mitochondrion; muscle myosin complex; ventricular cardiac muscle tissue morphogenesis; Z disc; sarcomere organization; myofibril; muscle contraction; stress fiber; striated muscle contraction; adult heart development; muscle filament sliding; atrial cardiac muscle tissue morphogenesis; in utero embryonic development; protein-containing complex binding; cardiac muscle cell development; regulation of heart growth; regulation of blood pressure; cardiac muscle hypertrophy in response to stress; cytoplasm; nucleotide binding; calmodulin binding; actin binding; identical protein binding; protein kinase binding; regulation of heart rate; regulation of heart contraction' ·

'extracellular matrix; metalloendopeptidase inhibitor activity; peptidase inhibitor activity; negative regulation of peptidase activity; enzyme inhibitor activity; negative regulation of endopeptidase activity; glycosaminoglycan binding; peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan; protein binding; calcium ion binding; extracellular space; extracellular region' ·
'regulation of extracellular exosome assembly; regulation of MAP kinase activity; exosomal secretion; positive regulation of ubiquitin-dependent endocytosis; extracellular transport; positive regulation of viral budding via host ESCRT complex; early endosome; negative regulation of epidermal growth factor receptor signaling pathway; ubiquitin protein ligase binding; Flemming body; nuclear receptor coactivator activity; cell differentiation; keratinocyte differentiation; endosome to lysosome transport; positive regulation of exosomal secretion; calcium-dependent protein binding; negative regulation of epidermal growth factor-activated receptor activity; ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway; virion binding; viral budding; viral release from host cell; protein homodimerization activity; early endosome membrane; positive regulation of DNA-templated transcription; ubiquitin binding; ESCRT I complex; late endosome; protein monoubiquitination; transcription corepressor activity; regulation of cell growth; protein modification process; protein transport; nucleus; nucleolus; protein binding; extracellular exosome; protein-containing complex binding; negative regulation of transcription by RNA polymerase II; regulation of cell cycle; negative regulation of cell population proliferation; cytosol; cytoplasm; cellular anatomical entity; membrane; plasma membrane; cytoskeleton; microtubule organizing center; endosome membrane; cell cycle; cell division; endosome; late endosome membrane' ·
'ubiquitin-protein transferase activity; zinc ion binding; ubiquitin protein ligase activity; embryo development ending in birth or egg hatching; ubiquitin ligase complex; positive regulation of protein catabolic process; olfactory behavior; suckling behavior; negative regulation of calcium ion transmembrane transport via high voltage-gated calcium channel; sensory perception of smell; ubiquitin-dependent protein catabolic process via the N-end rule pathway; in utero embryonic development; protein binding; membrane; transferase activity; metal ion binding; ubiquitin-dependent protein catabolic process; protein ubiquitination; cytoplasm'
'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' ·
'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' ·
'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' ·
'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' ·
'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' ·
'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'
▶ Code

16
'actc1a' · 'ank2b' · 'atp1a1b' · 'gsna' · 'hnrnpua' · 'hspa8b' · 'ndrg4' · 'nrap' · 'pdlim5b' · 'rtn4a' · 'smyhc2' ·
'sorbs2a' · 'syne1b' · 'tenm4' · 'tmem65' · 'tomm70a'
▶ Code

25
'abcb4' · 'camsap3' · 'crkl' · 'cttn' · 'dpt' · 'epdl1' · 'ezrb' · 'fermt2' · 'fmn1' · 'fn1b' · 'gsna' · 'ift74' ·
'lamb1a' · 'pcdh2ab9' · 'plaub' · 'pld2' · 'ppiaa' · 'rtn4a' · 'serpinb1l3' · 'serpine1' · 'slit2' · 'sorbs2a' ·
'tenm4' · 'tln2b' · 'tnfrsfa'
▶ Code

A tibble: 5 × 4

Symbol	Description	MitoCarta3.0_SubMitoLocalization	MitoCarta3.0_MitoPathways
<chr>	<chr>	<chr>	<chr>
Cox7a2	cytochrome c oxidase subunit 7A2	MIM	OXPHOS > Complex IV > CIV subunits | OXPHOS > OXPHOS subunits
Cox7c	cytochrome c oxidase subunit 7C	MIM	OXPHOS > Complex IV > CIV subunits | OXPHOS > OXPHOS subunits
Cox7a1	cytochrome c oxidase subunit 7A1	MIM	OXPHOS > Complex IV > CIV subunits | OXPHOS > OXPHOS subunits
Cox7b	cytochrome c oxidase subunit 7B	MIM	OXPHOS > Complex IV > CIV subunits | OXPHOS > OXPHOS subunits
Cox7a2l	cytochrome c oxidase subunit 7A2 like	MIM	OXPHOS > Complex IV > CIV subunits | OXPHOS > OXPHOS subunits | OXPHOS > OXPHOS assembly factors | OXPHOS > Respirasome assembly

Cox7a2: 'cox7a2a' **Cox7a2l:** 'cox7a2l' **Cox7c:** 'cox7c'

1: 'cox7a1' **Cox7a2:** 'cox7a2a' **3:** 'cox7a2b' **Cox7a2l:** 'cox7a2l' **5:** 'cox7b' **Cox7c:** 'cox7c'

▶ Code

64 · 29
60
'aco2' · 'adhfe1' · 'agk' · 'aldh9a1b' · 'atp23' · 'atp5f1d' · 'bcat2' · 'bckdhb' · 'chchd6a' · 'cox4i1' · 'cox5ab' · 'cox5b2' · 'cox6a1' · 'cox6b1' · 'cox6b2' · 'cox7c' · 'cyb5r3' · 'cyc1' · 'decr1' · 'etfb' · 'idh3b' · 'maip1' · 'mlycd' · 'mrpl2' · 'mrpl22' · 'mrps36' · 'mthfs' · 'nadk2' · 'ndufa10' · 'ndufa2' · 'ndufa3' · 'ndufa4' · 'ndufab1a' · 'ndufb10' · 'ndufb11' · 'ndufb4' · 'ndufb7' · 'ndufb8' · 'ndufb9' · 'ndufs5' · 'ndufs6' · 'ndufs8a' · 'nipsnap2' · 'pdha1a' · 'phb' · 'phb2a' · 'prdx4' · 'rida' · 'rmdn1' · 'snap29' · 'sod2' · 'tfam' · 'tmem177' · 'tmem65' · 'tomm70a' · 'uqcr10' · 'uqcrc1' · 'uqcrc2b' · 'uqcrh' · 'uqcrq'

▶ Code

6 Heatmaps

▶ Code

A data.frame: 6 × 11

	gene	KO1	KO2	KO3	WT1	WT2	WT3	NOP	ko_vs
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	alad	-1.8937150	-0.58330430	-1.4975788	0.672693	0.6583896	0.2379190	10	-1.84
2	mthfs	-2.8691737	-5.07133932	-7.4903233	-10.143908	-12.7743762	-8.8958321	1	5.46

	gene	KO1	KO2	KO3	WT1	WT2	WT3	NOP	ko_v:
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl:
3	mthfs	-2.8691737	-5.07133932	-7.4903233	-10.143908	-12.7743762	-8.8958321	1	5.46:
4	bcat2	1.5979720	2.63781594	2.7348600	-1.437596	-0.0244880	0.6275970	16	2.60:
5	atp1a1b	0.2911286	-0.07343499	0.1624315	-3.976195	-2.2186918	-1.8081526	1	2.79:
6	atp2a1l	-0.6378300	-1.01123993	-1.0630356	1.619401	1.4437790	-0.3482483	22	-1.80

241 · 11

▶ Code

'1C cycle' · 'Amino Acid metabolism' · 'ATP' · 'Autophagy' · 'cAMP' · 'Gluconeogenesis' ·
'Glucose Metabolism' · 'Glycogenolysis' · 'Glycolysis' · 'Glycolysis/Gluconeogenesis' ·
'Lipid/FA oxidation' · 'NADH pathway' · 'Nucleotide Metabolism/Catabolism' · 'OXPHOS' ·
'Protein Synthesis' · 'Pyruvate' · 'TCA' · 'TMA-Noxidation' · 'tRNA' · 'UDP-Galactose' · 'UDP-GlcNAc' ·
'UDP-Gluc' · 'Complex I' · 'Complex III' · 'Complex IV' · 'Complex V' · 'Cristae formation' ·
'Folate and 1-C metabolism' · 'Lipid metabolism' · 'Mitoribosome' · 'mtDNA maintenance' ·
'Pyruvate metabolism' · 'ROS and glutathione metabolism' · 'Xenobiotic metabolism' ·
'Mitochondrial Protein' · 'Branched-chain amino acid metabolism' · 'Chaperones' · 'Electron Carrier' ·
'Mitochondrial dynamics and surveillance' · 'Protein import, sorting and homeostasis' ·
'Actin and related' · 'Cardiac and related' · 'Muscle and related' · 'Proteolysis' · 'Calcium' ·
'Voltage Gated Potassium Activity'
46
'1C cycle' · 'Amino Acid metabolism' · 'ATP' · 'Autophagy' · 'cAMP' · 'Gluconeogenesis' ·
'Glucose Metabolism' · 'Glycogenolysis' · 'Glycolysis' · 'Glycolysis/Gluconeogenesis' ·
'Lipid/FA oxidation' · 'NADH pathway' · 'Nucleotide Metabolism/Catabolism' · 'OXPHOS' ·
'Protein Synthesis' · 'Pyruvate' · 'TCA' · 'TMA-Noxidation' · 'tRNA' · 'UDP-Galactose' · 'UDP-GlcNAc' ·
'UDP-Gluc' · 'Complex I' · 'Complex III' · 'Complex IV' · 'Complex V' · 'Cristae formation' ·
'Folate and 1-C metabolism' · 'Lipid metabolism' · 'Mitoribosome' · 'mtDNA maintenance' ·
'Pyruvate metabolism' · 'ROS and glutathione metabolism' · 'Xenobiotic metabolism' ·
'Mitochondrial Protein' · 'Branched-chain amino acid metabolism' · 'Chaperones' · 'Electron Carrier' ·
'Mitochondrial dynamics and surveillance' · 'Protein import, sorting and homeostasis' ·
'Actin and related' · 'Cardiac and related' · 'Muscle and related' · 'Proteolysis' · 'Calcium' ·
'Voltage Gated Potassium Activity'
46
132 · 11

A tibble: 6 × 12

unique_rownames	gene	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
alad	alad	-1.8937150	-0.5833043	-1.4975788	0.67269299	0.6583896	0.2379
mthfs	mthfs	-2.8691737	-5.0713393	-7.4903233	-10.14390754	-12.7743762	-8.895
bpnt1	bpnt1	-0.9682324	-1.8353367	-1.6240506	0.07364603	0.9653733	0.8287

unique_rownames	gene	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
atp2a1l	atp2a1l	-0.6378300	-1.0112399	-1.0630356	1.61940082	1.4437790	-0.348
atp2a3	atp2a3	-0.2727453	-1.6609984	-0.9738952	1.28363437	-0.3407920	0.8383
nt5c1bb	nt5c1bb	0.8670019	2.5939490	2.8636652	-1.15867845	0.2893536	0.175€

A matrix: 6 × 6 of type dbl

	WT1	WT2	WT3	KO1	KO2	KO3
alad	0.67269299	0.6583896	0.2379190	-1.8937150	-0.5833043	-1.4975788
mthfs	-10.14390754	-12.7743762	-8.8958321	-2.8691737	-5.0713393	-7.4903233
bpnt1	0.07364603	0.9653733	0.8287821	-0.9682324	-1.8353367	-1.6240506
atp2a1l	1.61940082	1.4437790	-0.3482483	-0.6378300	-1.0112399	-1.0630356
atp2a3	1.28363437	-0.3407920	0.8383122	-0.2727453	-1.6609984	-0.9738952
nt5c1bb	-1.15867845	0.2893536	0.1756364	0.8670019	2.5939490	2.8636652

▶ Code

pdf: 3
png: 2

Row labels (left side):
NADH pathway
Nucleotide Metabolism/Catabolism
OXPHOS
Protein Synthesis
Protein import, sorting and homeostasis
Proteolysis
Pyruvate
Pyruvate metabolism
ROS and glutathione metabolism
TCA
TMA-Noxidation
UDP-Galactose
UDP-GlcNAc
UDP-Gluc
Voltage Gated Potassium Activity
Xenobiotic metabolism
cAMP
mtDNA maintenance
tRNA

Right side labels:
ndufa3_1
ndufa2_1
ndufb9_1
ndufb4_1
cyb5r3_1
ndufs5_1
mdh1aa_2
ndufb8_1
ndufa10_1
ndufb10_1
ndufb7_1
ndufs8a_2
ldh3b_1
abcb4
etfb_2
eif2b1
agk_1
tomm70a_2
phb2a
atp23
phb_1
psme4a
csnk1a1
cnot4b
rnf123
usp38
pdha1a_1
pdha1a_2
aldh9a1b_1
sod2_1
prdx4
idh3b_2
aco2
fmo5
slc35a4
gnpda2
ugp2a_1
cnga3a
aldh9a1b_2
pde10a
tfam
farsb
iars1
Genotype

Code

A data.frame: 6 × 10

	Protein	KO1	KO2	KO3	WT1	WT2	WT3	NOP	ko_vs_
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	ndufa10	1.0072101	2.650823	3.3550487	0.6169489	0.98814359	-0.45752719	17	1.9551
2	ndufa2	1.2584117	1.779872	1.6508282	-0.9543852	0.72168044	0.11206961	8	1.6032
3	ndufa3	1.2857025	1.555973	2.0056984	-0.3260931	-0.07399171	0.49444447	1	1.5843
4	ndufab1a	0.6335561	1.691166	1.0971000	0.3571941	-1.36667690	-0.04514269	3	1.4921
5	uqcr10	-1.0111142	1.754500	0.3664659	-2.2776780	-3.26735167	-1.06381248	3	2.5728
6	uqcrc2b	1.0230850	2.646113	2.0944208	-0.4194865	0.99592987	0.28792496	28	1.6330

66 · 10

Code

'Complex I' · 'Complex III' · 'Complex IV' · 'Complex V' · 'Cristae Formation' · 'Fatty Acid Oxidation' · 'Folate And 1 Carbon Cycle' · 'Lipid Metabolism' · 'Mitoribosome' · 'MtDNA Maintenance' · 'NAD Biosynthesis And Metabolism' · 'Pyruvate Metabolism' · 'ROS And Glutathione Metabolism' · 'TCA Cycle' · 'Xenobiotic Metabolism' · 'Mitochondrial Protein' · 'Amino Acid Metabolism' · 'Branched-chain Amino Acid Metabolism' · 'Chaperones' · 'Mitochondrial Dynamics And Surveillance' · 'Autophagy' · 'Mitochondrial Ribosome' · 'Protein Import' · 'ROS/Glulutathione Metabolism'

24

'Complex I' · 'Complex III' · 'Complex IV' · 'Complex V' · 'Cristae Formation' · 'Fatty Acid Oxidation' · 'Folate And 1 Carbon Cycle' · 'Lipid Metabolism' · 'Mitoribosome' · 'MtDNA Maintenance' · 'NAD Biosynthesis And Metabolism' · 'Pyruvate Metabolism' · 'ROS And Glutathione Metabolism' · 'TCA Cycle' · 'Xenobiotic Metabolism' · 'Mitochondrial Protein' · 'Amino Acid Metabolism' · 'Branched-chain Amino Acid Metabolism' · 'Chaperones' · 'Mitochondrial Dynamics And Surveillance' · 'Autophagy' · 'Mitochondrial Ribosome' · 'Protein Import' · 'ROS/Glulutathione Metabolism'

24

2 · 10

A tibble: 6 × 11

unique_rownames	Protein	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
ndufs6	ndufs6	0.3872960	0.3114135	1.403355	-1.01001485	-0.50885979	-0.566998
ndufb11	ndufb11	1.1220066	0.9514735	1.959929	-0.00932997	0.29319824	-0.612837
ndufab1a	ndufab1a	0.6335561	1.6911659	1.097100	0.35719412	-1.36667690	-0.045142
ndufa3	ndufa3	1.2857025	1.5559725	2.005698	-0.32609309	-0.07399171	0.4944444
ndufa2	ndufa2	1.2584117	1.7798722	1.650828	-0.95438521	0.72168044	0.1120696
ndufb9	ndufb9	1.2566677	1.8606450	1.342288	-0.54845782	-0.10723745	0.0670988

A matrix: 6 × 6 of type dbl

	WT1	WT2	WT3	KO1	KO2	KO3
ndufs6	-1.01001485	-0.50885979	-0.56699868	0.3872960	0.3114135	1.403355
ndufb11	-0.00932997	0.29319824	-0.61283752	1.1220066	0.9514735	1.959929
ndufab1a	0.35719412	-1.36667690	-0.04514269	0.6335561	1.6911659	1.097100
ndufa3	-0.32609309	-0.07399171	0.49444447	1.2857025	1.5559725	2.005698
ndufa2	-0.95438521	0.72168044	0.11206961	1.2584117	1.7798722	1.650828
ndufb9	-0.54845782	-0.10723745	0.06709887	1.2566677	1.8606450	1.342288

▶ Code

pdf: 3
png: 2
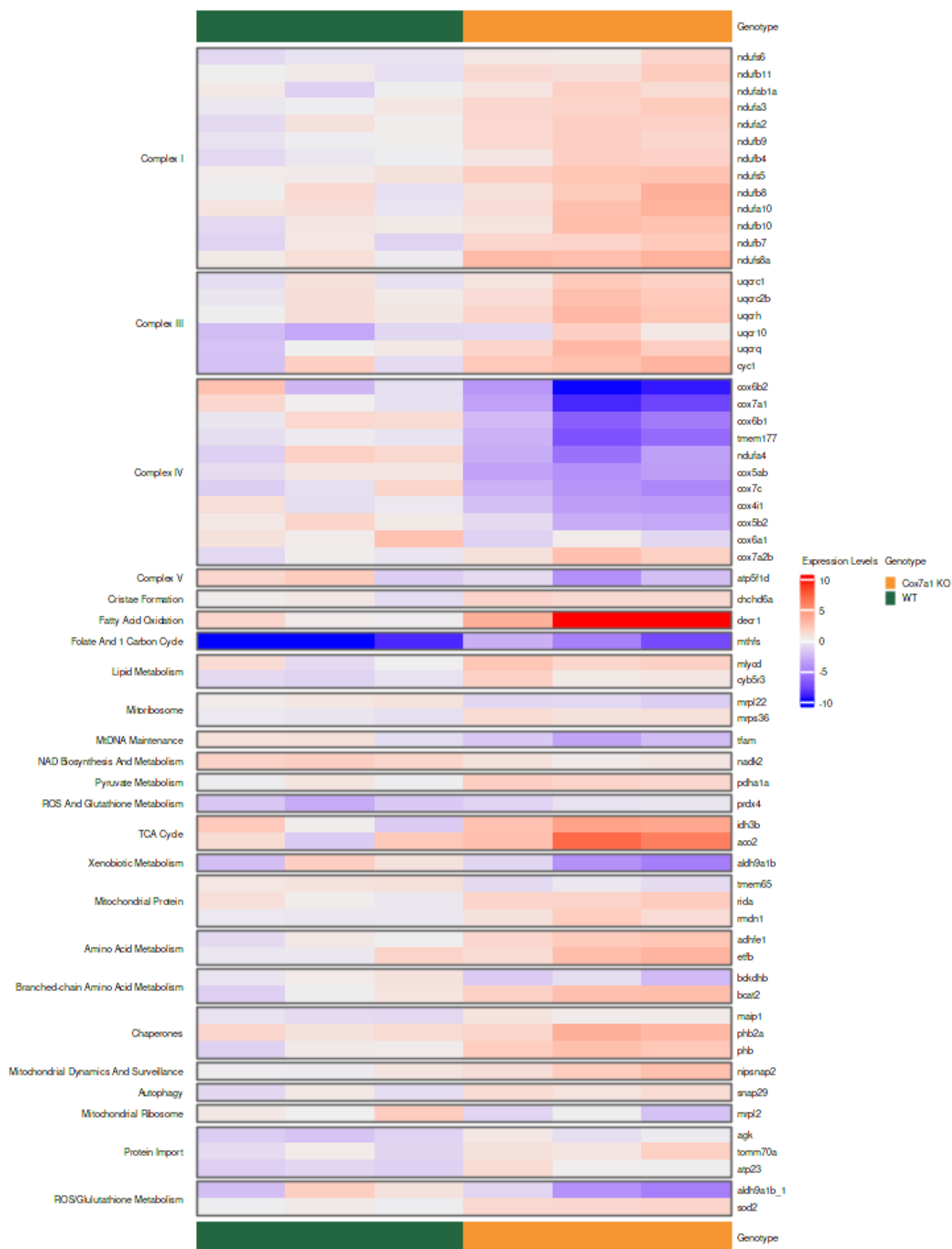
▶ Code

A data.frame: 6 × 11

	Protein	KO1	KO2	KO3	WT1	WT2	WT3	NOP	ko
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<d
1	alad	-1.8937150	-0.58330430	-1.4975788	0.672693	0.6583896	0.2379190	10	-1.
2	mthfs	-2.8691737	-5.07133932	-7.4903233	-10.143908	-12.7743762	-8.8958321	1	5.
3	bcat2	1.5979720	2.63781594	2.7348600	-1.437596	-0.0244880	0.6275970	16	2.6
4	ALDH9A1	-1.0758477	-4.27148319	-5.1340732	-2.182588	1.8254340	0.7438257	6	-3.
5	atp1a1b	0.2911286	-0.07343499	0.1624315	-3.976195	-2.2186918	-1.8081526	1	2.7
6	atp2a1l	-0.6378300	-1.01123993	-1.0630356	1.619401	1.4437790	-0.3482483	22	-1.

178 · 11

▶ Code

'1 Carbon Cycle' · 'Amino Acid Metabolism' · 'Aldehydes/carnithin Metabolism' ·
'ATP Synthesis And Related' · 'Autophagy' · 'CAMP Pathway' · 'Gluconeogenesis' · 'Glucose Uptake' ·
'Glycogenolysis' · 'Glycolysis' · 'Lipid/Fatty Acid Oxidation' · 'NADH Pathway' · 'Nucleotide Metabolism' ·
'OXPHOS' · 'Protein Synthesis' · 'Pyruvate' · 'TCA' · 'TMA N-Oxidation' · 'TRNA' ·
'UDP Metabolism Related' · 'Actin And Related' · 'Cardiac' · 'Muscle' ·
'Proteosomal Degradation/Protelysis' · 'Calcium Signalling And Related'

25

'1 Carbon Cycle' · 'Amino Acid Metabolism' · 'Aldehydes/carnithin Metabolism' ·
'ATP Synthesis And Related' · 'Autophagy' · 'CAMP Pathway' · 'Gluconeogenesis' · 'Glucose Uptake' ·
'Glycogenolysis' · 'Glycolysis' · 'Lipid/Fatty Acid Oxidation' · 'NADH Pathway' · 'Nucleotide Metabolism' ·
'OXPHOS' · 'Protein Synthesis' · 'Pyruvate' · 'TCA' · 'TMA N-Oxidation' · 'TRNA' ·
'UDP Metabolism Related' · 'Actin And Related' · 'Cardiac' · 'Muscle' ·
'Proteosomal Degradation/Protelysis' · 'Calcium Signalling And Related'

25

88 · 11

A tibble: 6 × 12

unique_rownames	Protein	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
alad	alad	-1.8937150	-0.5833043	-1.497579	0.67269299	0.6583896	0.237
mthfs	mthfs	-2.8691737	-5.0713393	-7.490323	-10.14390754	-12.7743762	-8.89
ilvbl	ilvbl	-1.0025913	-4.0601677	-2.013272	0.20263726	0.8198455	-0.49
bcat2	bcat2	1.5979720	2.6378159	2.734860	-1.43759576	-0.0244880	0.627

unique_rownames	Protein	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
ALDH9A1	ALDH9A1	-1.0758477	-4.2714832	-5.134073	-2.18258779	1.8254340	0.743
bpnt1	bpnt1	-0.9682324	-1.8353367	-1.624051	0.07364603	0.9653733	0.828

▶ Code

'Complex I' · 'Complex III' · 'Complex IV' · 'Complex V' · 'Cristae Formation' · 'Fatty Acid Oxidation' · 'Folate And 1 Carbon Cycle' · 'Lipid Metabolism' · 'Mitoribosome' · 'MtDNA Maintenance' · 'NAD Biosynthesis And Metabolism' · 'Pyruvate Metabolism' · 'ROS And Glutathione Metabolism' · 'TCA Cycle' · 'Xenobiotic Metabolism' · 'Mitochondrial Protein' · 'Amino Acid Metabolism' · 'Branched-chain Amino Acid Metabolism' · 'Chaperones' · 'Mitochondrial Dynamics And Surveillance' · 'Autophagy' · 'Mitochondrial Ribosome' · 'Protein Import' · 'ROS/Glulutathione Metabolism'

▶ Code

pdf: 3
png: 2

7 Volcano plots

▶ Code

'gene' · 'gene_mouse' · 'protein' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'NOP' ·
'ko_vs_wt_logFC' · 'ko_vs_wt_P.Value' · 'ko_vs_wt_adj.P.Val' · 'gene_full_name_zf' · 'GO_description_zf' ·
'associated_phenotype_zf' · 'GO_name_zf' · 'GO_family_zf' · 'gene_full_name_mouse' ·
'GO_description_mouse' · 'associated_phenotype_mouse' · 'GO_name_mouse' · 'GO_family_mouse' ·
'Description' · 'MitoCarta3.0_SubMitoLocalization' · 'MitoCarta3.0_MitoPathways' ·
'confirmation_status_muscle' · 'confirmation_status_ventricle' · 'info_genecards_uniprot_nadia'
'gene' · 'KO1' · 'KO2' · 'KO3' · 'WT1' · 'WT2' · 'WT3' · 'pval' · 'logFoldChange' · 'NOP'
4040 · 10

A tibble: 6 × 10

gene	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
ass1	-5.153913	-13.878287	-10.127414	3.102007	1.614356	-2.870240
ORFNames=zgc:162509 {ECO:0000313|ZFIN:ZDB-GENE-050809-100};	2.914659	14.445267	8.732459	-1.426478	-4.607301	1.159704
osm	3.793709	14.891488	9.918484	-6.357533	3.016443	1.058804
usp38	-3.395814	-8.901054	-11.060259	-15.078312	-20.319190	-14.655742
myhz1.2	-4.961302	-5.220350	-8.114330	18.489280	-6.904081	-4.711620
ba1	-5.602232	-8.497147	-13.872898	8.516233	-6.312119	-6.031472

▶ Code

▶ Code

▶ Code

A tibble: 15 × 10

gene	KO1	KO2	KO3	WT1	WT2	WT3	pval
<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl
zgc:162509	2.9146591	14.4452666	8.732459	-1.4264778	-4.6073007	1.1597040	0.00
osm	3.7937086	14.8914883	9.918484	-6.3575331	3.0164434	1.0588039	0.01
usp38	-3.3958137	-8.9010539	-11.060259	-15.0783124	-20.3191902	-14.6557418	0.00
pcdh2ab9	-1.4559199	-7.5875340	-9.431745	-13.7700134	-16.1866828	-12.5094588	0.00
rnf123	-4.3013214	-7.3144955	-9.668344	-14.9984992	-16.1921003	-12.7682378	0.00
LOC110437804	-1.5053579	-6.1424277	-6.791214	-12.1810727	-13.2783436	-11.4169663	0.00
ift74	-5.7593055	-9.5788620	-10.266730	-14.7862093	-17.7906143	-15.3345319	0.00
decr1	3.4801039	9.9239165	10.096107	1.3792279	0.2121305	-0.1296590	0.00
cnga3a	-3.7538779	-4.6571801	-7.886207	-9.5688260	-18.1980418	-9.7773900	0.01

gene	KO1	KO2	KO3	WT1	WT2	WT3	pval
<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl
ptgr1.1	2.2833801	4.1757566	11.485449	-0.8378945	-1.0686034	0.6468778	0.01
cnot4b	-0.8359325	6.8192386	6.742998	-4.0872132	-1.0067215	-0.8925613	0.01
si:ch211-196f19.1	6.6393783	-0.8403702	6.658096	-0.9448848	-1.3482062	-2.1089130	0.02
mthfs	-2.8691737	-5.0713393	-7.490323	-10.1439075	-12.7743762	-8.8958321	0.00
tln2b	-3.4492390	-4.8683380	-7.700331	-9.6048075	-12.1432753	-9.0708311	0.00
extl2	-2.2210629	-3.9436559	-5.566005	-8.9098153	-11.1099435	-5.5604536	0.01

pdf: 3

png: 2
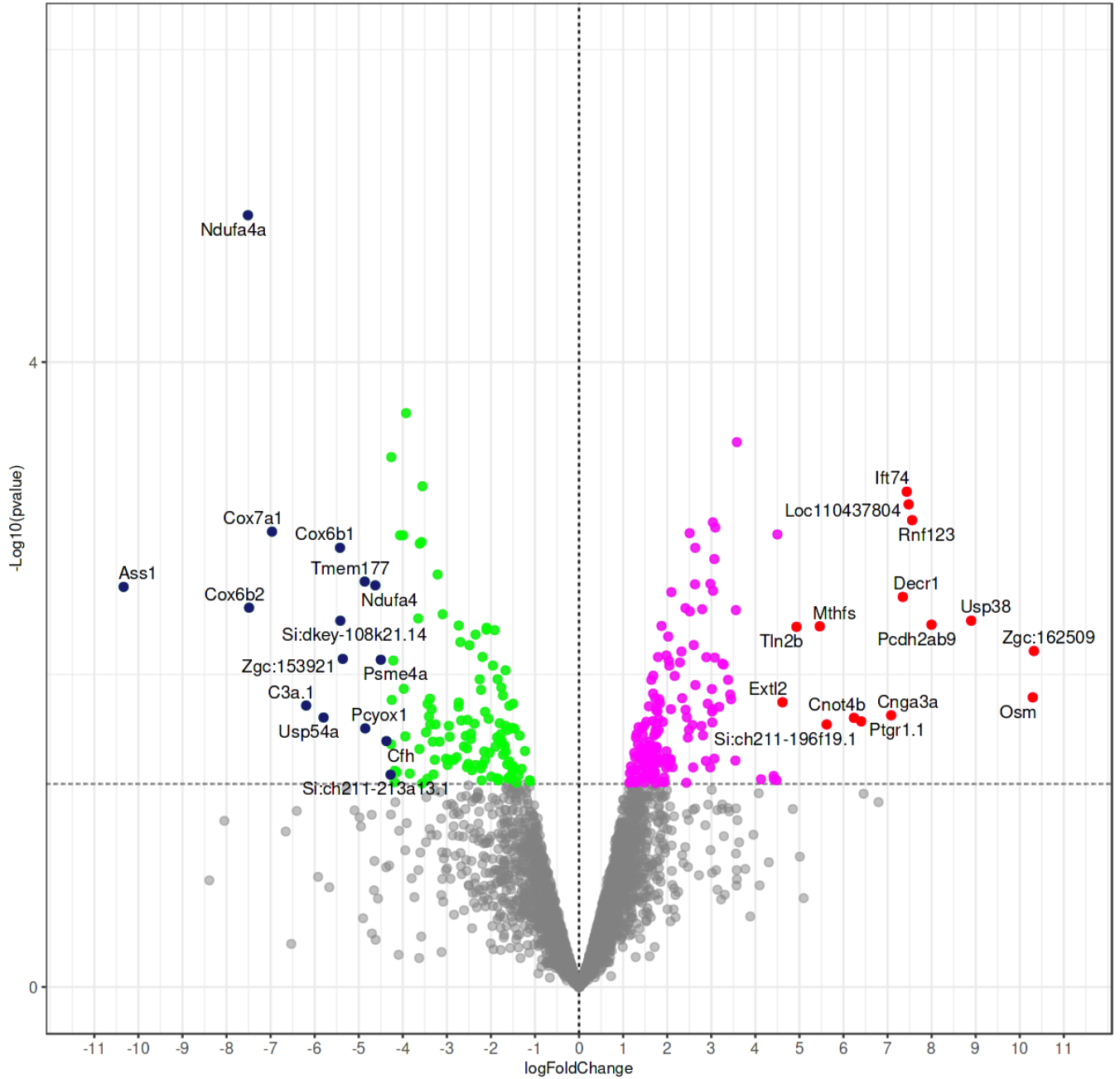
gene	gene_mouse	protein	KO1	KO2	KO3	WT1	WT2	WT3
<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
cox7a1	NA	E9QDH1	-3.503921	-8.936727	-7.756023	1.290831	0.04860092	-0.6341581

8 Save Rdata and write the session info

```
R version 4.3.2 (2023-10-31)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 22.04.3 LTS

Matrix products: default
BLAS:   /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.10.0
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.10.0

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=de_CH.UTF-8        LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=de_CH.UTF-8    LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=de_CH.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=de_CH.UTF-8 LC_IDENTIFICATION=C

time zone: Europe/Zurich
tzcode source: system (glibc)

attached base packages:
[1] grid      stats4    stats     graphics  grDevices utils     datasets
[8] methods   base

other attached packages:
 [1] ggVennDiagram_1.2.3  limma_3.56.2            openxlsx_4.2.5.2
 [4] paletteer_1.5.0      ComplexHeatmap_2.16.0 org.Hs.eg.db_3.17.0
 [7] org.Mm.eg.db_3.17.0  AnnotationDbi_1.62.1   IRanges_2.34.1
[10] S4Vectors_0.38.1     Biobase_2.60.0         BiocGenerics_0.46.0
[13] clusterProfiler_4.8.1 lubridate_1.9.2        forcats_1.0.0
[16] stringr_1.5.0        dplyr_1.1.2            purrr_1.0.1
[19] readr_2.1.4          tidyr_1.3.0            tibble_3.2.1
[22] ggplot2_3.4.2        tidyverse_2.0.0

loaded via a namespace (and not attached):
```

```
  [1] RColorBrewer_1.1-3       shape_1.4.6              jsonlite_1.8.7
  [4] magrittr_2.0.3           farver_2.1.1             GlobalOptions_0.1.2
  [7] zlibbioc_1.46.0          vctrs_0.6.3              memoise_2.0.1
 [10] RCurl_1.98-1.12          ggtree_3.8.0             base64enc_0.1-3
 [13] htmltools_0.5.5          gridGraphics_0.5-1       plyr_1.8.8
 [16] cachem_1.0.8             uuid_1.1-0               igraph_1.5.0
 [19] lifecycle_1.0.3          iterators_1.0.14         pkgconfig_2.0.3
 [22] Matrix_1.5-3             R6_2.5.1                 fastmap_1.1.1
 [25] gson_0.1.0               clue_0.3-64              GenomeInfoDbData_1.2.10
 [28] digest_0.6.32            aplot_0.1.10             enrichplot_1.20.0
 [31] colorspace_2.1-0         rematch2_2.1.2           patchwork_1.1.2
 [34] RSQLite_2.3.1            fansi_1.0.4              timechange_0.2.0
 [37] httr_1.4.6               polyclip_1.10-4          compiler_4.3.2
 [40] bit64_4.0.5              withr_2.5.0              doParallel_1.0.17
 [43] downloader_0.4           BiocParallel_1.34.2      viridis_0.6.3
 [46] DBI_1.1.3                ggforce_0.4.1            MASS_7.3-60
 [49] rjson_0.2.21             HDO.db_0.99.1            tools_4.3.2
 [52] ape_5.7-1                scatterpie_0.2.1         zip_2.3.0
 [55] glue_1.6.2               nlme_3.1-162             GOSemSim_2.26.0
 [58] shadowtext_0.1.2         pbdZMQ_0.3-9             cluster_2.1.6
 [61] reshape2_1.4.4           fgsea_1.26.0             generics_0.1.3
 [64] gtable_0.3.3             tzdb_0.4.0               data.table_1.14.8
 [67] hms_1.1.3                tidygraph_1.2.3          utf8_1.2.3
 [70] XVector_0.40.0           ggrepel_0.9.3            foreach_1.5.2
 [73] pillar_1.9.0             yulab.utils_0.0.6        IRdisplay_1.1
 [76] circlize_0.4.15          splines_4.3.2            tweenr_2.0.2
 [79] treeio_1.24.1            lattice_0.22-5           bit_4.0.5
 [82] tidyselect_1.2.0         GO.db_3.17.0             Biostrings_2.68.1
 [85] gridExtra_2.3            graphlayouts_1.0.0       matrixStats_1.0.0
 [88] stringi_1.7.12           lazyeval_0.2.2           ggfun_0.0.9
 [91] evaluate_0.21            codetools_0.2-19         ggraph_2.1.0
 [94] qvalue_2.32.0            RVenn_1.1.0              ggplotify_0.1.0
 [97] cli_3.6.1                IRkernel_1.3.2           repr_1.1.6
[100] munsell_0.5.0            Rcpp_1.0.11              GenomeInfoDb_1.36.1
[103] png_0.1-8                parallel_4.3.2           blob_1.2.4
[106] DOSE_3.26.1              bitops_1.0-7             viridisLite_0.4.2
[109] tidytree_0.4.2           scales_1.2.1             crayon_1.5.2
[112] GetoptLong_1.0.5         rlang_1.1.1              cowplot_1.1.1
[115] fastmatch_1.1-3          KEGGREST_1.40.0
```